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SEXUAL SELECTION THROUGH MATE CHOICE IN EVOLUTIONARY COMPUTATION

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Sexual Selection Through Mate Choice in Evolutionary Computation

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To my family.

Resumo

A Computação Evolucionaria agrega um conjunto de algoritmos com aplicação em múltiplos contextos e num crescente número de indústrias. No seu formato canónico, os Algoritmos Evolucionários são uma metáfora bem justificada de Selecção Natural. Em suma, é espectável que a combinação entre alto desempenho e um número proporcional de oportunidades de reprodução conduza a população através do espaço de procura e em direcção a zonas onde a procura de soluções potencialmente óptimas seja mais produtivo. Nesta perspectiva, compensar directamente indivíduos altamente competitivos pode trazer benefícios directos ao esforço de procura. No entanto, pode ser argumentado que numa perspectiva mais alargada e dependendo das características do problema alvo, a abordagem pode não ser a mais apropriada. Em problemas multidimensionais, multimodais, cujo espaço de procura seja altamente rugoso, é relevante explorar outras abordagens capazes de potenciar o processo de procura.

Esta tese apresenta Selecção Sexual através da Escolha de Parceiro como um método auto-adaptativo alternativo, para a avaliação de candidatos para reprodução. A abordagem afasta-se dos ganhos imediatos resultantes da avaliação por desempenho e introduz um grau de liberdade de escolha no processo de selecção de parceiros. Ao permitir a cada indivíduo o uso da sua própria função de avaliação, representada no seu genótipo, é alcançada uma maior autonomia evolucionária capaz de introduzir forças divergentes daquela imposta pela Selecção Natural. Como resultado, o processo evolucionário é mais aberto e afasta-se da selecção baseada em aproximação a um ou mais objectivos. O padrão de evolução resultante é fora do convencional e benéfico para o processo global de procura, muito devido às sinergias entre as forças de Selecção Natural e Selecção Sexual. É proposto que modelos de Escolha de Parceiro sigam as seguintes regras: i) cada indivíduo deve escolher o seu parceiro de reprodução baseado na sua própria percepção dos outros e nas suas próprias preferências; ii) as preferências de escolha deverão estar sujeitas a descendência com modificação, de forma semelhante a qualquer outra característica; iii) Escolha de Parceiro introduz a sua própria pressão de selecção e está também sujeita a pressão. Esta tese apresenta uma estrutura genérica para um algoritmo que modela este processo e ainda duas abordagens distintas para a representação de preferências usando Programação Genética, cada uma seguindo as suas próprias regras adicionais. A primeira abordagem sugere que as preferências sejam representadas como um parceiro ideal, com o qual candidatos possam ser comparados (PIMP). A segunda abordagem sugere representar uma função que agregue percepção, preferências e interacção entre sinais num contexto de avaliação (CMP-GP).

É estudada a hipótese de que Algoritmos Evolucionários que incluam modelos de Escolha de Parceiro, adoptando assim uma perspectiva mais aberta de procura através do relaxamento de objectivos, podem trazer melhorias a processos de optimização. Este estudo abrange as abordagens PIMP e CMP-GP, abordando ainda mecanismos de Escolha de Parceiro de forma genérica. De forma a estudar o assunto metodicamente, a hipótese é desdobrada em várias questões a investigar e que se focam tanto em indicadores de desempenho como em demonstrar e validar empiricamente os comportamentos introduzidos pela Escolha de Parceiro. Estas últimas direccionam-se a impactos relacionados com selecção, percepção e efeitos a nível de população. Esta tese faz vários contributos no sentido de integrar e compreender o papel da Escolha de Parceiro na Computação Evolucionária. A teoria é amplamente discutida, incluindo marcos históricos no seu estudo e uma síntese moderna, assim como princípios e impactos. A modelação de Escolha de Parceiro como um modelo genético e a sua gradual adaptação a um operador com aplicações em optimização é também discutida. O estado da arte da sua aplicação com múltiplos fins é apresentado e categorizado. Usando estas contribuições como base, esta tese apresenta então um modelo genérico de Escolha de Parceiro e duas abordagens distintas, que são aplicadas num conjunto de 52 problemas de Regressão Simbólica. Segue-se a análise dos resultados relativos a desempenho e comportamento, com o apoio de um conjunto de métricas que se focam nas diferentes questões propostas. O estudo é ainda alargado para incluir operadores e mutação e a sua interacção com Escolha de Parceiro. Por fim, são tiradas conclusões em relação às questões investigadas e a hipótese central é abordada, confirmando-se o esperado neste contexto específico.

Abstract

Evolutionary Algorithms are valuable optimization tools on a wide range of contexts and with applicability on an increasing number of industries. Their canonical layout is a well justified metaphor of Natural Selection. Overall, it is expected that matching high fitness with proportionate reproductive opportunities will guide the population through the search space, towards areas worth exploiting for possibly optimal solutions. Rewarding competitiveness can bring direct benefits to search efforts. However, on a broader perspective and depending on the characteristics of the target problem, the approach may not be the most appropriate. In multimodal, multidmensional, rough search landscapes, other strategies are worth exploring in hopes of greater benefit to the global search process.

This thesis introduces Sexual Selection through Mate Choice as a self-adaptive alternative for the evaluation of mating candidates. The approach looks away from immediate fitness gains and introduces a degree of freedom of choice when selecting mating partners. A much pursued higher evolutionary autonomy is achieved, by allowing individuals to encode and make use of their own evaluation functions, as part of the genotype. This autonomous choice can introduce selective forces that diverge from Natural Selection, potentially producing unorthodox search patterns. Overall, this will impact and benefit the global search effort, despite moving away from objective oriented selection and introducing a degree of open-ended evolution. Still, synergies between Sexual and Natural Selection are relevant. It is proposed that Mate Choice models follow three assumptions: i) individuals must choose who they mate with based on their perception of others and their own mating preferences; ii) mating preferences are subject to descent with modification through inheritance like any other trait; iii) Mate Choice introduces its own selection pressure while being itself subject to pressure. This thesis introduces a framework following these assumptions. Furthermore, two approaches based on Genetic Programming representations of mating preferences, each following its own additional and specific assumptions, are studied. The first approach suggests representing preferences as ideal mating partners to whom candidates can be measured against (PIMP). The second approach suggests the representation of a contextualized mate evaluation function, coupling perception, preferences, and interactions between signals (CMP-GP).

It's hypothesized that Evolutionary Algorithms modeling proper Mate Choice mechanisms can improve on optimization by adopting a widening perspective on search and the relaxation of objectives. This hypothesis is addressed both on PIMP and CMP-GP and regarding Mate Choice in general. In order to methodically explore the subject, a number of research questions are introduced, focusing on performance indicators but also on empirically demonstrating and validating the behavioral changes imposed by Mate Choice. Particularly, these research questions focus on aspects of selection and perception, and on the effects that Mate Choice has on populations. This thesis makes several contributions towards integrating and understanding the role of Mate Choice in Evolutionary Computation. It covers theory on the subject, focusing on historical milestones and a modern synthesis, and introduces conditions, principles, and impacts that are associated with Mate Choice. The modeling of Mate Choice as genetic models and its transition to optimization operators is also covered, as well as impacts on search efforts. Furthermore, the state-of-the-art is compiled in comprehensive categories. Supported by the theoretical discussion, this thesis introduces a general framework and two distinct designs, applied to a set of 52 Symbolic Regression instances. An analysis of performance and behavior follows, supported by a number of metrics that are introduced and focus on the different research questions. This analysis is then extended to include impacts of mutation in combination with Mate Choice. Finally, conclusions are drawn on research questions and the proposed hypothesis is confirmed under the discussed setup and assumptions.

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Chapter 1

Introduction

Nature-inspired algorithms have had increasing attention from researchers over the past few decades. On the one hand for the purpose of better understanding natural behaviors through simulation, and on the other hand as optimization tools. Through continuous efforts, such algorithms have become valuable for targeting a wide range of problems, and most recently found applicability on multiple industries. Traditional optimization algorithms have nowadays many flavors, inspired by different behaviors observed in nature, and focusing on different strategies to build solutions that fit a target objective. Regarding Evolutionary Algorithms, their canonical layout is well justified as a metaphor of Natural Selection [68, 101, 131, 203], which has influenced the overall structure and particular design of operators. In the end, it's expected that linking high fitness with matching reproductive opportunities will contribute to population synergies capable of progressing through the search space, leading to areas that can be exploited for valuable, possibly optimal solutions.

Rewarding competitiveness and performance through higher reproductive rates is an intuitive concept, which holds potential search benefits while remaining relatively simple. Therefore, it may come as a surprise that such a strategy, even when coupled with mechanisms to introduce diversity, sometimes underperforms. Surely, in unimodal or smooth search landscapes, this metaphor of Natural Selection can perform sufficiently well, even when searching through multiple fitness peaks by leaning on stochastic initialization, large enough populations, mutation, and adequate selection pressure. However, as both the research field and industry focus on harder and harder target problems, that effort may prove to be insufficient. In likely multimodal, multidimensional, and rough search landscapes, the direct rewarding of proximity to the objective as evaluated by fitness may be non-advantageous or downright hindering to the global search efforts. In those scenarios, attributing reproductive opportunities in proportion to fitness may actually represent a limitation.

As an alternative, search doesn't have to be explicitly guided by one or multiple well defined objectives. In the right scenario, widening the search efforts by introducing open-ended approaches, self-adaptation, or diverging selective forces may allow for important synergies that on the grand scale contribute positively towards an objective. The idea may be counter-intuitive or paradoxical, but the search path towards best results may not follow a straight line but require a wider perspective on the value of the fitness function and how it translates to reproductive success. This thesis presents an exploratory study on the possibility of using Mate Choice as a self-adaptive alternative for the evaluation of individuals, one that is able to look away from immediate fitness gains and allow a relative freedom of choice in mating, introducing behaviors that on the long run may potentially result in a more profiting search effort.

1.1 Background

Since the early days of Evolutionary Computation, models have been tried on a growing range of problems and contexts. On their canonical form, evolutionary models can be used for optimization with very few requirements: i) a genotypic representation for candidate solutions and corresponding mapping to phenotype; ii) and a fitness function to evaluate and compare between such candidates. However, a lot of effort has been put into specializing behaviors to better fit certain contexts. Listing them all and their potential gains would be an unreachable goal, but a few things are worth bringing up regarding the range of algorithmic solutions that have been brought up over the years: i) there's no silver bullet that will ultimately adapt and improve on every context; ii) domain knowledge is relevant when designing problem specific operators or parameters; iii) custom algorithms can have very slight to very deep modifications; iv) these mods can take place on different levels of the algorithm, such as using island models on a population level or imposing specialized mutation operators on the gene level.

Whereas the range of approaches available in the literature is outstanding, the subset that could be said to introduce a degree of open-ended evolution, or to focus on diverging selective forces is comparatively small. Both have been customarily explored in Artificial Life or Evolving Systems to study natural populations, but historically, when optimization is considered, Natural Selection has an unchallenged central role. Applications try to make the best of this role, sometimes relying on mechanisms introduced to balance, restrict, or sway an excessive impact, for instance in hopes for higher diversity. However, whatever the outcome, those scenarios are by design restrained from achieving the evolutionary freedom of open-ended evolution or other aforementioned strategies. In order to do so, the roles of selection for reproduction need to be rethought, for instance by having pairs of individuals selected independently and valuing different characteristics, or by fomenting partner interactions during selection.

Sexual Selection through Mate Choice can provide a valuable framework for such interactions by introducing the ability for each individual to choose its mating partner according to its own preferences. The idea has been thoroughly explored in Evolutionary Theory, being first introduced by Darwin [59] and contributed to by many renowned researchers over the years [12, 54, 97, 307, 322]. A modern view justifies the emergence of many prominent traits through the impact of Mate Choice rather than Natural Selection [12, 54], and the number of studies is growing. In Evolutionary Algorithms, Mate Choice can provide for a much pursued evolutionary autonomy, as long as the models follow appropriate assumptions, and therefore contribute to a degree of open-ended evolution. It has been shown in Natural Sciences that Mate Choice introduces selective forces divergent from Natural Selection, which in optimization, can contribute to unorthodox search patterns, potentially better suited for global efforts on multiple contexts.

1.2 Motivation

The presence of Sexual Selection in optimization research spans over the last couple of decades. Although the number of studies is somewhat small, they introduce a wide range of ideas. Part of the proposed models focus on introducing particular behaviors that are characteristic in nature, such as incest prevention or other forms of restricted mating. Others try to capture the exploitative and exploratory roles of genders, or aim at improving performance through specialized pairing and reproduction rules. Some of these mechanisms are designed by analyzing specific contexts and are developed on purely engineering grounds, for their utility when facing particular challenges. Depending on their design, the level of autonomous evolution introduced in the algorithm may vary, but often is relatively small. There are of course exceptions that allowing for higher freedom of choice and relative autonomy.

Overall, this reality is contrasting with how Sexual Selection is expressed in nature, where its self-adaptive character, fueled by autonomous choice and a gene-centered view of mating preferences, is key. There seems to be a void in Evolutionary Algorithms in regards to approaches that introduce Mate Choice as an open-ended methodology rather than a utility focused, conservative, goal-oriented behavior. This may be partially explained by challenges in designing complex systems, barriers in studying dynamic behaviors, or an overall resistance to invest in systems that may be difficult to justify in a purely utilitarian, well established way. Despite those challenges, the transference of knowledge from Natural Sciences into artificial models has always found purpose, as shown by the growing range of available algorithms mimicking the behaviors of species (ants, bees, birds, etc.). Ways to model Mate Choice in Evolutionary Algorithms closely following its simplistic, basic assumptions may prove to be a useful addition.

As suggested, this thesis focuses in studying only Mate Choice approaches that can introduce a relatively high degree of choice freedom and thus add a possibly diverging, self-regulated selection force that emerges in an open-ended fashion. For the purpose, the models shall follow a small set of assumptions that can be summarized as such: i) individuals must choose who they mate with based on their perception of others and on their own mating preferences; ii) mating preferences are subject to descent with modification through inheritance like any other trait; iii) mate choice introduces its own selection pressure while being itself subject to pressure. By following these assumptions, a framework shall be proposed along with two approaches, each with its own characteristics in regards to the evaluation of mating candidates and the representation of mating preferences. For the purpose, the use of trees-based genotypes and Genetic Programming operators will be explored, as a vehicle to model perception of distinctive traits, their independent evaluation in light of individual preferences, and their interactions into evaluation systems of evolving dimensionality and complexity.

1.3 Hypothesis and Research Questions

This thesis follows an inevitable exploratory frame, aiming at transferring knowledge on Mate Choice coming from Natural Sciences into a proper framework that can introduce new paradigms of search in Evolutionary Algorithms, while proposing mechanisms that can best incorporate autonomous and open-ended evolution in collaboration with goal oriented efforts. In a performance focused scope, it's hypothesized that Evolutionary Algorithms coupled with proper Mate Choice mechanisms can improve on optimization by adopting a widening perspective on search and the relaxation of objectives. While pursuing confirmation for this hypothesis, others have to be considered and addressed. Particularly, it's hypothesized that multidimensional mating preferences can be properly modeled using a Genetic Programming representation, with two particular approaches in mind: representation of an ideal mating partner to measure candidates against (PIMP); representation of an explicit perception system, preferences, and interactions, organized as a contextualized mate evaluation function (CMP-GP).

While the stated hypothesis can be partly addressed using performance indicators and theoretical knowledge, empirically demonstrating the behavioral changes in Evolutionary Algorithms as an impact of Mate Choice can be challenging. In the effort to do so, a number of research questions were organized. Regarding performance, the following ones are relevant: i) how do the approaches compare over a large test set with varying characteristics; ii) are performance differences between approaches statistically significant; iii) how do design choices, particularly in regards to mutation, compare in terms of performance gains. Further focusing on behavioral analysis, the following questions are addressed: i) is Mate Choice truly taking place or are the results the product of some other unexpected behavior; ii) do mating preferences have a Fisherian or Wallacean character; iii) does gender emerge with Mate Choice; iv) is perception of trait variation being promoted with Mate Choice; v) is evaluation contrast being promoted with Mate Choice; vi) what are the dynamics of preference dimensions and complexity; is diversity being promoted with Mate Choice; vii) does Mate Choice promote the emergence of complex innovations; viii) does Mate Choice contribute to escaping local optima.

1.4 Contributions

This thesis makes several contributions towards the integration and understanding of Mate Choice in Evolutionary Computation. Firstly, it introduces the subject from a theoretical point of view, focusing on relevant background information: i) describes historical breakthroughs in Natural Sciences towards a modern overview of Mate Choice; ii) further highlights basic conditions and principles for adaptive Mate Choice; iii) discusses the modeling of Mate Choice in genetic models and the transition from those models into the application of self-adaptive mate evaluation functions in Evolutionary Algorithms, through a step-by-step discussion of increasing complexity; iv) compiles and expands on discussions regarding the impact of Mate Choice in search efforts and potential resulting advantages; v) summarizes relevant past contributions made in the context of optimization algorithms or related subjects, organizing diverging designs into comprehensive categories.

Secondly, supported by the theoretical discussion and the review of existing designs, this thesis also makes the following practical contributions: i) introduces a general framework and clarifies which are the necessary assumptions and requirements for the emergence of Mate Choice in Evolutionary Algorithms; ii) expands on that framework by introducing two different representations and approaches, distinguishing between them and offering proof of concept for both; iii) applies both approaches to a set of 52 Symbolic Regression instances, totaling 10 different experimental setups; iv) introduces metrics for the analysis of each research question and consequently to the proposed hypothesis; v) shows an extensive, comparative, and well supported discussion on the impacts of Mate Choice following each approach, both regarding performance and behaviors; vi) discusses the performance impacts of mutation on top of Mate Choice; vii) draws conclusions on the hypothesis and research questions.

1.5 Outline

The remaining of this document is organized following the order depicted above. Chapter 2 introduces Sexual Selection and the topic of Mate Choice, covering breakthroughs in Natural Sciences and culminating on a modern overview on the topic. Chapter 3 focuses on how to model Mate Choice, beginning with simple genetic models and moving toward complex mate evaluation functions in Evolutionary Algorithms, also addressing impacts and behaviors. Chapter 4 covers related work and previous applications of Mate Choice in optimization algorithms following a variety of design choices and assumptions in the literature. Chapter 5 clarifies the assumptions and requirements for Mate Choice to be modeled in Evolutionary Algorithms, introduces a framework for doing so, and expands on that framework by suggesting two approaches for the representation of mating preferences and the evaluation of mating candidates. Chapter 6 introduces the experimental setup used for studying and comparing each approach, in regards to performance as well as changes in behavior, detailed by research questions and associated metrics. Finally, Chapter 7 draws conclusions on the research questions and the tested hypothesis, suggesting further steps to study Mate Choice in the context of optimization.

Chapter 2

Sexual Selection

In 1831 the HMS Beagle departed for what would be a five year voyage. On board was Charles Darwin, a naturalist that throughout the journey, and his life, would study and contribute to various research fields, ultimately establishing himself as a prominent geologist, naturalist and overall science figure. On the course of his studies, Darwin grew a collection of fossils and other artifacts regarding which he published extensive analysis. He was also in close contact with a high diversity of fauna and took note of its distribution and characteristics. Incited by the observation of both, Darwin began a discussion that would prove to be a breakthrough in Natural Sciences. Either through drafts in his travel journals or by correspondence with fellow researchers, he lead a challenge on established ideas on the origin of species and helped bring research on that topic into a new direction.

2.1 Evolutionary Background

After returning home, Darwin expanded on those ideas and thoroughly studied what would eventually be regarded as the forces responsible for the evolution of species. In 1859, as a first synthesis of his findings, he published a new theory on a volume entitled *On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life* [58]. The theory of Natural Selection, as it would be known for the coming ages, was co-proposed and supported by Alfred Wallace [60, 306], another prominent researcher, and despite initial criticism by the community, gathered a number of followers and contributors.

2.1.1 Evolution by Natural Selection

As an emerging idea in Natural Sciences, Natural Selection took on itself the main role in Evolutionary Theory. It was succinctly described by Darwin as the result of competition within or between species affecting their individuals relative rate of survival. In Layman's terms, the theory can be described through two key concepts: i) descent with modification; ii) common descent. Descent with modification is the observable fact that siblings are slightly different in appearance and behavior when compared with their parents or each other. Common descent is the hypothesis that all living things have a common ancestor and although they differ extensively between them, they are the result of many iterations of descent with modification. Even in present days, we are limited in observations of common descent, but at Darwin's time, evidence was mostly restricted to fossils, anatomy, and species distribution.

Common descent may have been a topic of discussion among naturalists for some time by the mid 1800s, but the arguments against were simply too big for it be taken seriously. Researchers found that descent with modification produced random variation while common descent was the prime of order and complexity. Arguably, random variation alone could by no means produce order and complexity as observed in nature. Darwin's contribution was to show that it was indeed possible, through the introduction of a selective force which he named as Natural Selection. According to his ideas, this would be the process by which random changes resulting from descent with modification could be selected for by nature in a orderly, non-random way, therefore allowing for order and complexity to emerge over many generations.

Lacking modern technology for lab experiments, computer simulation, or mathematical models, Darwin used selective breeding as an auxiliary tool to explain his thoughts. Selective breeding has been an ongoing day-to-day part of breeder's and farmer's lives. It has not only allowed the domestication of many species, but has also introduced speciation to best fit the needs or aesthetic preferences of humans. While variation is always the result of descent with modification, domestication and artificial speciation have been achieved by the slow but simple process of granting only the best regarded specimens a chance to contribute to future generations. The end game of Darwin's argument was that nature itself was capable of a similar selection, not by conscious choice but because adversity and difficulty to survive introduced environmental pressure and competition. The result would be akin to indirectly deciding to what extent new individuals created by descent with modification are allowed to survive and reproduce. Over many generations, positive traits are maintained and passed on to future generations while negative traits are selected against and are eventually discarded, ultimately adapting living things to their habitats, promoting successful innovations and speciation as a response to a changing and diverse environment.

Since Darwin, the scientific community contributed extensively to the study of evolution by Natural Selection and provided increasing evidence to support it, having allowed it to overcome competitive ideas into overall acceptance by researchers worldwide [21]. A genetic basis was established by Mendel [194, 300] and eventually both works were combined in a framework that includes also contributions from other contemporary researchers [66, 71, 99, 102, 252, 256, 319]. This would become known as the Modern Synthesis [139] and would have continuous impact over many research fields ever since.

2.1.2 The Enigma of Ornamentation and Mating Behaviour

Despite the community's acclaim for his work, Darwin continued to further explore his ideas and battled with what he saw as gaps in the theory of Natural Selection. He expected to be able to explain the emergence of characteristics across species as adaptations to their respective habitat, so that they were in some way valuable in each species' struggle for survival. This proved sometimes to be a difficult task. He questioned, for instance, how was it that conspicuous traits such as animal ornamentation or mating behavior could be accounted for by survivability. Some of such traits, as he observed on multiple species (most often on males), were costly to maintain, consumed great energy, and were complex while adding little to no gain to an individual's ability to survive. In fact, in some cases such traits could be deleterious to survival and should be disfavored in competition. They were therefore an enigma for Darwin, who had trouble in seeing their purpose and how they could be maintained under the pressure of Natural Selection [12, 54, 58].

Evidence has since then been extensively documented, including a wide number of examples on many animal classes. Conspicuous traits involving coloration, for instance, can be found on multiple species of birds, insects, mammals, and even fish [12, 54, 59, 197]. In some cases such coloration has been proved to be deleterious to survival due to increasing exposure to predators [12]. The development of horns or antlers in males for the purpose of fighting sexually competing peers have also been studied as traits of little survival value [159]. Calling, which can be found across many species of birds, insects, mammals, and amphibious such as frogs [119] are also prevalent in nature. Scent related traits have also been found relevant in this line of research [12].

Darwin's view: Choice by Good Taste

Darwin stood by the ideal that evolution and the emergence of traits were the result of competition and the relative advantage that they brought in relation to others. Ornamentation, courtship behavior, means for male competition etc. were to be though of as any other trait and to have no specially tailored explanation. Given that Natural Selection explained the evolution of species and the origin of traits as the result of competition for survival, Darwin envisioned the existence of another trait-shaping selection force, capable of shaping species in complex and diverse ways. The key would still be competition, but rather than competing for survival, traits emerging through descent with modification would be selected for their advantages in gaining access to mating partners. Darwin's innovative idea was that such features were selected because they brought males (usually) advantages in access to female partners, in spite of potentially risking survival abilities [59]. The costs to survival would be compensated by advantages in reproductive success, making features that bring advantage in competing for mating more likely to pass on to offspring.

Darwin organized his ideas in the theory of Sexual Selection, described as the result of competition within species affecting its individuals relative rates of reproduction [59]. There would be of course the question of distinguishing which characteristics develop under which selection pressure. Darwin answered that question by suggesting that traits under Sexual Selection would meet certain criteria such as developing only on sexually active individuals, mostly during mating seasons and were specific to one gender only. Furthermore, their use would have to be either to fight off other competing mating candidates or to attract the attention of potential mates through display [12, 59]. Evidences of features that fit such criteria were mostly found on males and were found to be abounding in nature.

The topic was fascinating to Darwin who first touched the subject in his 1859 publication [58] and ended up dedicating a full volume to the topic: *The Descent of man, and selection in relation to sex* [59]. Two processes were described by Darwin as contributing to differential mating success: i) intra-sexual selection through competition of one sex (males usually) for access to individuals of the opposite sex (females usually); ii) inter-sexual selection due to sexual preferences leading to variable reproductive success (usually female mating preferences acting on male features). The first one has been popularized as Male Competition while the latter became most known as Mate Choice. Darwin's research interests were mostly on Mate Choice, leaving behind other topics such as how Male Competition contributes to the emergence of weaponry and sexual dimorphism [59].

Mate Choice [59] aimed to explain the emergence of aesthetic features such as ornamentation and courtship behavior in a way that was in line with the pillars of Darwin's evolution theory, or in other words, how they were associated with competitive advantages. According to Darwin, such competitive advantages were gained by males meeting the taste of selective females. Those that best fit the mating criteria of females in the population would gain reproductive advantage by being selected more often for reproduction, in disregard of being or not among the fittest males in that population. The idea would conflict with the principle that Natural Selection ruled over reproductive success, by suggesting that complex and rich ornamentation and behavior was the result of males competing to meet female taste for splendor and nothing else.

Early days of Sexual Selection and specially Mate Choice were bound with difficulties [54]. Choice was regarded as dependent on consciousness and was seen as an inherently human capability, while other species were driven by instinct. This feeling was specially strong when taxa with few apparent senses and intelligence were considered. Therefore, the idea of female Mate Choice was considered impossible even if Darwin first promoted it as an instinct based process. Also, it may have been difficult to advocate in a 19th century Victorian society that roles in evolution could be unbalanced between genders the way that Darwin described. A male-centered view of the world was still in vogue while Mate Choice put females at the guiding role [198]. The subject of choice was for these reasons a very touchy subject, which led several authors to publish their views against the idea. Wallace while agreeing on the subject of Natural Selection, had opposite views on Sexual Selection [307]. Westermarck [15] and T. H. Morgan [205] later commented on Mate Choice with great criticism as did Huxley [139], who would make great contributions to the modern thesis of Evolutionary Theory.

Interestingly, choice was accepted as a widespread ability in the animal kingdom. Food choice for instance was considered as unconscious, even as an inheritable preference, molded by evolution and varying benefits. Going from there to female Mate Choice and the resulting inner-species competition was however a big leap, for sure beyond the limits of acceptable science at the time [196]. Even if Mate Choice was to be considered as an adapting force, there were still questions regarding its usefulness. Food choice had arguably emerged because it was purposeful for survival, something that was more difficult to argue regarding Mate Choice. Because naturalists had at the time a species thinking of evolution (with adaptations happening for the good of the species), until Mate Choice could itself be explained as a purposeful result of selective forces, it would always struggle to be taken seriously by most researchers [12, 54, 307].

In summary, Darwin claimed that conspicuous traits emerged by adapting to the selective forces imposed by female Mate Choice. However, while that could explain the evolution of ornamentation or courtship behavior, it did little to explain the usefulness of choice. To the eyes of many, and specially taking into account the possibly deleterious aspect of Mate Choice, Sexual Selection as seen by Darwin not only was not adaptively explained, it had the potential of being maladaptive [12, 54]. Explaining the origin of Mate Choice (specially the gains of choice for splendor) and consequently the conditions necessary for Sexual Selection and Natural Selection to co-exist and compete became possibly the biggest challenge for Darwin's views on Sexual Selection.

Wallace's view: Choice by Good Sense

Wallace considered Darwin's views regarding Sexual Selection to be non-realistic. After all, Natural Selection was a means of finding an harmonious order and good sense in an otherwise chaotic continuous process of descent with variation. In his own way, Wallace had the same strong will to keep to the ideals of competitiveness and relative advantage that was characteristic of Darwin. Perhaps even more, and for that reason he was a strong advocate of Natural Selection. He argued in favor of its central role in evolution and was not keen on having a second selective force adding complexity. In a rather simple way, Wallace regarded Sexual Selection as a contributing process of Natural Selection, not much more than the process by which females selected the best males to breed. In many cases, features that for Darwin were under the pressure of Sexual Selection, were described by Wallace as the product of Natural Selection. For instance, calling may have a significant task in social roles such as warning of predators in proximity. Antlers, horns and body size can be used for protection from predators, or ultimately to fight over resources rather than mates. Species identification and sex recognition can also benefit from such attributes [307].

Wallace was quite successful on such arguments, mostly because he found utility in features and therefore good reason for its emergence as the result of Natural Selection. Nonetheless, he could not and did not attempt to overlook the observable fact that females in many species choose mating partners in favor of certain characteristics. His idea on the subject was however very different from Darwin's, as he argued that choice must be sensible and by no doubt coincide with Natural Selection. Otherwise, it would be selected against. Simply put, he claimed that Sexual Selection, as an inner-species force, should reinforce Natural Selection, by sensibly choosing mating partners in favor of the good of the species. He regarded it as having a secondary role at best [12, 54, 307], a view that was in-line with the species-level thinking of evolution (with adaptations happening for the good of the species) that was in vogue at the time.

The subjects that best fit Wallace's ideas were not the same that best fit Darwin's theories on good taste. Darwin had a particular drive to try to explain the exuberance in certain species. When explaining how was it that females seemed to favor complex ornamentation or extravagant behavior, Wallace argued that while females seemed to be selecting aesthetically, they were actually doing so sensibly. By his regards, the most healthy and vigorous males would be at the same time the most adorned, and so beauty and quality simply happened to coincide [308]. If the most ornamented males were not the fittest, they simply couldn't survive, which would contribute to a correlation. It should be noted that Wallace did not accept ornamentation to act as honest indicators of male vigor, health, stamina, sexual maturity, or others, but rather as a side effect. Selection for those ornaments could happen, not for beauty's sake, but only as a side effect of a sensible choice [54, 307].

For Wallace, Mate Choice had only to do with good sense, with females always going for good and useful qualities in males (by a Natural Selection sense). In his understanding, ornaments had nothing to do with choice, so that for instance in a species where males exhibit brightly colored feathers, a colorblind female would still have a preference for the brightest male simply because she is going for quality and not for beauty [54]. His theory that mating preferences have emerged because they represent good sense successfully avoided the problem of explaining the emergence of female Mate Choice that haunted Darwin's good taste theory. However, it raised an equally important problem. If ornamentation and complex behaviors play no role in choice, how is it that such features have emerged despite the costs of maintaining them. Wallace made an attempt to explain such phenomena by suggesting that characteristics that may not find usefulness are the result of adaptation to the point where species can put surplus energy to non-selective goals without risking survivability.

Moreover, as aforementioned, Wallace [307] explained ornamentation as identification badges, allowing individuals to identify peers and possible mating partners. He also suggested that extravagant displays were the result of nature's predilection for exuberance in colors, songs, or others, an idea that was extended into courtship behavior. Arguably, such richness was default and Natural Selection was responsible for inhibiting them outside mating seasons, and more so on females because of their proximity to offspring [198]. Finally, males would be more likely to shows such displays due to surplus energy, male vigor, higher health and therefore less need for camouflage, or simply as non-selective side effects [54] of descent with modification. Such ideas in a way were add-ons to the simplicity of Natural Selection.

In summary, Wallace claimed that Mate Choice was useful as a process of Natural Selection, having emerged for the purpose of females selecting the fittest males for reproduction. While that put Mate Choice as an adaptively explained idea, it failed to demonstrate the emergence of costly ornamentation and complex courtship behavior. In the light of Natural Selection, researchers failed to see how did they contribute to survival. Wallace purposed multiple ideas to explain such features. Still, explaining the origin of ornamentation and costly behavior would become the main challenge for Wallace's good sense theory.

2.1.3 The Interplay of Sexual Selection with Natural Selection

For Darwin, evolution can be seen as the interplay between two major forces, Natural Selection and Sexual Selection [59]. The first impacts species by favoring adaptations to the environment that improve survivability. The second affects each gender in relation to the other in order to maximize their reproductive advantages. On an individual level, failing according to Natural Selection would mean low survivability, while the outcome of failing in Sexual Selection would mean few or no offspring. On a genetic level, either results on less chances for individual genes to replicate themselves into future generations, thus both Natural Selection and Sexual Selection have an influence on a population level through its genetic pool, leading to changes over time.

Wallace's ideas put Sexual Selection on a much weaker role and the majority of evolutionary power was for Natural Selection. At most, the first was a process of the second, adapted for the purpose of selecting the fittest mating partners. Maximization of survival and reproduction abilities would evolve hand in hand, with adaptation to the environment as a common goal. On an individual level, low survivability and few or no offspring were both the result of low quality by Natural Selection standards. Genes associated with higher quality individuals should consequently have a higher chance of replicating onto future generations both by their relative advantage in survival, and by the reinforcement provided by Sexual Selection, ending up shaping the population through its genetic pool. This contribution of Sexual Selection for the benefit of Natural Selection was attractive to most researchers and their views on species-level evolution. Although they saw the gaps in the good sense theory, it was still regarded as a better fit than Darwin's good taste ideas, specially since they had their own unexplained flaws.

In Darwin's good taste theory, having Sexual Selection reinforcing Natural selection by adapting features in the same direction is certainly a possible outcome of the interplay between them, being up to the researchers to investigate if they are the result of Natural Selection, both forces, or mostly Sexual Selection. Such scenarios, some of which have been addressed before, were seen as feasible by researchers [12, 54] as the result of Darwin's propositions. For instance, the development of body size and weaponry as a result of male competition, or certain colors in birds [58], were seen as possible due to their utilitarian aspect. However, researchers were skeptical on how the idea generalized to non-utilitarian characteristics, which Darwin had primarily aimed to explain. Following his ideas, Sexual Selection opposes Natural Selection many times which raised questions on how could such scenarios have emerged in nature. This conflict was what first attracted Darwin to explore the topic of Mate Choice and Sexual Selection, but it was also what brought up skepticism from other prominent figures.

Darwin's ideas may have been ahead of his time, as mathematical and scientific tools were not yet available that could help support them. Computers and simulations that could be used as analogy were also yet to be. We know now that choice is not necessarily dependent on consciousness nor is it a characteristic exclusive to humans but it would take time to reach such knowledge. With the beginning of the 20th century, Mendel's work [300] on genetics was blooming, getting the attention of the research community. This was extremely important to corroborate Darwin and Wallace's ideas on Natural Selection, in particular heredity and adaptability, while also bringing new ideas on mutability. Nonetheless, it deviated attention from other topics. Sexual Selection was mostly left unstudied as it was, with Wallace's ideas having perhaps the upper hand in the works that would come next [12, 54]. The discussion was barely kept alive.

2.1.4 Filling the Gaps

By the late 1880s discussion on Sexual Selection was left at a deadlock. On the one hand, Darwin could explain the emergence of conspicuous traits and behavior as the result of taste, but could not clarify the adaptive value of female Mate Choice. On the other hand, Wallace promoted his ideas on adaptive female choice but struggled to justify the emergence of ornamentation or costly behavior. In the mean time, despite having put the discussion away from the research community's mind, the genetic world was having an indirect impact on the understanding of Sexual Selection. Researchers were starting to slowly shift their view of evolution from a species level into a view that better accommodated intra-species competition, an individual and genetic level. Such changes would prove to be fruitful for Sexual Selection research and to the work of filling the gaps left by Darwin and Wallace on their respective theories.

Contributions to the Good Sense Theory

The new perspectives on competition allowed for new understandings on the inner dynamics of species. Male-male competition for instance gained a new sense and different authors suggested that such an arms race could to some point explain the emergence of ornamentation. If, for the purpose of competition with their peers, males focused on evolving certain features rather than diversifying their strategies, the process could result in over-specialization effects, or in other words, the exaggeration of certain features [61, 64]. Arguably, this could explain large body size, certain coloration and callings, etc. simply as attempts by each male to be better than others. In a way, this idea could be seen as an extension of pre-existing ideas of male competition [59] for the evolution of weaponry, but accounting for conspicuous traits as well.

Mate Choice based ideas also started floating around the community. Wallace did not assume any relation between conspicuous traits and quality in an individual (they were side effects), however, if one would make such an assumption, then for instance body size could be seen as a marker for robustness or energy, bright colors could be seen as markers for male vigor, and so on. The underlying idea was that fitter individuals would be more likely to successfully magnify such features, and so selection for those features could be useful as they would be honest indicators of gene quality. For clarity, selection for those features would not happen because they matter but simply because they were markers for quality. Still, that would put markers evolving under the pressure of females attempting to select the best males and males trying to best be accepted by females [54]. This idea differs from the aforementioned example where colorblind females would still be able to select the best males, putting them now at a disadvantage as they would struggle to differentiate between better and worst markers.

Marker utility for ornamentation and other features raised multiple questions. The idea was founded on the certainty that markers would act as honest indicators of quality, but if males engaged in the process of over exaggerating their ornaments to seem more worthy, then they would end up acting as dishonest advertisement. In order for females to be able to select for quality, they would need to be able to distinguish between honest and dishonest mating candidates. This would lead to an arms race where both males and females try harder to outwit each other. In a way, this scenario goes against Wallace's view of good for the species evolution, but on an individual level, females are still trying their best to select mating candidates of higher quality, thus safeguarding the sensible value of Mate Choice.

These ideas alone were sufficient to revitalize Wallace's ideas by providing the means to explain exuberance and therefore fill the gap in the good sense theory. Others would also contribute. Zahavi may have made the boldest contribution [322] by suggesting that extreme ornamentation could handicap the survivability of individuals, and advocating that the impact would make them honest advertisement of genetic quality. Wallace and Zahavi had opposite views regarding the importance of ornamentation and display costs. The first was a strong advocate that females would select mating partners independently of the cost of their conspicuous traits while the second suggested that females would choose rich ornamentation precisely because of their high cost.

Zahavi's handicap model introduced the idea that beings exhibiting risky displays such as heavy tails, bright colors, or loud callings would have to compensate such burdens through high survival features. Females would be able to explore the increase in competition in males, brought by the cost of maintaining such traits, and promote the behavior by understanding that males that succeed in survival while handicapped likely hold high genetic quality and are therefore sensible choices for mating. Such advances on Wallace's school of though pushed researchers into thoroughly questioning details more and more. One of the subjects that was perhaps most challenging was the observable fact that despite having females sensibly choosing for the same goal, heritable genetic differences were maintained in male populations. Arguably, such differences should diminish more and more under the pressure of favoring high quality males.

The question was of interest as a general topic in Evolutionary Theory but was addressed on this specific subject by Hamilton and Zuk [123]. They suggested an arms race between organisms and their parasites to be at the bottom of it. As they emphasize, parasites and their hosts are continuously trying to overcome each other, either by adapting resistance to parasites or trying to beat such resistances. Knowing that males with parasites would be less healthy and consequently be less capable of appearing vigorous or maintaining exuberant displays, female choice would be most sensible to push males into advertising their health. Also, the dynamic nature of the host-parasite environment would mean that the best males or the best genes at some point, may not be the best a few generations later (due to adapting parasites). Therefore, there would not only be an advantage in adapting Mate Choice into favoring apparently healthy partners but also, and at the same time, there would be a relative advantage for males in producing extreme traits in order to distance themselves from unhealthy ones. Such forces could possibly explain the emergence of ornamentation and handicaps, as their costs would be most burdening for unhealthy males [123].

Zahavi's handicap model [322] and Hamilton and Zuk's model of host-parasites [123] have been shown to be mathematically and biologically stable, and so the modern ideas that came to build up on Wallace's good sense theory brought his legacy into a new level of discussion. By abiding by the rules set out by Wallace, one might say that researchers could see a whole picture now, without gaps, explaining both the value of sensible Mate Choice and the role of conspicuous traits. It could perhaps be said that some studies brought good sense closer to Darwin's ideas, by promoting ornamentation as adapting to female Mate Choice. One should not forget though that choice is in this case utilitarian and that the main contributions were explaining how utility can shape traits into such extremes that they seem less than sensible, while still being.

Contributions to the Good Taste Theory

Ronald Fisher, a mathematician that influenced various fields of study, contributed heavily to tackle the challenging questions that surrounded Darwin's view on Sexual Selection: i) are there selective advantages in Mate Choice; ii) what are the selective forces behind female Mate Choice; iii) can physical traits in males adapt to female preference. Such questions were not straightforward and as aforementioned, their reliance on female taste had a negative impact on the community's opinions. Still, Fisher came up with an elegant answer [97, 98], which not only explained the emergence of Mate Choice but did so while abiding by the main pillars of Darwin's ideals of competitiveness, without resorting on any specially tailored process or explanation.

He theorized that the tastes of individuals were much like any other characteristic under the influence of selective pressure and thus subject to evolutionary change. Accordingly, through descent with modification alone, a mating preference for a specific characteristic may find itself in relative majority in a population. At that point, males that best fit the majority preference will be in relative advantage when compared to others, and thus be selected more often. While this idea was easy to grasp, what was entirely ground breaking was the suggestion that independently of the survival value of the majority preferred trait, females would have an advantage in following the preference in fashion in the population.

In more detail, reproduction enforces that both preferences and the preferred traits are passed on to the resulting offspring, independently of their gender and as contributions coming from both parents, allowing for females to express the preferences and for males to express the traits in their respective phenotypes. Therefore, following the largest trend in the population and choosing a fashionable mate should be helpful in producing attractive male offspring, while choosing otherwise, may produce offspring that are less likely to be chosen for reproduction in the next generation. This phenomena has been often called the Attractive Sons theory [54] and shows how choosing an attractive mate can be adaptive for females, even if selecting with no regards for fitness. Simply put, while good taste may result in the selection of traits that reduce the chances for survival in a lineage, it may also increase the chances of reproduction by introducing males that are attractive to a larger female base, boosting the potential for a positive growth rate in future generations.

These ideas were on their own a great contribution from Fisher, as they could theoretically explain the emergence of Mate Choice. However, they still could not fully explain the emergence of complex ornamentation. Fisher showed however that the inheritance of mating preferences alone could produce such phenomena. He discussed that females with a preference for a given feature will breed offspring that inherit both, so that the coming generation will experience a genetic connection between the two. As the preference is more and more expressed, the more the corresponding trait is genetically linked to that preference. Such a linkage is what feeds each growing fashion, with females with a certain preference becoming increasingly more likely to select for the corresponding feature and as a side effect, selecting for their taste as well (the preference genes that are linked to their respective traits) [54, 12].

So what would start as the Attractive Sons effect, with a small but relative advantage for expressing and selecting a given trait, would result in a runaway process of positive feedback, where both preferences and corresponding features reinforce each other in a loop with increasing momentum. Arguably, even if the process started with favoring an utilitarian feature, it would feed itself to the point where there was no longer utility involved but the preference would be maintained by its own selective pressure. Eventually, Natural Selection would take its toll due to the excessive cost of a feature being higher than the reproductive gain provided. Still, such a model of hand-in-hand evolution of preferences and traits could, according to Fisher, explain the emergence of exaggerated ornamentation and behavior.

Fisher's theoretical model implied a number of ideas that are worth mentioning: i) it saw mate choice as an innate, instinctive and inheritable process, in no way dependent on human consciousness; ii) while observations were most easily found on species with highly developed perception systems (capable of more intricate ornamentation and complex courtship behaviors), simpler species could as easily maintain their own processes; iii) it hinted that both mental and physical traits should be regarded as the product of evolutionary change through descent with modification; iv) the feedback loop between mating tastes and corresponding features meant that evolution was subject to a dynamic, self-adaptive environment; v) such an environment was extremely challenging to analyze using the tools available at the time; vi) the interplay between Natural Selection and Sexual Selection as suggested by Darwin would have great significance.

Despite the effort, Fisher's work was mostly neglected at his time. While he addressed some of the most relevant questions brought up regarding Darwin's propositions, it was only with a second edition of his 1930's work [98, 99] in 1985 that interest in the topic re-emerged. At this point, science was more open minded to the subject of good taste and female preferences, and Fisher's Attractive Sons theory implied a form of good sense in choosing mates by taste, by eyeing its reproductive benefits for females, an idea that could only be popularized by having an individual-level view of evolution. Researchers were also better prepared technologically. Mathematical models have since been proposed to test Fisher's ideas [157, 168, 211], with highlight to Kirkpatrick's two allele model which was one of the earliest models to demonstrate Fisherian runaway Sexual Selection as a stable mechanism [157]. Over time, the Fisher-Darwin model of good taste has gained its space in Sexual Selection theory by showing how good taste and good sense are after all not such opposing ideas.

2.2 Modern Overview

Modern science has recognized the different impacts of Natural and Sexual Selection but has also realized that it is extremely difficult to have them studied as separate forces in nature. On the one hand the players in each force have been rightfully recognized: external environment, physical and biological agents for Natural Selection; sexual mating candidates and sexual rivals for Sexual Selection [109]. On the other hand, despite

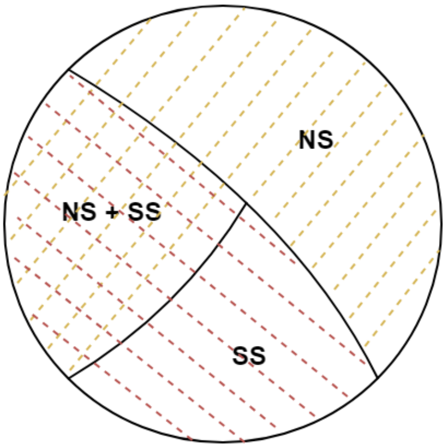

Figure 2.1: Relations between Sexual and Natural Selection in regards to the emergence and adaptation of traits.(adapted [12]).

depending on such well separated agents, the strict differentiation envisioned by Darwin and the deep dependence implied by Wallace continues to be disputed on occasion. The issue is far from the battle between schools of thought on the turn of the 19th century and has in fact matured to a point where researchers have found relevance in both. Nowadays ideas from both school of thought have shown to have a place in evolutionary theory, leading to a sort of balance as is shown by Andersson's review [12].

2.2.1 Sexual Selection in Neo-Darwinism

Along his review on the subject [12], Andersson promotes Sexual Selection as one among many forces involved in Natural Selection. As both Natural Selection and Sexual Selection are more and more scrutinized, they've come to accommodate different selective processes, and so its natural that Sexual Selection is now seen as one among many. This view, as stated above, is not a reinstatement of Wallace's ideas as by no means does Sexual Selection have to be a positive reinforcement for traits that make good sense for Natural Selection. It should be rather viewed as a compromise, where Sexual Selection plays a part, just not with a role as prominent as Darwin suggested. As Brown argued [33], when compared to Artificial Selection, the fitting place of Sexual Selection is as a subset of Natural Selection. However, some authors such as Endler [257] still see usefulness in Darwin's distinction due to differences in impact between mating competition and that for survival. This document will keep referring to mating competition forces as Sexual Selection and other remaining forces as Natural Selection. This choice is not a matter of disagreement but rather due to usefulness and clarity.

As opposing ideas started merging, the challenges moved from explaining the emergence of mating preferences or ornaments into identifying which traits are promoted by Natural or Sexual Selection, as well as exploring the mechanisms within Sexual Selection. These challenges have been demanding since the beginning of studies on sexual behaviors and, due to its dynamics, continue to be. Figure 2.1 shows the relation between Sexual and Natural Selection in the emergence and development of features. As shown, features may belong to one of three groups: i) *N* is the group of features

Table 2.1: Processes of Sexual Selection and their impact (adapted [12])

Process	Impact
Scrambles	Enhanced sensory and motion means; early and fast location of mates
Endurance Rivalry	Longer reproductive endurance during mating season
Contests	Traits that improve success in fights; alternative tactics to avoid stronger opponents
Mate Choice	Ornamentation and behaviour that attract mating partners; offering of resources supporting of breeding
Sperm Competition	Strategies that prevent rivals from accessing the mate; ability to dislodge competing sperm

that have evolved by means of Natural Selection alone, due to their contributions to survival; ii) *S* includes features that evolve by means of Sexual Selection alone due to contributions for mating competition; iii) *S+N* groups features that are under the influence of both Natural and Sexual Selection by contributing positively to the struggle of surviving and that of mating.

Separating observed features by group can be a tricky process, as the role of traits under consideration need to be carefully investigated. A naive approach could put all features related with reproduction under the umbrella of Sexual Selection, however some of such features, for instance traits that improve fertility or pregnancy have no purpose in mating competition [12]. Therefore, while improving reproductive success, they have probably evolved by Natural rather than Sexual Selection. Sensory or other characteristics that help males find and reach females are also disputable and difficult to know for sure which force contributed to their emergence. Additionally and as previously discussed, many features such as body size, weaponry, and calling can contribute for Sexual Selection while having roles in fending off predators, social behaviors, among others [12, 54, 59]. In some cases, their usefulness is difficult to attribute to a group of selective influence. For instance, certain frogs use bright colors to signal predators that they are poisonous unfit prey, which raises the possibility of such signals being the result of Natural Selection alone. Such hypothesis can raise complex discussions, specially since colorful ornamentation is often the result of Sexual Selection [12].

These examples bring forth the difficult analysis involved in putting the emergence of a feature on its rightful group of selective forces. While some characteristics found in nature are doubtlessly related to Natural Selection and others are doubtlessly related to Sexual Selection, the borders between each individual group *N* or *S*, and group *N+S* (from Figure 2.1) can sometimes be fuzzy. As a bottom line, it could be said that traits in the latter group are those where Sexual Selection points in the same direction as Natural Selection, while features in the *S* group result from Sexual Selection pointing to its opposite direction. However, population and environment dynamics can over time contribute to this fuzziness. Moreover, as discussed previously, features can emerge as utilitarian for survival and through a Fisherian process be exaggerated to a point where they are no longer selected for their survival role but rather for their beauty. The opposite, where features that emerge to meet female preference end up finding a role in social behavior or survival is also possible. These processes mean that the evolution of features can be linked to multiple selective forces over time.

In their endeavor to further explore the connections between sexual behavior and evolved characteristics, researchers have focused on the mechanisms of competition that comprise Sexual Selection. Darwin had initially proposed a combination of two mechanisms: i) male competition; ii) female mate choice [59]. This simpler model has since then adapted to accommodate more evidence and knowledge, resulting on a view that better partitions Sexual Selection into a set of mechanisms: i) scrambles; ii) endurance; iii) contests; iv) mate choice; v) mate competition. Andersson [12] addresses each process and an adapted summary of each one can be found in Table 2.1, which for the purpose of this document will suffice. It's important to address that these mechanisms are in themselves not exclusive, in fact some (or all of them) may occur together, such as scramble preceding contest, followed by Mate Choice. This makes their relative importance and their links to different features difficult to analyze.

In summary, Sexual Selection is now a process whose place in Evolutionary Theory is well established, having evolved from two competing theories into a model that has profited from both Darwin's and Wallace's lines of thought. Its relation with Natural Selection is now more than ever well understood, as one among other selective forces, although one that may not always point in the same direction as the remaining. Its selective agents have been described as mating candidates and sexual rivals, which are also its target, thus making population and social dynamics particularly relevant. Due to these characteristics, identifying without a doubt which traits are the result of Sexual Selection, Natural Selection, or both has been a particularly challenging quest. During their effort to catalog such features, researchers have contributed to a more specific description of the inner processes of Sexual Selection, as well as to the conditions under which traits fall under their influence.

2.2.2 Conditions for Sexual Selection

In a very straightforward way, the only conditions for Sexual Selection to happen are genetic variation in the gender under pressure (most often the males) and means for reproduction. In nature, such variation can manifest itself in different forms of competition, which vary depending on the particularities of each species. Polygamous species, where males have access to several females, often present the most extreme behaviors and ornamentation because higher freedom makes competition more crucial for males: an opportunity for stronger males and a demand for weaker ones. Such a system emphasizes differences between males so that on extreme scenarios the most attractive male can gain access to all females or the least attractive male can fail to access even one. The struggle is so that it leads to a stronger investment in Sexual Selection related features, an effect that is boosted by a greater scrutiny from females who, when facing wide availability from males, impose more demanding preferences [59, 98, 233].

Polygamous systems are very common but Sexual Selection is present in monogamous species as well. While males are usually ready to mate sooner than females, the most sexually fit females are also usually ready to mate sooner than others, which in this case is relevant. For males, this suggests advantages in mating sooner, in order to hopefully pair with the female who is more likely to produce fit offspring. For females, mating sooner gives access to a wider range of candidates to select from and so a better chance of selecting an attractive male. It should be kept in mind that in monogamous species, unless there's cheating, when males are selected they cease to be available, which fuels their struggle to be chosen sooner rather than later by a healthy, fecund female. Such a competition is rather intense specially if the species has an unbalanced sex ratio, which can lead to mating candidates to be left out [158, 213, 233]. Overall, competition for mating can be very intensive early in the season but also very beneficial due to the pairing of the best females with the most competitive males.

Across most species, females and males have almost opposing strategies regarding mating. Females are most often very selective in regards of who they pair with while males invest in mating with as many females as possible. The reason behind female choosiness is most likely related to their high parental investment, not only during pregnancy but also during the first stage of the offspring's life [12, 241, 317]. Such an investment keeps females from being able to reproduce again, possibly for a long time, and for that reason they benefit from being specially exploitative of the male gene pool. Males on the other hand have a lower certainty of paternity than females, and so take less benefits from the female approach [6, 181], investing instead in trying to explore as much as possible the female genetic pool for a chance of producing many, fit, attractive offspring. It should be noted that exploitation and exploration are here referring to the genetic level, whereas on an individual level both genders are exploitative, in the sense that by mating, both males and females will for a period be unavailable to other individuals (similarly to many other natural resources) [12].

Gender dynamics are interesting and abundant in nature. However, they are not an absolute necessity for Sexual Selection, given that means for recombination prevail. Theoretically, a single gender population where individuals are capable of mating with each other and produce offspring will develop means of competition for mating and trigger selective forces as a result. The premise is the same as always, that the relative advantage for each individual to mix its own genes in beneficial ways will be enough for the emergence of sexual selective strategies. Andersson suggests for instance that it would not be surprising to find such strategies in bacteria [12]. Regarding the mechanisms presented in Table 2.1, intra-sexual [138] processes such as scrambles, contests and endurance rivalry are still viable as their benefits on a unisex species remain unchanged, as does for sperm competition, which is a post-copulation mechanism.

Mate Choice, as inter-sexual selection [138], may at first sight lose some of it advantages specially if the cost of reproduction in females is disregarded (other strategies may arguably be more beneficial such as mating as many times as possible despite the quality of mates). However, Fisher-Darwin theory shows that producing attractive offspring is beneficial nonetheless. Given that individuals have at least some sensory and are capable of choice, tastes are bound to emerge and runaway processes are therefore feasible, as are other behaviors related to Mate Choice. In fact, individuals would accumulate both the choosiness of females, and the struggle for being fit and attractive, as is characteristic of males. Overall, it could be said that, despite the possible absence of reproductive costs, on a genetic level, producing poorly attractive or less than fit offspring will come with a cost for the genes involved, over a few generations.

2.2.3 Principles of Adaptive Mate Choice

As partly discussed in previous sections, the dynamics between Natural and Sexual Selection makes it sometimes challenging to establish the source for the emergence of particular traits. Moreover, as previously demonstrated, Natural Sciences research has found that Sexual Selection can emerge through a number of processes (see Table 2.1). It's also been discussed that some of these processes represent intra-sexual competition, such is the case for scrambles, endurance rivalry, or contests. Despite the occasional exception, it's been observed in nature a relation between such means of Sexual Selection and Natural Selection.

The contributions of each selective force for the evolution of features are however almost never well balanced. For instance, in some species agility can have an important role in contests, but it's likely to be much more under the influence of Natural Selection than Sexual Selection because of its extreme importance in escaping predators. Antlers on the other hand can have a role in fighting off predators on occasion but their role is much more likely to be of higher importance as weaponry in male competition. In such species, antlers are likely to be more under the influence of Sexual Selection than Natural Selection.

It's important to know that the degree of influence that each force can have on each specific trait is not only unique but also dynamic over time. Most intra-sexual processes are likely to fall under the *N+S* group in Figure 2.1 and thus represent instances where both Natural and Sexual Selection point in the same direction, although with different strengths and means for each trait. Notwithstanding the continuous discussion about the connections between Natural and Sexual selection, in these cases it's not difficult to come up with a stable system, where both selection forces have a somewhat harmonious role. Inter-sexual selection by means of Mate Choice is however a more challenging topic. Conspicuous traits are very often linked to female choice over male features and behavior, a process that unlike others is often seen as counterproductive for survival efforts (group *S* in Figure 2.1). Nonetheless, mating preferences for possibly detrimental characteristics have been shown to prevail in stable systems. Sexual Selection through Mate Choice has represented an unique opportunity to explain such traits and how are they able to exist stably over time.

Adaptive Conspicuous Traits

Historically, selection for conspicuous traits has always been a complex and fracturing subject in evolution research. As discussed above, from the beginning there have been competing ideas, starting with Darwin's good taste versus Wallace's good sense. Researchers have supported either one, by contributing to filling the gaps in both ideologies. While science has come a long way in many points of Sexual Selection theory, the selective forces responsible for the emergence of conspicuous characteristics across species are still actively debated. Apart from Mate Choice mechanisms, other processes have also been brought forward, usually leaning on good sense ideas to explain the emergence of ornamentation or display by alternative means. Some have been successfully refuted [109, 257], but the remaining ones are plausible and mutually compatible, making them not only difficult to refute but also making it more complex to determine their exact influence on ornament evolution [12].

Andersson [12] covers some of the theories that have been discussed by the community. It has been argued for instance that sexual dimorphism can be accounted for by ecological differences, with sex differences emerging as a response to intra-species competition for resources [59, 170, 261]. Such dimorphism can arguably emerge by imperfect genetic correlations between sexes [262], but even if they arise due to Sexual Selection, Natural Selection may maintain and enlarge its presence due to differences in selection pressures between sexes [50, 51]. For instance if each sex has a different exposure to the habitat then differences in diet or even coloration can be enforced by Natural Selection alone. While such a theory can account for some dimorphism, it can hardly explain costly ornamentation, signaling or risky behavior as would be expected. An alternative theory proposed by Baker and Parker [17] suggested emphasized coloration as a signal for predators, warning that they are preying a poisonous or weaponized individual [280]. By their account, the advantage brought by better avoiding predators would fuel the emergence of such signals. Presently, it's considered that such a mechanism may contribute for traits in specific species, specially if strong coloration is present independently of their social or sexual role [17]. Still, the idea fails to generalize and does not seem to be a global explanation for emergence of conspicuous traits.

Male competition has also been suggested as a possible source for the emergence of conspicuous traits. As some authors argue [43, 109, 243, 311, 313, 314], evolution of these features can be explained by their potential role as badges of vigor or presence, not by being attractive to females but rather by being intimidating to competing males. Simply put, some accounts of bright color or other displays may arguably emerge not by direct Sexual Selection but by making tough competitors recognizable to weaker ones. Through such signals, stronger individuals should be able to passively fend off weaker competitors without having to engage in active contests [17]. The relative advantage pushes males into investing more and more in such displays of strength. It follows that these characteristics may emerge from social competition for resources or territory rather than specifically for access to mates.

Unlike adaptation to the environment, such means of male competition would be enforced by the male population on itself, much like females would impose their preferred choice on the male population. Instead of being ruled by mating preferences, such a competition would be ruled by the recognition of strength among males and the consequent withdrawal of weaker males in benefit of apparently stronger ones. The parallelisms between ideas regarding the emergence of ornamentation through Male Competition and Mate Choice are immense. Zahavi [321], among others, has suggested that alike Mate Choice, the emergence of ornamentation through indicators of strength can take an unpredictable direction and through successive improvements [314, 323] lead to divergence in coloration or displays across species as well as produce extreme ornamentation [243, 314]. The view is consistent with a good sense perspective, where males should avoid those that show greater ornamentation handicaps, as their show of extravagance while being capable of escaping predators indicates that they would be fierce rivals in direct contests [17].

In summary, dimorphism as a result of different ecological opportunities between genders, as well as the emergence of conspicuous traits as warning signals of unprofitable preys for predators may account for a few instances of extravagance in males but fail to generalize and therefore aren't regarded as valuable explanations for the widespread emergence of costly and risky displays. Male Competition however has obtained respectable opinions from the science community, specially as mathematical models have suggested that it can lead to instability in traits [12, 221]. It has been argued that such a strategy based on indicators is sustainable as a stable system [219, 220, 267]. The similarity of some ideas with those of Mate Choice are great but should not come as a surprise. In a sense, female Mate Choice is not a contrast of Male Competition, as males are competing with each other even when females choose their mates. On the contrary, the notion that Male Competition much like female Mate Choice may directly or indirectly promote conspicuous or non-conspicuous traits, even if by different means and with different strength, brings up the inter-linkage between mechanisms of Sexual Selection.

Female Choice of Male Traits

As of nowadays, different plausible mechanisms have been proposed for the emergence of conspicuous traits. While some have been addressed already, female Mate Choice stands as the most well established one in the scientific community. Historically, not only has Mate Choice been the most prominent focus of Darwin's and Wallace's discussion on Sexual Selection, many contributions have been accumulated on female choosiness and the resulting pressure that favors conspicuous traits. In a modern view, that same relevance is maintained. Despite possible influence by other means of selection in the emergence of conspicuous traits, Mate Choice is still regarded as the main motor for the emergence of such features [12, 54], and remains the theory that best accommodates the most amount of evidence, either directly or indirectly. It's impact can come in different levels of complexity. For instance and in possibly the most simplistic scenario, it could be said that male traits may evolve simply because they make males more easily detectable by females. Therefore, loud callings, bright colors or other signals may be reinforced because individuals are noticed more often [217, 220, 221, 312].

While such adaptations can bring evolutionary advantages to the best performing males, it represents a method of improving passive attraction [316]. Much like the emergence of conspicuous traits by male competition described above, this process is a way of getting ahead of other males, possibly through a relatively better response to sensory bias in females, rather than by meeting their specific mating preferences. Therefore, much like the discussed mechanisms, it doesn't represent an evolutionary explanation for mating preferences. As a bundle, all these different particularities are part of Sexual Selection theory, in the sense that they favor ornaments that best stimulate their targets [12]. However, its debatable that they represent Mate Choice. Nonetheless, some authors nowadays define mating preferences and choice in a broadly way, as patterns that make females more likely to mate with some mating candidate more often than with others [118, 157, 232]. Even if that makes sense on an individual or population level, on a genetic level it probably makes better sense to distinguish which genes are acting in active choice. For that reason, this document will refer to Mate Choice as the active and direct process where females evaluate and compare several males and have a preference for the most attractive ones.

It's been described in previous sections, among other topics, the chronologies of research on Mate Choice, specifically focused on the evolutionary value of the process, and the consequent benefits in evolving both female choice and male traits. Independently of the school of thought, the procedure of selection abides by a common backbone (with possible variations): i) each female is presented with displays of ornamentation and courtship behavior by multiple males; ii) the male that catches the female's eye will be allowed access to reproduction while others will move on. Different tactics by females have been observed, for instance the evaluation of multiple male courtships in parallel and the selection of the most attractive in relation to rivals. Alternatively, sequential comparison is also possible, making it so that competing males never actually meet each other (interesting as there is less direct intra-sexual competition and a higher role of inter-sexual selection). Other strategies such as threshold acceptance of males are also viable, where males are evaluated due to their absolute rather than relative value, although relative advantage may also result from the benefit of accessing females earlier rather than later [1].

Preferences and the way that females choose their mates, specifically how female preferences evolve to favor conspicuous traits, remains a controversial topic in Sexual Selection [189, 251, 265, 318]. Figure 2.2 shows how Cronin [54] has organized the bulk of nowadays female Mate Choice theory. At the root, there's the historical distinction of ideas, Fisher-Darwin's good taste on one side and Wallace's good sense on the other. Good taste has a certain purity to it, due to its reliance on a simple scheme. It explains the evolutionary advantage of mating preferences through the Attractive Sons hypothesis, which shows how the evolution of choosiness can result from a self-reinforcement loop which enforces that both preferences and preferred traits are passed

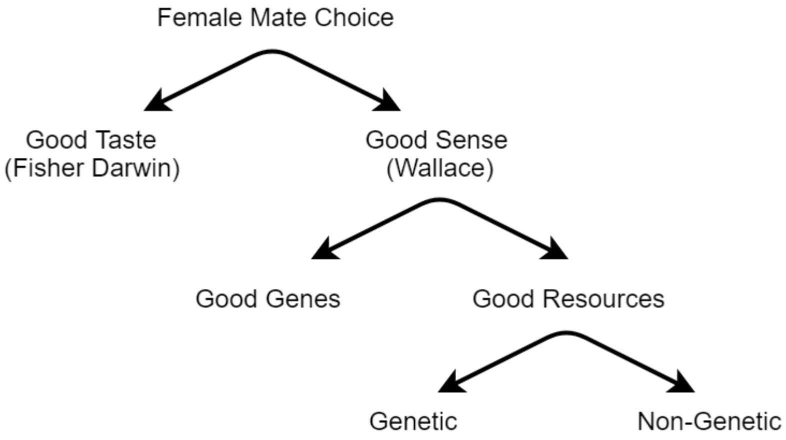

Figure 2.2: Strategies of Female Mate Choice (adapted [54])

onto the next populations. By choosing fashionable males, females can bring adaptive advantage to their offspring and so to their own mating preferences as well (see Section 2.1). Due to the factor that Fisher-Darwin's mating preferences select features for beauty's sake, it may promote those that reduce the viability of males over increases in attractiveness. For that reason it may some times be referred to as maladaptive [54].

The Wallacean side of the tree is somewhat more complicated. It further distinguishes between two types of selection: selection for good genes; selection for good resources. Choosing males sensibly for good genes is the bottom line of Wallace's ideology, and includes preferences for males that show greater energy, agility, etc. or even the most extreme handicaps. Females can also select for best apparent resistance to parasites or other honest signals of good genes. Preferences evolve for ornaments associated with males that can contribute for the breeding of viable, fit children (see Section 2.1). Within selection for good resources, females are selecting not only for males themselves but also for the quality of resources that they can provide (such as nests, food, protection etc.). In some instances, the quality of the resources provided is dependent on each male's ability and can be seen therefore as an extension of their phenotype, an external ornament that results from their genetic quality. In such cases, female preference for resources can emerge as a mean to sensibly profit from the males that will pass on the best abilities to offspring. There can therefore be similarities between choosing males for their physical ornaments or displays, and for their ability to provide resources, as they both are indicators of genetic quality. Together, they are sometimes called adaptive, in contrast with maladaptive Fisher-Darwin choosiness.

There is however, an aspect of selection for good resources that is distinctive from other means. More than an ornament, many resources provided by males have a direct impact on females rather than on their offspring quality, either benefiting their protection, food reserves, or exposure to the habitat, among others. Sometimes, females will end up selecting for resources alone, with no particular interest in deducing which male may actually have better genes. The differences in resource quality in such cases may be purely environmental. Still, by contributing to the survival ability of females and maybe even to that of offspring during their childhood, preferences for relevant resources can be enforced. Due to their significance to female survival, sexual productivity or overall fitness, selection for resources may sometime be regarded as direct selection. By contrast, adaptive or maladaptive selection is sometimes regarded as indirect selection because appropriate decisions will impact offspring fitness and consequently bring evolutionary advantage indirectly to mating preferences in future generations. While direct selection of preferences has been discussed by the research community [251], indirect selection has represented an overwhelming slice of the whole effort put into studying Mate Choice, from Darwin's and Wallace's time to current mathematical and computational models.

2.2.4 Some Aspects of Mating Preferences

The widespread recognition of the Fisher-Darwin model as a plausible explanation for Mate Choice was not immediate. The historical difficulties that it faced, and which for a long time made Wallace's school of though more attractive and seemingly more plausible, have been discussed in previous sections. However, among the many contributions that would result from the Mendelian genetic interpretation of evolutionary theory [194, 300], emerging views on inheritance would contribute to a new view of evolution. It was claimed that selection as a whole would be best investigated from the perspective of genes, instead of regarding individuals or even species as a block unit in evolution. Among many other research topics, this would have a great impact on Sexual Selection related research, firstly by re-boosting the interest in Fisher-Darwin good taste, but also by contributing to other relevant topics on the inner workings of mating preferences and their impact on a genetic level.

Gene centered evolution

The original Darwinian perspective on evolution explores it as happening at the level of individual organisms. Briefly, competition for a given resource will result in higher survival and reproductive rates to the relatively best adapted individuals in a population, consequently allowing their features to pass on more often to future generations. Much like any other study, this individual level view was most certainly bound by the available tools, capability of observation, and knowledge at the time. Researchers were also able to observe macro-evolution, at the level of species or above. However it would be only through the works of Mendel and his successors that evolution would start to be understood on a smaller scale [194, 300]. Through the study of DNA, inheritance, and gene-expression, particularly how phenotypes are the expression of an individual's genetic code and how only that code is passed on through reproduction, a synthesized theory of evolution was proposed where the gene takes the main role as the unit of evolution [62, 63, 120, 122, 227, 317].

Gene centered evolution, or the Selfish Gene theory as was popularized by Richard Dawkins [63], regards a gene not as being any possible piece of a DNA sequence but rather as every instance of a particular variation of DNA bit present in nature (also referred to as allele) [63, 116]. The theory puts competition as truthfully happening on the gene level. Alleles, while not facing selection directly, express themselves by influencing phenotypic characteristics which will present variation, given that there is genetic variation as well. By acting on phenotypic features, selective forces act indirectly on corresponding genes, allowing the most beneficial ones an advantage that translates into a wider representation in future generations. Dawkins used the following analogy [63]: consider a pool of rowers, some with characteristic A and some with characteristic B who are randomly assigned to boats; the boats then race in heats and there's a speed advantage to the boats that have most rowers with the same characteristic; between heats, the winners are returned to the rowers pool for the next round. Over time, a predominantly and then completely taken over pool would show rowers with the same characteristic.

This analogy tells us several important things about gene centered evolution. Firstly, it shows that while individuals (boats) are competing with each other, their performance at each generation (heat) is the expression of the collection of genes that has been attributed to them (rowers). Secondly, genes when combined may cooperate for a mutual goal but individually are competing with each other, so that over time, either genes with characteristic A or genes with characteristic B will take over the gene pool and the other will be depleted. Thirdly, at no point during the analogy is mentioned that either characteristic A or characteristic B is directly beneficial for the carrying individual. Genes compete for their increased frequency in the gene pool alone, not for the benefit of an individual or species. Finally, the time frame of selection for genes is different than that for individuals which are themselves temporary expressions while genes are much more persistent through time.

More formally, genes organize themselves in genotypes who express into phenotypic features on the individuals that encode them. Such individuals are ephemeral from a genetic point of view, while genes persist for much longer periods of time through the lineage and inheritance allowed by many co-existing instances [63]. By grouping in genotypes, they may cooperate for the global goal of spreading in future generations but, overall, genes selfishly compete for their own personal propagation. The effects of genes are dependent on multiple variables, some of which environmental but also related to gender. For instance, probably most of the genes that affect ornamentation, behavior or mating preferences are encoded in ordinary chromosomes and are present in both genders, with their expression being activated or inhibited by hormones [12]. Their phenotypic effect can be beneficial, detrimental or neutral, with their role being determined both by survival and reproductive success [54]. Overall, their evolutionary success is determined by the cumulative effect on their multiple instances, not by any one individual particularly.

Such a view of evolution has ideas that align with those of Fisher-Darwin's Mate Choice by good taste. As discussed previously, probably the most prevalent criticism for the idea was the possibility of having detrimental mating preferences (from an individual level perspective). Indeed, when comparing with Wallace's good sense, Fisherian preferences are definitely selfish. Fisher's self-reinforcement loop suggests preferences selecting for themselves by correlating increasingly with preferred traits, even at the risk of decreasing survival abilities. Wallace's theory by no means loses credibility with the emergence of gene centered evolution, but the intuitive bias that made it more attractive for researchers loses its appeal. In fact, in light of gene level competition, both good sense and good taste are equally viable as they both represent utility-based means of Mate Choice, ones that can explicitly favor the propagation of genes for their own selfish gains.

Preexisting preferences

Facing an already developed conspicuous trait and trying to figure out how the corresponding mating preference emerged is usually a defying task. Researchers have to consider multiple alternatives: i) that the feature was favored by a Fisherian runaway process, for beauty's sake; ii) that it serves an utilitarian purpose and has been favored by good sense; iii) if it's a resource, that it is being selected for the ability of the male or alternatively for its direct profit; iv) that it emerged as a side effect of other adaptations (non-related to Sexual Selection). If this was not in itself a challenge, by consequence of the above discussion on gene inheritance, mating preferences may or may not be expressed in the phenotype and otherwise remain undetected by researchers, unless triggered.

The simple explanation for such preferences to remain undetected or hidden is that there may not be variability in males for them to have a role in their evaluation and differentiation. In Layman's terms, no male is currently showing the ornaments that would otherwise be favored by a given preference. Alternatively, all males may be showing the same ornamentation, as if they were exact copies. In both scenarios, lack of variability renders selection for that trait as useless [178]. How preferences for a non-existing trait can emerge requires some explanation. Following Fisher-Darwin's ideas, taste can emerge through simple variation. Additionally, preferences may at some point be relevant and spread in a population and later through speciation, genetic drift, or other causes, be rendered useless. Moreover, they can be influenced by sensory bias or purely occur arbitrarily or as secondary effects [59]. In such cases while not being fueled directly by self-reinforcement, they may still be maintained and even propagate through genetic linkage with favored genes (meaning that they are very often found together) [52]. While at that point they bring no evolutionary advantage, advantageous genes have no choice but to promote them as companions. So, in contrast with what would be intuitive, and like any other gene, preferences may remain dormant and propagate stealthily.

There are many documented observations of preferences that preexist traits in different genus, and that under the right conditions can be activated. Burley for instance developed an experiment with zebra finches where stripes of randomly selected colors were artificially added to their natural black and white feather patterns. Mating preferences were found in both males and females for particular colors, and because such colors had never existed in this finch species, the preferences preexist the traits. Arguably, and given the opportunity for males to naturally produce such colors, a runaway process could be in place. How these preferences have come to emerge and be maintained in zebras finches is highly debatable, possibly through a secondary effect or a sensory bias [37, 38, 39, 40, 41, 54]. Similarly, Platy fish males whose fins have been added fake extensions, similar to those of the Swordtail fish, have strongly increased their reproductive success with females even though the species in nature lacks that feature [24]. Arguably this could be a reemergence of an old preference, as other species from the same genus such as the Swordtail are known to use that feature in selection. Alternatively it could mean that a preference for long tail features preexists the self-reinforcing process that lead to that feature in the Swordtail fish. Other examples are known [54, 119].

By definition, preexisting traits are non-utilitarian, as they have no role in selection or differentiation of favorable mating partners. At a first glance, they are much more deeply connected with Fisher-Darwin theory than with Wallace's selection for good sense. In a way, preexisting preferences can be a possible origin for Fisherian preferences, and by variation of male traits trigger a runaway process, however it can't be said that this is a sure assumption nor can a broader study be avoided [229]. While the good sense of preexisting preferences is less intuitive, the resilience and perseverance of genes in competition can keep them actively replicating even when they don't contribute directly to increase their chances of replication, making so that once sensible choices can be kept dormant in future generations. Finally, there can be many multiple preexisting preferences in a genetic pool at the same time [85, 229], being up for its dynamics to determine which may eventually be relevant for Mate Choice and which may not.

Preferences multicomponency

So far, conspicuous traits have been addresses independently of their frequency in each individual subject. Theoretically, we could define a base case as one where female preference emerges for a particular trait alone, with either Fisher-Darwin's or Wallace's models applying. Depending on the utility of the developed trait, its purpose and means for emergence may be determined, the correlation between preferences and traits could be tracked, as could the propagation of relevant genes on a population. Possibly, the whole process would be clear, regarding the influence of both natural and sexual selective forces. There are however many examples of species in nature where males combine multiple ornaments such as coloration, particularly lengthy tails, calling and so on, sometimes also investing in courtship behavior to best show off their full display of conspicuous traits. Such scenarios move away from the base case and by consequence, when preferences for multiple traits are considered, the complexity of such a study increases dramatically.

Rowe studied animal signaling and reception, showing how complex the issue can be, as it effects multiple processes, from sensory stimulation, to how they are psychologically processed and responded to [113]. From her analysis, it is shown that multiple stimuli augments sensory reaction in receiving animals, but more importantly, it discusses how the combination of multiple sensory can contribute to relevant Mate Choice related points of interest: i) combining multiple stimuli can improve detection and recognition thus making a contribution to more ambitious scrambles or passive competition among males; ii) it can also contribute to a more thorough discrimination between candidate males, allowing for a multidimensional analysis of male characteristics; iii) finally, it can improve memorability of signals. Overall, the resulting interactions between signals shows that multicomponency is more than the sum of each component [113]. Not only are multiple stimuli apparently capable of producing responses more effectively, they seem to be much more complex than a linear combination of their parts, possibly assuming different weights or more complex interactions.

Multicomponency may have great potential, specially in species with more capable sensory systems or that show higher brain capacity. However, how they operate is regarded as highly dependent on the psychological aspects of the species in question, rather than being a simple direct reaction to sensory stimuli (as could maybe be assumed in a one-component model), or even a direct combination of stimuli. For that reason, understanding the workings of female choice relying on multicomponent preferences is an exponentially more demanding task, one that we can not expect to understand by studying each part independently. The emergence of multicomponency in preferences is still a highly debatable subject. Rowe suggests that receiver psychology may have created a strong selective pressure for the emergence of displays involving multiple signals, due probably to it's increased informative role benefiting females [113]. Moller and Pomiankowski discuss that multicomponency is predominantly found in polygamous species of birds rather than on monogamous ones, due to their increased investment in attractive traits. They conclude that most traits can't be considered Wallacean indicators of fitness but are rather likely to have evolved by Fisherian means [204].

Speciation and hybridization

Sexual Selection can impact species and populations in deep ways through their genetic pools. As discussed previously, male competition and specially Mate Choice can drive ornamentation and behaviors to extremes, with sensory constraints often acting as the main limitation and Natural Selection acting as the controlling force, keeping self-reinforcement and runaway processes from going too far. Such an evolutionary engine has been capable of shaping species by influencing the reproductive success of individuals and consequently, gene frequency [59]. More than that, the enforcement of mating preferences has been shown capable of speciation [12, 54]. In the early days of evolutionary theory, speciation was thought of solely the product of isolation leading to different lineages, to the point where interbreeding was no longer possible. One of the most illustrative example was that described by Darwin regarding the Galapagos archipelago [58], and how from island to island, variations of tortoises and finches had resorted on different diets, habits, and acquired different sexual preferences. In a short summary, migration of sub-populations from island to island resulted on founder-effects and adaptation to local geographic conditions, thus drifting genetically from their ancestry into what would become new species [58].

Despite environmental pressure being regarded traditionally as the main cause for speciation, Mate Choice plays a great role. Firstly, isolation and adaptation may lead to differences in sensory sensitivity, which can influence means for successfully identifying mating partners. Mating preferences can be influenced by such changes, by rendering some of them unusable and leading to the favoring of others. More interestingly, Fisherian self-reinforcement can lead to increasing differences in mating preferences, also reinforcing mate recognition mechanisms to the point of isolation [157, 168, 169, 230, 288]. It has been observed that in closely related species, not only are bigger differences more often found in sexual related features [58, 59, 168] but also that such differences appear to be poorly related to survival adaptation [12]. It has been suggested that the phenomena is consistent with Fisherian preference runaway [168]. Genital stimulation and reproductive organs have also been found to differentiate through means of female choice, sometimes into highly complex systems that make reproduction between otherwise close species unfeasible, thus further promoting their isolation [81, 82].

Speciation through habitat isolation is also known as allopatric speciation and represents one end of the spectrum of possible means of speciation. On the other end, there's sympatric speciation, where species emerge from existing ones even when their populations share the same habitat. Studies have suggested different means for Mate Choice to give rise to speciation in such cases. Changes in the habitat can lead to a subset of the population to adapt and either through changes in sensory biases or preferences become the subject of speciation. In some cases, mutation can also account for partial adaption inside a population. For instance a particular population of finches has reportedly produced individuals whose beaks abide by two ideal sizes, with selection against those in between promoting a split in the population [137]. Moreover, signal exuberance and a reinforcement of complex sensories, can also lead females to be specially selective with their partners, considering as potential mates only a small fraction of the whole available males. Frogs for instance are known to be particularly sensible, with most species of frogs having their own particular calling [28]. The sensibility of the inner ear of the frog to frequencies also seems to relate to the number of species in a particular lineage [250]. Finally, females may be particularly sensible for mating with closely related males in order to avoid interbreeding with other species, which has been known to be more prone to produce less attractive or less viable offspring.

Species and population dynamics are not limited to speciation alone. Moreover, speciation is far from being a clean and sure process. It depends deeply on environmental variables, in some instances it can happen very fast while in other occasions the differentiation between different species can remain fuzzy for many generations. One may imagine that on a theoretical island model, given that enough isolation is maintained, migration can lead to very fast adaption to new habitats and that a very strict differentiation between species can emerge, both in terms of survival habits and reproduction related traits and behavior. Mechanisms for species differentiation, possibly incompatible reproductive organs, and overall offspring quality will keep those species from interbreeding. However, in nature such levels of isolation are often not found, either when allopatric speciation occurs and most specially when moving in the spectrum towards sympatric speciation. Often related populations have contact with each other and along the process, as long as reproduction is viable, hybridization is a possibility. From an individual or population point of view, there would be more gain in the exploitation of each population, in hopes of producing viable or attractive offspring. However, from a genetic point of view, propagation is key and therefore exploration is as valid a strategy as any. Sometimes hybridization can lead to merging of species, to one of them being absorbed, but new speciation may also occur [34, 73, 167, 171]. Mating preferences have a major role in allowing for such processes. After all, despite the role of the reproductive organs, they are what either forbids or allows for such dynamics between species, that otherwise would, by force of Natural Selection alone, be simply adapting to their habitat.

Chapter 3

Modeling Mate Choice

The role of Sexual Selection, and particularly Mate Choice, was for a long time diminished for several reasons: i) the community wasn't ready to accept its challenging ideas; ii) Wallace while gaining the attention of the community put it as a particularity of Natural Selection; iii) both Darwin's but also Wallace's ideas showed important gaps; iv) there were not enough documented examples nor were there ways and tools to verify the validity of the ideas. That would change, as has been described in the previous chapter, with the aid of the Selfish Gene theory and Fisher's studies which contributed heavily to reboot interest in the topic. Contributions have been made since then based on increasing amounts of data related to many species. Despite such progress, Mate Choice lacked mathematical proof that the discussed ideas could prevail as a stable system. The problem was particularly relevant for Fisher-Darwin's ideology, due to the potential standoff between Natural and Sexual Selection. Even with good taste being interestingly sensible on a genetic level, it was questioned if Mate Choice by good taste could withstand being challenged by Natural Selection.

With the rise of the computer world, simulations within artificial systems mimicking the works of nature came as helpful tools for Natural Sciences. They represented a way to model genetics and test artificial life, in a relatively easy, inexpensive, time-efficient, and most importantly controlled way. Many of the evolutionary ideas in Neo-Darwininan science passed the test of simulation and consequently saw their importance reinforced and mathematically validated. New research fields would arise from this era of innovation, such as Evolutionary Computation which nowadays encompasses several genetic models but has its seeds in the 1950s. Evolutionary Programming was introduced by L. Fogel in the 1960s [101], Genetic Algorithms were proposed by J. Holland in the 1970s [131] and Evolutionary Strategies were developed by Rechenberg and Schewefel during the 1960s and the 1970s [239, 258]. Genetic Programming was first idealized during the 1960s and established itself during the 1990s [165]. All would follow the popular ideas at the time on genetics, inheritance and selection by survival value.

Despite their role in the understanding of the biological world, genetic models have also found other purposes in science and engineering. Evolutionary Algorithms for instance have since their early days been developed as optimization tools, with growing applications in many research fields and industries, each with its own challenges and needs. Customization of Evolutionary Algorithms has been a regular practice to meet such needs, with researchers often finding it useful to incorporate mathematical or otherwise engineering mechanisms to improve the application of the algorithms on particular problems. Sometimes, it has also been found to be beneficial to incorporate biological knowledge. While it can't be expected that all the variables and operators in today's understanding of nature to be relevant or even viable in genetic models, some pieces may be surprisingly fit. The transferring of knowledge between multiple sciences such as Evolutionary Biology, Evolutionary Anthropology [45], or Evolutionary Psychology [42], and genetic models, has been a relevant part of what the scientific community deals with. Regarding Mate Choice, genetic models have played a continuous role to a better understanding of Fisher-Darwin's and Wallace's schools of thought [12]. Perhaps more interestingly is the idea that Mate Choice can introduce new potential in Evolutionary Algorithms to deal with certain optimization tasks.

3.1 Fisherian and Wallacean Models

Mathematical and genetic models have made important contributions to the theory of Sexual Selection. Ideally, such models mimicking population dynamics and biological behavior should achieve generality, precision, realism, and simplicity [12, 179], as scientific means to reproduce controlled experiments on the behavior of natural populations. Many times, maintaining the compatibility of such characteristics is an impossible task, so that models have to be devised to work under assumptions that establish the conditions under which they are run. Likewise, these assumptions influence how models are studied, analyzed, and how predictions are made [9, 12]. Common assumptions have included the male-female distribution in initial populations, number of offspring in each reproduction step, the initial genetic distribution, the lack of mating cost, or the disregard of external factors such as mutation of mating preferences. Still, by formulating those assumptions with clarity, comparisons between models can be made, hypothesis formulation can derive and overall guidance of empirical work benefits.

While state of the art models for Sexual Selection can be quite complex, initial models were surprisingly simple. Still, they successfully provided mathematical evidence for many of the ideas that were at the base of Sexual Selection theory. O'Donald was the pioneer of Mate Choice modeling and what would end up being called the few-locus models (locus refers to the position of genes in a chromosome) [211, 212]. O'Donald relied on a polygenic, diploid, two-locus approach, however simpler models have been shown to work as well, and while their results have been extended to polygenic and diploid approaches, neither are necessary requirements for showing the effects of Mate Choice. The models that came after that of O'Donald, mostly follow a common backbone which has been summarized in Algorithm 1, with appropriate assumptions and customization applying when relevant. Analysis also relied on the following ideas present in the algorithm: i) gene allele frequencies are calculated from genotypes and compared to those of previous generations; ii) over many generations, variations are analyzed and conclusions are driven regarding allele frequency evolution and its effects.

The following subsections cover specifics on models for Fisher-Darwin Sexual Selection as well as Wallace's fitness indicator mechanisms. For the two-locus model (Fisherian), Kirkpatrick's haploid approach [157] as well as Lande's polygenic model [168, 169, 170] will be briefly discussed, while for the three-locus model (Wallacean) three indicator models will be addressed and compared, based on the simulations by Maynard Smith [192, 263, 265] and other authors [146, 228, 231, 232]. Overall, conclusions are in-line with previously discussed theory and while some of the most relevant ideas will be further addressed, full analytic results and discussion are unnecessary

```
assume initial allele frequencies;
assume initial population size and male-female ratio;
for n generations do
    calculate mating frequencies in both sexes based on mating preferences
      and other aspects;
    calculate genotypes frequencies among offspring in new generation;
    apply natural selection;
    calculate genotypes frequencies among adults in new generation;
    calculate allele frequencies from genotypes frequencies;
end
allele frequencies are assessed throughout the generations;
```

Algorithm 1: The few locus model

to be presented and can be consulted elsewhere [12]. It should nonetheless be noted that few-locus models are more tractable than polygenic models, which usually rely on quantitative genetics and may not produce elegant analytic results or solutions. Still, it can be concluded that more than ever, Fisher-Darwin's and Wallace's ideas can be seen as closely related, relying on very similar models and mechanisms that differentiate on a few assumptions. Fisherian models need less assumptions and are therefore more attractive, however Wallacean models are themselves rendered as very close in terms of genetic workings.

3.1.1 The Two Locus Model

Kirkpatrick's model [157] represented individuals as two-locus chromosomes, one for preferences (P) and one for traits (T). In the model there are two types of males, those encoding T_1 don't invest energy on producing an ornament and so have a survival ability of 1, while those encoding T_2 express a conspicuous trait but have their survival reduced by an established selection coefficient s, $1-s$. Accordingly, there are two types of females, those encoding P_1 select mating partners randomly, and those with the P_2 allele show a preference for T_2 males. For a given preference strength a_2, P_2 females mate more often with T_2 males than with T_1 males. It should be highlighted that, as described, males carrying a conspicuous trait in this model have a cost on survivability, but having a preference for that trait has no direct cost for females, either on their ability to survive or on their certainty to reproduce. There is, therefore, no direct selection of mating preferences.

As would be theoretically expected, as the model runs following Algorithm 1, a linkage disequilibrium emerges between the two loci, with the P_2 allele becoming associated with T_2 allele through Fisherian self-reinforcement. The simple fact that P_2 females tend to mate with T_2 males more often allows the allele to spread, not as a result of a direct selection but rather through maintaining a linkage to alleles that are favored by Sexual Selection. While T_2 has a negative impact on survivability, their favoring in selection allows the pairing of both preference and conspicuous traits, in a straight resemblance of the Fisher-Darwin Attractive Sons theory. By assessing the frequency of T_2 and P_2 alleles, Kirkpatrick showed that the system is stable along an equilibrium line (Figure 3.1), along which gene frequencies remain fixed [12, 157].

A few thing are worth notice in regards of the equilibrium line, which is represented in Figure 3.1: given values for a_2 and s, for any frequency of P_2 alleles, there

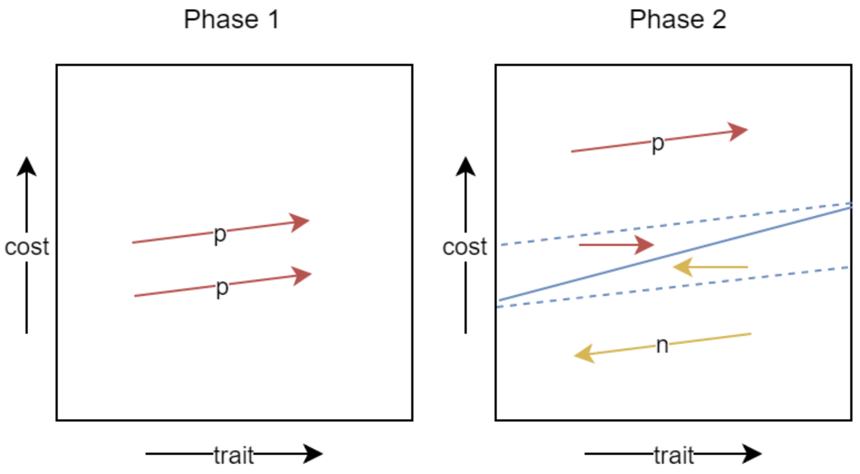

Figure 3.1: Line of equilibria in Kirkpatrick's model (adapted [12])

is a corresponding frequency of T_2; on a first phase (left side of Figure 3.1), if there is only a rare preference for a trait, its frequency is likely to remain null; however, if for some reason such as genetic drift or mutation, the preference becomes more common, the male trait may spread, bringing the process to phase two (right side of Figure 3.1); if the mating preference is strong enough to overcome s, then the frequency of the male trait can increase; the equilibrium point will remain along the line and may vary due to changes in gene frequencies; if changes are small, the equilibrium point tends to return to the line (usually not to the previous place); large changes may result in boundary equilibria where the ornament frequency is either lost or fixed in the population. Overall, Kirkpatrick's equilibria line represents a stable model in the sense that deviations will always lead to the population evolving back to it.

Further research by Seger [259] tested a similar model, although with a tournament like selection process, where each female chooses a mating partner from among a lek, or subset of the male population, rather than having potential access to all males. Similarly, P_1 females choose a male from the lek randomly while P_2 females have a higher chance of mating with a T_2 male, if one happens to be present in the lek. Such changes make it so that when T_1 males are common, most tournaments may not include T_2 males and the other way around. Depending on the male frequencies, P_2 females may have a chance of choosing according to their preference or not, which results on male fitness being frequency dependent. The result of such a model is that displacements away from the equilibrium line are larger and more in accordance with a true runaway process, causing possible disequilibrium and rapid evolutionary periods in the modeled population.

Kirkpatrick [157] and Seger's [259] models, while achieving mathematical proof for Mate Choice to be possible as a stable system, were simplistic in the sense that survivability, preferences and conspicuous traits were each the direct result of two loci. In nature, traits are regarded to be the result of polygenes, with multiple genes having an additive influence on traits. Lande's model [168] is as close an approximation to few-locus models as one could expect, with the difference that preferences and conspicuous traits depend on many autosomal genes. Most of the assumptions remain the

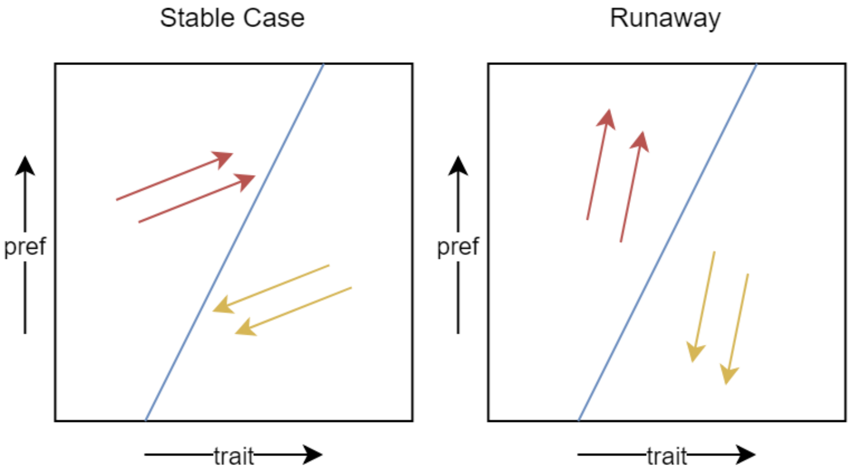

Figure 3.2: Line of equilibria in Lande's model (adapted [12])

same, females behave similarly, and males can have access to multiple females and provide only genes. Male survival is maximum when the ornament is of optimum size and decreases through a Gaussian function whose width represents the selection coefficient. Lande tested three approaches for P_2 female preferences: i) with absolute preferences, each female favors a given size for male ornament, with preference decreasing through a Gaussian function (similar to Natural Selection but with per female center and width); ii) with relative preferences, females have a preference for those ornaments who are relatively larger than average; iii) finally, each female preference increases exponentially with the size of the male trait.

Results were similar with either approach, with male ornaments being pushed into optimum size through Natural Selection and at the same time to a larger-than-optimum size through mating preferences. On the one hand, Natural Selection applied before reproduction reduces the number of males with larger costly ornaments [12]. On the other hand, Mate Choice then disfavors those who are less risky with ornament size. The result is a shift in male trait sizes. If the system has not reached equilibrium, both preferences and ornaments evolve and develop a covariance by means of self-reinforcement. The process reaches an equilibrium when the survival cost of an ornament is large enough to offset the reproductive advantages. When in equilibrium, Sexual Selection and Natural Selection balance each other, variation is reduced due to the removal of extreme individuals until uniformity is found. Mutation can nonetheless restore variation [168].

Lande also expanded on Kirkpatrick and Seger's conclusions regarding the equilibria line. While Lande reached similar conclusions as the previous studies, he showed that the line can represent stable (left side of Figure 3.2) or unstable (right side of Figure 3.2) models depending on its slope and the slope along which ornaments and preferences evolve. The system is unstable if females are critical on their choice of males to the point that Natural Selection becomes relatively weak. This allows for runaway processes away from the line of equilibria, either pointing toward larger or smaller ornaments, as previously discussed by Fisher [98]. Natural Selection or otherwise selection for extreme and rare males establish when such processes end. Overall, the two-locus model and later a polygenic alternative have shown that Fisher-Darwin's good taste can work under very few assumptions and can produce stable systems, although susceptible to runaway processes.

3.1.2 The Three Locus Model

Individuals in this few locus model are represented as chromosomes encoding the following three locus: the first locus can either encode the presence of an ornament (A) or its absence (a); the second locus can either represent high (B) or low (b) viability; the third locus is for female preference, either preferring ornamented males (C) or choosing a partner randomly (c). Similarly to the previously discussed models, males express ornaments and females express mating preferences, while each gender carries the genes for both. The assumptions also remain mostly the same, however no solutions analytically comparable to the Kirkpatrick's equilibrium line are achieved. Still, regular analysis through gene frequency remain helpful in showing that Wallace's ideas of ornamentation as indicator mechanisms can prevail as stable systems under certain assumptions.

Three variants of indicators have been tested and discussed by Maynard Smith [263, 264, 266] and other authors [8, 10, 11, 156, 228, 231, 232, 289]: i) with pure epistatic indicators, all males with allele A will express an ornament; ii) with condition-dependent indicators, males will express an ornament only if they encode allele A simultaneously with the allele for high viability B; iii) with revealing indicators, all males with allele A express an ornament, but while males with allele B keep it in prime shape, those with allele b keep it in poor shape. In each of the three approaches, females have no direct cost from mating, however, the allele for general viability makes B females fitter. The higher the selection coefficient, the bigger the fitness differences from b females. Regarding males, each approach has its own mean of establishing their viability. Overall, there is a viability cost for males developing ornaments (all with allele A in approaches *i* and *iii* and those with both allele A and B for approach *ii*). The cost of producing an ornament coupled with general viability determines the male's survival ability.

There are a few particularities that arise from such model differences. For instance, in model *i* all males develop the trait causing those with poor survivability to risk it even further. They do so in order to join other males in the struggle to access all available females, both carrying c or C preferences, as to hopefully benefit from it. Model *ii* allows only males with high viability to express an ornament, in case they carry both alleles simultaneously, saving weaker males from accumulating costs but also making them less attractive to C females. It also makes ornaments honest displays of virility, in contrast with model *i* where ornaments may be dishonest. Model *iii* also allows for the distinction between male quality through the condition of the displayed ornament, but adds a cost to all males carrying allele A, independently of their viability. In all models, the self-reinforcement of ornaments and preferences for such traits is expected and achieved. If B emerges for instance by mean of mutation, A benefits from coupling with such individuals, either because the cost of maintaining the ornament is less impacting on their survival ability or because they are the only ones who have enough energy to display it. The result over some generations is that ornaments are more likely found among B carrying males, making C carrying females more likely to mate with high viability males.

The global result is the coupling of preferences and high viability, C and B, through the linkage of C and A and the association of A with B. There is a linkage disequilibrium between these alleles, through the association with high viability. As a side effect, *a*, *b* and *c* gradually become linked as well. The process is in many ways similar with a Fisherian process, however the assumptions imposed in the model make it so that a sensible association emerges, in accordance with Wallacean ideas. That similarity was emphasized by Pomiankowski [228, 231, 232] when comparing the three models, who also brought up that indicator models by themselves cannot account for the propagation of ornaments and preferences, requiring a threshold frequency of preferences for ornamentation for a self-reinforcement process to kick in. While that would be very much in line with Fisherian models, no line of equilibria was found to exist. On the contrary, indicator mechanisms may increase the likelihood of fixation of preferences and traits and thus may contribute heavily to the emergence of deleterious traits [127, 289].

Analysis has also shown that pure epistatic indicators, on top of seeming less realistic, have a weaker impact as a driving assumption for the emergence of self-reinforcing selection of mating preferences and respective ornaments [11, 228, 231, 232]. Furthermore, results have shown to generalize to diploid models [289]. Polygenic models have also been developed, such as the one by Iwasa et al. [146], whose assumptions are mostly similar to Lande's Fisherian model [168], with general viability, preferences, and ornaments depending on various polygenes. In such models, further assumptions include small fitness variations over phenotypic variations, and a cost for cryptic female choice. More importantly, in order for Iwasa's model [146] to work, it must be assumed that deleterious mutations produce viability loss, and that ornament size increases with male general viability. This final assumption aligns with condition-dependent and revealing indicator models, partly explaining why they seem to work more often than models where ornaments are not dependent on male condition [146].

3.1.3 Discussion

Both the schools of thought of Fisher-Darwin and Wallace have one way or another been demonstrated to be viable through mathematical models, and so have had their ideas strengthened. In a way, Fisher-Darwin's models come out on top due to their acclaimed simplicity, either in few-genes and polygenic models. Ideas such as the self-reinforcement of preferences and traits through their increased coupling, or runaway processes, have also had positive arguments in their favor. While maintaining the required assumptions to a reasonable low, analytic and quantitative analysis have contributed to the establishment of Fisherian good taste behavior as a viable scenario. While Wallacean good sense requires more assumptions both in few-genes and polygenic models, results are also enthusiastic, even arguably providing better means for the rapid propagation of conspicuous traits, on specific scenarios.

Such models have shown similar results with diploid and haploid representations, and identical behaviors are achievable not only with few-genes models but also with polygenic models, even if requiring a few more assumptions. Although the discussed experiments rely on populations with two genders, both encode the same locus, expressing preferences or traits accordingly. As argued, effects are likely to extend to unisex populations, where individuals may contribute either through a male or a female role. Also, it may be expected for results to extend to monogamous populations, even though it's likely that the spreading of relevant genes takes a slower pace and reaches less extremes. The studied models also trace only one trait, and so preference multicomponency and the corresponding expression of multiple ornaments is not addressed. The models show, however, that ornament adaptation may change direction due to mutation, drift or other factors followed by new momentum. Given the means to express multiple ornaments, evolutionary chances for new preferences and ornaments to propagate may happen while preference for others recede. Finally, the discussed models determine their assumptions based on promoting either Fisherian or Wallacean preferences. Given broader assumptions, both may exist concurrently.

Despite the great value and knowledge provided by the modeling of Mate Choice in genetic models, and the differences between them, what could be regarded as most striking is the great similarity between Fisher-Darwin and Wallacean models. On a close look, the processes behind the emergence of ornaments for good taste or as indicator mechanisms are mostly the same, relying on self-reinforcement through what is popularly known as the Fisherian feedback loop, even to the point of producing runaway processes. Simply put, what most influences the ornaments on their purpose is determined by a few assumptions on how those ornaments express themselves, and how they impact viability. Such models have therefore contributed to the building of bridges between both ideologies, bringing them closer together on common ground.

3.2 Selection through Mate Choice in Evolutionary Algorithms

Research in Evolutionary Algorithms has boomed over the past few decades. Independently of the reasons that have contributed to this boom, Evolutionary Algorithms are nowadays regarded has a very successful family of metaheuristics. The family has since the early days come to accommodate multiple algorithms, relying on a set of operators and strategies to find better solutions to many optimization problems and tasks. Of course, as metaheuristics, Evolutionary Algorithms don't aim at finding an optimal solution (although they may), but rather at finding a good enough solution, given limited computational resources. Moreover, they may require only broad expertise on the problem being tackled, making them well tailored for a great number of general problems, even those where humans lack complete knowledge. In return for relatively low design effort, the algorithm provides a guided search through a solution space without having to test every possible variation, even possibly acting as a black box.

Unlike genetic models used for the studying of biological behavior, Evolutionary Algorithms are invariably goal oriented. It may be said that reaching for that goal is the essence of an Evolutionary Algorithm, with its inner workings, competitions, and dynamics contributing to that global task. While being uncharacteristic of the previously discussed models, such a view has had a great influence on the developments made to Evolutionary Algorithms from an effectiveness or efficiency perspective. Overall, many contributions focused on engineering rather than natural processes have been made during the years. Still, Evolutionary Algorithms remain relatively faithful analogies of Natural Evolution through Natural Selection. It has been discussed however that Natural Evolution has found it profitable across many species to include other forms of competition, among which Sexual Selection through Mate Choice. A parallelism becomes obvious for Evolutionary Algorithms by introducing the idea that the most advantageous way to reach the best solution for a global task may not be to focus completely on reaching for that goal but rather to balance that effort with methods capable of producing other dynamics or even ignoring the goal. The introduction of Mate Choice may be a viable nature-inspired means to do that.

For the purpose of discussing the possible benefits that Mate Choice can bring to Evolutionary Algorithms, various important knowledge nuggets relating to the mod-

```
initialize population;
evaluate each individual in the population using fitness function f(i);
repeat
    select individuals for reproduction;
    breed offspring by applying genetic crossover and mutation;
    evaluate offspring using fitness function f(i);
    replace old population with new one;
until termination condition is met;
return individual with best fitness;
```

Algorithm 2: A generic Evolutionary Algorithm

eling of Mate Choice are going to be covered in the next subsections. Firstly, Evolutionary Algorithms are going to be compared to other Genetic Models, both covering similarities and discussing differences. Secondly, a template for Mate Choice is going to be introduced, its deviation from traditional selection operators reviewed and opportunities examined. Finally, ways to model multidimensional Mate Choice, or rather the evaluation of mating candidates in more complex ways will be discussed.

3.2.1 Evolutionary Algorithms vs Genetic Models

Algorithm 2 sums up the steps that usually take place when running an Evolutionary Algorithm, which may sometimes be subject to changes when convenient, by including new assumptions. For instance, new offspring may merge into the previously existing population under certain rules, mutation and crossover may have higher or smaller chances of happening, sometimes even having zero probability, and so on. Independently of whichever tailoring, the assumptions needed for an Evolutionary Algorithm are different than those for other, previously assessed Genetic Models. This is particularly true regarding allele frequency. While there is added value in keeping track of allele frequencies throughout evolution on a Genetic Model (or distinct traits in polygenic models), the same isn't so straightforward for Evolutionary Algorithms. There are multiple reasons for that being so, which are relevant for studying the impact of Mate Choice and will be covered independently for clarity.

Firstly, Evolutionary Algorithms rely on stochastic initialization. While Genetic Models have very well defined initial conditions, under which it should be possible to predict or follow changes in the population in a clear and noise-free way, traditional initialization in Evolutionary Algorithms bars that option. Coupled with multiple reruns, stochastic initialization offers broader search opportunities but makes it harder to predict the evolutionary path of a population based on its initial conditions. If Mate Choice is implemented on top of that, its self-adaptive and dynamic nature make the problem of tracking much harder if using the same means. This situation is further reinforced if few assumptions are made regarding the expression of ornaments and preferences, in a closer remark to Fisherian rather than Wallacean preferences. In short, given an unknown distribution of genes relative to viability, preferences or ornaments, it may be expected for evolution to take any possible direction, on the one hand pushed by Natural Selection towards a goal, but on the other hand pushed by Mate Choice and preferences. As previously discussed, Mate Choice is highly dependent on initial conditions. It may be triggered by an initially established preference or genetic drift mid run. For that reason, it is likely that its behavior won't remain stable between runs.

Secondly, Genetic Models are mostly focused on the studying of evolutionary behavior, whereas Evolutionary Algorithms ultimately aim at finding a good solution to an optimization problem. This difference may have strong implications. In both algorithms, gene level competition is undeniable, however when applying an Evolutionary Algorithm, individuals as whole organisms have a greater significance than simply being vessels for genes. Of course, independently of the model, gene competition is directly influenced by the relative quality of each individual, as aggregates of genes, and the resulting individual level competition. However, in Evolutionary Algorithms specifically, individuals are evaluated as whole organisms, and there is an expectation for the population to produce better and better individuals, due to their roles as candidate solutions. For these reasons, individual and population levels have a higher significance than on other Genetic Models, where the gene level is arguably the most relevant. Regarding Mate Choice, such a view may put a weight on preferences or traits, and their corresponding genes, to contribute positively to their host individuals more that focusing on their own selfish gain. In a way, when designing mating preferences, this view could influence the introduction of Wallacean assumptions, with the good of the individuals or of the population in mind.

Thirdly, polygyny and phenotype mapping also add complexity in Evolutionary Algorithms when compared to other Genetic Models. The few-locus models described previously map genotype to phenotype nearly directly, and thus have the advantage of warranting the tracking of gene frequencies, which allows for analytic results and observations such as the line of equilibrium. It has however been discussed that polygenic models allow for no such discussion. It does not mean that similar behaviors are not implicit in their workings but, due to their nature, observations and their discussion need to be done through the tracking of the phenotypic expression of preferences and traits. How they relate to specific genes remains, nonetheless, difficult to assert. Still, assumptions in polygenic models allow for the meaning of preferences and traits to be directly inferred, mostly because each characteristic depends exclusively on their corresponding genes. In the end, much like in few-gene models, the mapping between genotype and phenotype is so that a set of genes influences one and only one aspect of the phenotype in quite a straightforward way. The same can't be taken for granted when dealing with Evolutionary Algorithms. Most often, genotype to phenotype mapping is much more complex, with genes influencing one or more aspects of the phenotype, and often not encoding viability in a straightforward way. Alternatively, fitness and conspicuous characteristics may be extracted from the phenotype through evaluation or other means. In short, the connection between phenotype and genotype in Evolutionary Algorithms may not be as direct as in other Genetic Models. This characteristic makes traditional analysis strategies difficult to apply.

In summary, Evolutionary Algorithms and other Genetic Models have different ambitions and therefore have design, behavior and analysis differences. Regarding design, representation and phenotype mapping strongly influences how Sexual Selection may contribute to achieving a well defined goal in Evolutionary Algorithms, in contrast with a more behavioral-analysis focused approach, characteristic of other Genetic Models. On the subject of behavior, it should be expected divergence to result from various differences, starting with the stochastic nature of Evolutionary Algorithms, but also from its dynamics from gene to population level and how they link with its goal-oriented nature. Finally, regarding analysis, polygeny and complex representation of preferences and traits when tackling specific problems, is likely to render unhelpful traditional analysis means used in other Genetic Models. While this subsection highlights differences that are very relevant when considering the transfer of knowledge from other Genetic

Models into Evolutionary Algorithms, it should be kept in mind that plenty of characteristics are maintained. For that reason, exclusive designs or behaviors should not be expected, but rather different assumptions and an increase of complexity.

3.2.2 The Mate Choice Operator

Throughout the last few decades, there has been a timid but continuous interest in introducing Sexual Selection ideas into Evolutionary Algorithms, through the design of tailored selection operators. This investment has materialized in a reasonable collection of papers and ideas but, for the most, Sexual Selection through Mate Choice can't be said to have had a particularly relevant impact. There are a number of potential reasons accounting for the topic to remain uninteresting for some, or a curiosity for others: i) selection inspired by Natural Selection has had a long history within Evolutionary Algorithms, often regarded as a default or first choice, being distributed with many frameworks; ii) such operators can often work as black boxes, generalizing to many problems; iii) they rely on minimum assumptions to work properly, such as fitness variation within a population; iv) on many applications, Natural Selection inspired operators achieve satisfying results or at least some mean of progress; v) for that reason, there's a certain confidence in the usefulness of such operators; vi) for improvements in particular domains, researchers often focus on specially tailored approaches to tackle certain tasks or collections of problems.

In addition to the aforementioned reasons, there are a few additional ones that are directly related with the complex workings of Sexual Selection through Mate Choice: i) the process is not straightforward to model, as it may depend on more complex assumptions to represent mating preferences, ornamentation and choice; ii) many of the aforementioned particularities of Mate Choice, specially its self-adaptive dynamic nature and its relation with Natural Selection, increase design complexity; iii) as a result, its behavior can be difficult to assess and analyze, whereas Natural Selection has had many means of analysis proposed over the years; iv) such increase in complexity may require more advanced knowledge than a standard approach, possibly keeping less skillful researchers (such as those with different backgrounds) from coming aboard.

Despite the challenges, there have been advances in the design of Mate Choice operators, fueled by curiosity, their prospective value, or sometimes as a byproduct of studies with different focus. The following two subsections aim at highlighting operational differences when designing a Mate Choice operator. First, traditional selection will be briefly discussed, and then a template for Mate Choice will be presented and contrasted. At this point, analysis of the Mate Choice operator will be kept on a high level, using a mostly general template. Still, the impact that design choices can have on behavior will be introduced as a relevant topic. Chapter 4 will later cover how Mate Choice operators can and have been customized over its research history.

Traditional Selection

Figure 3.3 demonstrates how traditional selection works. On a high level, individuals are selected consecutively and independently from an existing population, by means of a predefined selection operator. Individuals may be selected from zero to many times, following the principle that fitter ones have higher chances of reproduction, the same way that they would access resources more easily. On a more particular level, on most implementations the selection step takes exactly the same actions every time. In a form of competition that can rely on various rules, such as proportionate selection

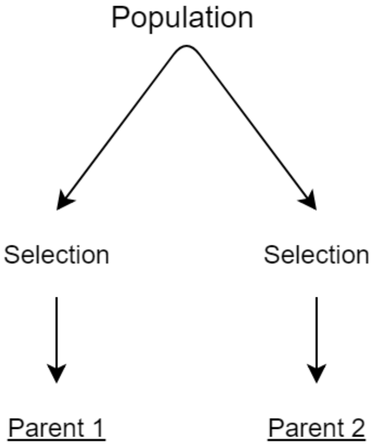

Figure 3.3: Diagram of traditional selection method

probabilities in Roulette Wheel [16] or *best-of-N* in Tournament Selection [16], traditional selection determines the reproductive success of each candidate solution based solely on its fitness at tackling the target problem. Traditional Selection operators are therefore metaphors of Natural Selection as the sole meaningful selective force, disregarding the impact of Sexual Selection in reproductive success and relying on what can be reduced to a reproduction-of-the-fittest view. In a way, it's a good analogy of early Darwinian and Wallacean views of Natural Evolution.

For their relevance in the ongoing study, there are a few characteristics of these operators that should be brought up. As seen in Figure 3.3 and as previously introduced, individuals are selected in an independent fashion, and for all purposes are in isolation. They are not allowed choice of who they mate with and so, unless designed otherwise, they are paired randomly. Competitive advantage arises through there being a greater rather than lesser chance that, when selected, individuals are mating with a partner whose fitness is above average. Such a selective force impacts offspring in a fitness improving direction. From a gene level perspective, competitive advantage comes with coupling with genes for good fitness, for a higher chance of being selected. There is of course a stochastic factor involved, as a means to give less fit individuals a chance of competing. While this may sometimes result in short bursts of evolution in diverging directions, the effect can't be said to be the result of an active force comparable to Sexual Selection.

Selection through Mate Choice

The introduction of Mate Choice in Evolutionary Algorithms can drastically change the structure of selection operators. Individuals are no longer isolated nor are they selected independently, based on an external evaluation metric alone. As seen in Figure 3.4, individuals are capable of interaction to a certain degree, allowing them to influence each other's and their own reproductive success. On a high level, this is accomplished by introducing female and male roles in selection, in determent of the gender neutrality characteristic of traditional selection. The assumption of such roles can have multiple implications, with Female Mate Choice being by far the most relevant one, a true key

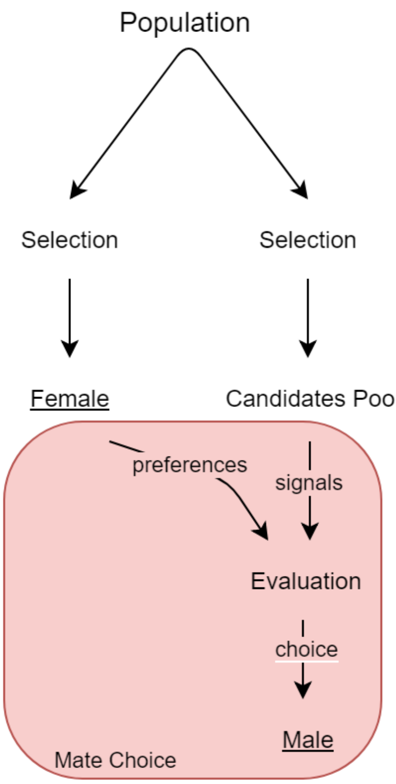

Figure 3.4: Diagram of selection through Mate Choice

player in the selection of partners for reproduction. As a general template, that alone can allow for the introduction of new selective forces and inner-population dynamics singular of Sexual Selection theory. On a particular level, at each selection step an individual is selected for a female role and, given access to a set of male mating candidates, should be able to perceive information on each of them, and choose as a mating partner the one that best matches its mating preferences.

As previously stated, despite some fragility, there has been some opportunities for the discussion of interesting and innovative ideas regarding Mate Choice in Evolutionary Algorithms. While Figure 3.4 shows a template or backbone for Mate Choice, multiple design variants can be found in the literature, each following their own inspirations. In the end, designing a Mate Choice operator requires only a few assumptions, however, those assumptions can have deep impacts on the workings of an Evolutionary Algorithm. Some may be more important than others but for the purpose of wholeness, all will be covered briefly for a better understanding of their influence. This will allow for a better understanding of Chapter 4, where different examples of multiple design choices and their application on different problems will be reviewed, particularly regarding the variety of design choices that can be found when applying Mate Choice operators in Evolutionary Algorithms.

As a starting point, there's the matter of selection of females and male candidates, and the preliminary step of gender determination. In nature, sex determination is most often achieved through a main sex locus, whose allele will trigger the expression of genes related to male or female characteristics [117] (usually chromosomal differences are present as well). The same method is simple to achieve in Evolutionary Algorithms during reproduction, by inheritance of sex-determination genes. Alternatively, approaches that bend the process to meet mathematical or engineering goals can be introduced. For instance, it may be assumed that each reproductive step always produces a male and a female, or two-step sex determination can be assumed. In that case, on a first step, all offspring are created, and on a second step gender is determined to meet certain population criteria (ex: fittest half are female and the remaining are male). In akin approaches, gender is fixed for the active period of each individual or changed at well established periods. As a side effect, it implies the partitioning of the population into two distinct groups.

Perhaps more interestingly, individuals may act as simultaneous hermaphrodites [22]. Taken for granted that this choice requires no additional energy or other costs, and by placing adequate restrictions to self-fertilization, such a gender system can produce interesting dynamics. In that scenario, gender is no longer determined at any point, giving each individual the opportunity to be selected either as a female or as a male and temporarily act accordingly. From a gene level perspective, it would mean that the whole gene pool would be available for both selection processes rather than being partitioned, allowing the expression of each gender as appropriate. For each individual and for the system as a whole, such an approach imposes no additional effort, bringing the advantage of relying on less assumptions on how and when to determine each individual's gender.

Independently of which individuals are available for selection as females or males, there's always the need to establish the means by which they are selected. Once again, there are distinctive views that can be adopted. For instance, one may assume that all females are likely to have a chance at reproducing and make it so that every individual available as a female reproduces once. On the other hand, such an assumption puts all females at an equal level, whereas, as previously discussed, variance is likely to give fitter females advantageous positions towards accessing males. For that reason, traditional approaches may be suitable for allowing stronger females a higher chance of producing offspring in their lifetime. Male selection can be a bit more complex though, specially considering male competition and Mate Choice. Similarly to females, an approach may put all males as available mating candidates for each selected female. Alternatively, Natural Selection may be applied to make the fittest ones available more often than others. Curiously, fitness based approaches may also be suitable to mimic male competition (ex: tournament between males to determine which one has access to the female). For that purpose, instead of using raw fitness as a comparison metric, better suited metrics for the purpose may be considered to determine inner-gender competitive advantages, although that is likely to require new assumptions to be included.

Carefully reasoning these choices can be extremely important and may result on different behaviours within Evolutionary Algorithms. Gender determination and the operators actively selecting for each role will impact inner-population dynamics in various ways. Even Natural Selection may be in some way rethought, since on top of its previous role, its interactions with Sexual Selection will be determining. For instance, the stricter selection of females is, the more cryptic they will be on males, in the sense that only a few preferences are taken into consideration, possibly favoring a small subset of males. Over time self-reinforcement is likely to spread such preferences into the whole population. Following the same idea, the number of male mating candidates as well as the pressure put in selecting each of them (considered both Natural Selection and male competition) can influence the ability of less fit but potentially attractive individuals to contribute to reproduction. In short, balancing selection pressures is sure to have an important role in designing Mate Choice operators. The task may be challenging, depending on each problem and goals. If hermaphrodite models are considered, then all individuals may be under the pressure of all forces during the same generation, in turns depending on the selection step taking place. That scenario should be considered when establishing assumptions on the aforementioned balance.

At the point where there's a selected female and a set of male mating candidates, many strategies may be applied for the female to select its mating partner from among available candidates. In order to do so, females shall access bits of information regarding each mating candidate and give preference to those who best meet their preferences. What information is displayed by males and accessible by females shall be regulated by the operator's assumptions. In the end, such assumptions will determine the rules of Mate Choice. For instance, assumptions may establish that preference is given for a certain phenotypic characteristic, or for proficiency on a certain tasks. Also, by adopting a more goal oriented or engineering view, information access may not be solely phenotypical (such as expected in nature) but females may access information on specific locus, genotypical digests, genealogical or other potentially useful information. Similarly to other Genetic Models, preference may emerge through evolution, in any direction, under the rules set by assumptions, potentially taking Fisherian or Wallacean roles, depending on their connection with individual fitness. In previous models, there has usually been a direct viability cost associated with the display or ornamentation. In Evolutionary Algorithms, at times that cost results indirectly, through the genetic impact of developing traits for attractiveness rather than for fitness, instead of being imposed directly through the assumptions regarding their expression.

In summary, designing a Mate Choice operator involves a few critical steps: i) how to build female and male selection pools; ii) how to select each female from the corresponding pool; iii) how to select a set of mating candidates from the available pool; iv) how to evaluate each male candidate following the active females preferences; v) how to select the best candidate for reproduction. Altogether, these steps are drastically different from a traditional fitness-based selection method. Individually, how each step is setup will impact the workings of the operator, and should therefore be done in accordance with the design assumptions and needs. Furthermore, the global design can influence the balance between Natural and Sexual Selection, through their interaction means. Particularly of relevance are the assumptions on Mate Choice, or how to evaluate and choose the most appropriate mating partner, following a female's preference. It could be said that those assumptions are the major player in the strategy. As a result of applying a Mate Choice operator, behavioral changes should be expected: i) the reproductive success of individuals is determined by both their survival ability and attractiveness; ii) the mating preferences of individuals will determine which candidates are good matches and are more likely to pass on their genes. The process changes from being a struggle for producing fit offspring to a competition involving fitness and attractiveness, where mating preferences have a ruling role.

3.2.3 Complex Attractiveness Evaluation

The few-locus models previously discussed rely on the expression of a single feature and the corresponding preference. While, for the purpose of studying the ability of Fisherian and Wallacean processes to persist in stability, such constraints are sufficient and lead to a strong performance, they make no contribution to what may happen when more than one conspicuous trait is present. Species flaunting more than one ornament are however very common, which suggests evolutionary advantages under certain conditions. Modeling multiple preferences for Mate Choice in Evolutionary Algorithms can also represent opportunities, specially in scenarios where information can be accessed regarding multiple aforementioned characteristics on mating candidates. Miller and Todd [287] have pointed out that the development of appropriate models that can account for the interactions and processing of multiple components into an overall mate value is one of the major challenges of Mate Choice related research. Independently of the scope, how to model preference multicomponency and complexity, or in simpler terms, how to model multiple dimensions of preferences and how they may be processed together, through the impact that they may have on each other and globally in the process of Mate Choice, should be further discussed.

Multidimensional preferences

Having Kirkpatrick's model [157] as a base (for being the one involving less assumptions), by deduction, an extension to support the evaluation of multiple traits would simply imply replacing the trait locus with a vector of locus, one for each ornament. Similarly, a vector of preference locus would be used, each corresponding to an ornament. Females instead of either choosing partners randomly or for an ornament, may in this case choose for zero, one or for multiple ornaments. They do so according to their own preferences. Individual evaluation of each trait can be straightforward: if the female has a preference for a specific trait and if a mating candidate shows that trait, then the male should be favored in competition with others. All preferences considered, those males expressing a larger number of preferred traits should have relative advantages in Mate Choice. How to combine such individual evaluations of traits into a single mate value for a mating candidate can have deep impacts even if rather simple approaches are applied. For instance, an *AND* operator between female preferences and male trait vectors can produce a vector marking locus where both preference and ornaments are active. The number of hits can be used as a function for mate value. Alternatively, a *XNOR* operation would produce a vector marking locus where both preferences and ornaments are either active or inactive. In the latter case, there would be a benefit for males that don't express irrelevant ornaments. Other functions may be applied with little effort, for instance weighted functions that may deem the importance of each trait as unbalanced.

By moving away from binary representations and generalizing, these mating preferences can be seen as a position on the phenotypic space that represents an ideal mating partner. Independently of the number of dimensions, that position can be encoded as a set of coordinates, or as a vector. If similarity between this phenotypic position and mating candidates represents a likelihood of mating, then this measure can extend as a function defined over the whole phenotypic space, with the chances of reproduction being encoded as an additional dimension. In the end, the model uses $n+1$ dimensions to represent attractiveness (as a height) for each particular female. Miller and Todd have explored a closely related approach [199, 200, 201, 286, 287, 288]. They describe encoding preferences as cone-shaped probability-of-mating functions, where genes represent key parameters for that function. In their studies, each individual has its own sexual reference position, which can be determined in different ways: i) individual-relative preferences put the sexual reference position at the location of the individual's own phenotype; ii) parent relative preferences put it at the location of a parent's phenotype; iii) population relative preferences put it at the average location of all phenotypes in the population; iv) space-relative preferences put it in an absolute position in the phenotype space [200, 201, 288]. Given a sexual reference position, the peak of a probability-of-mating function can be determined in one of two ways: with non-directional preferences, the cone is centered at the sexual reference position [288]; with directional preferences, the cone is displaced a certain distance in a particular direction [200].

In order to encode this information, in addition to their phenotypic traits, individuals may genetically determine which sexual reference position to rely on (may also be set as a global assumption), and in case directional preferences are used, the direction is determined by n genes, one for each dimension, and one for distance. Together, those genes represent a mate preference vector, or displacement vector for the cone shaped probability-of-mating function. Moreover, an additional gene determines the width of the cone, or in other words, the radius of the probability-of-mating function which to some degree loosely models adaptive cryptic female choice. Over generations, both genetic material relative to an individual's own traits and its mating preferences are subject to change, evolving through selection pressure. If the whole population is considered, mating functions can easily be stacked, showing which regions of the phenotypic space are more attractive following Mate Choice preferences [200].

Miller and Todd's work adds to the discussion on multidimensional preferences by showing how functions can be encoded through their key parameters. Therefore, not only can ideal mating partners be encoded through their phenotypic position, thus supporting non-binary representations, but also strategies can be evolved. Experiments mostly focused on populations with neutral Natural Selection, meaning that individuals were only subjected to Mate Choice. There are however a few experiments where the relation between Natural and Sexual Selection is addressed to some extent. More on that topic will be covered ahead. It may be said that the initially described binary approach, while simple in design, supports multiple dimensions of preferences. If assumptions are mostly maintained, then the behavior is likely to remain closely similar to that of an unidimensional scenario, although possibly taking place concurrently on more than one dimension. The latter approach should also follow suit, while at the same time allowing further generalization towards real-valued representations and providing additional control on the behavior of the aggreation function that ties multidimensional preferences together.

On the other hand, preference complexity can't be said to be achieved by the approach. Unless preferences have an associated cost that can indirectly influence the successful perception of certain traits, which would be very unlikely in an Evolutionary Algorithm, then the processing of preferences and traits into a mate value can be seen as a simple aggregate of different stimuli. There is a strict independence in the expression of preferences and therefore in the interpretation of multiple ornaments. Such a model opposes the ideas discussed in Section 2.2.4, where it is suggested that preferences multicomponency is more than the sum of each component, and most likely much more complex than the linear combination of each part.

Gene Interactions in Preferences

The described model, as succinctly discussed above, supports multidimensional preferences but not preference complexity. In other words, the evaluation of each single trait is context free or in total absence of preference interactions. Despite its value, there is more to multi-preference evaluation than linearity [113]. Lerena [178] has explored the subject and described the issue using, among others, an illustrative example similar to the following: consider a species where males may express tails and crests as ornaments; with linear preferences, the contribution of each trait to an attractiveness value is blind to the presence of the other (displaying a crest should be more attractive than its absence and flaunting a tail should be more valuable than the opposite); with complex preferences, the context of all traits is relevant for the attractiveness value of each one (showing a crest may only be valuable if the tail is in good shape, and hold no value or even be repulsive if a well shaped tail can't be maintained). From a genetic perspective, the principle holds: the contribution of an allele to a female's preferences may be subject to context through gene interactions (such as epistasis [226]). In Evolutionary Algorithms, gene interactions and the resulting complexity are usually present, its significance in the representation and expression of mating preferences should come with no surprise.

There aren't many studies in the literature that focus on the artificial modeling of preference complexity, specially if filtered for optimization algorithms. Still, Lerena's study includes important contributions to the current discussion, although focusing on both Natural and Artificial Systems modeled under very specific assumptions: evolution is open ended (there's no Natural Selection applied on traits, or costs associated with preferences); cognitive and evaluation noise may be present in Natural System related experiments; preference mutation happens on a perception level; other common assumptions. These are arguably more appropriate for modeling Natural Systems [178] and have been adjusted in order to provide relevant knowledge in noise-free Artificial Systems. Restrictions are also made on preferences, with only two types (with different dimensionality or different complexity) evolving concurrently. In the end, insight is given regarding competition between different levels of complexity, while the interactions themselves are less relevant. It is argued that under Natural Selection, specific relations may be favored [178].

With that being said, Lerena suggests modeling preference complexity using NK-models [310] which are mathematical models suitable for representing landscapes of tunable size and ruggedness. The appeal for using NK-preferences is therefore evident. The system is individual-based, so that each individual consists of the following two chromosomes: i) a binary vector of size M, determining which traits are expressed as ornaments; ii) a binary preferences vector of size N ($N \leq M$) ruling which traits are relevant for Mate Choice, and a NK-table establishing the value of each trait vector in the light of the preference vector. In a way, the preferences vector is alike to a sensory system or bias, whereas the NK-table determines, for every possible context, the contribution of each particular trait to a global attractiveness function).

In other words, the preferences vector determines the input to an evaluation system whose output is described by the NK-table. N will determine the number of dimensions, or components, while K will determine the degree of interaction between such components (the complexity). $K = 0$ corresponds to the previously described system where each component contributes linearly to the overall attractiveness value. By increasing K, the system allows the contribution of each trait to be dependent on a larger context (other traits). Gender may be determined randomly at birth [176], or a simultaneous hermaphrodites model may apply [178]. Initialization is stochastic on all parts of the representation and recombination takes place by interchanging chromosomes and not through intra-chromosomal changes. Mutation may affect both preference and trait vectors but NK-tables are immutable and are passed on through inheritance. When evaluating a potential mating partner, each locus in the female's preference vector matches a trait locus. Females access the target male's trait-vector, XOR it with their own preferences vector, thus producing a comparison vector that encodes the context under which the male is being evaluated. The NK-table is used to determine the female's attractiveness for that particular male.

Lerena's modeling of preferences is particularly interesting for the control that it gives over dimensions and complexity. The system allows for the modeling of a NK-landscape whose size and ruggedness can be easily controlled by the the tuning of two parameters, N and K. As individuals are only subject to Sexual Selection, their reproductive success and the evolutionary process are influenced mostly by the degree of interaction between preferences or the ruggedness of the NK-landscape induced by mating preferences. The assumptions on the system and the NK-landscape make it so that the NK-tables set the underlying laws of evolution, by specifying the evaluation function for Mate Choice. It's relevant to recall that such rules compete for inheritance through the production of attractive sons, but that their competition in the genetic pool is limited, as their are not subject to inner recombination. They are large blocks of immutable genetic code. In the end, results in Artificial Systems point to larger preference dimensionality, and a smaller number of interactions, having a competitive edge.

Evaluation Functions for Mate Choice

Viewing mate choice as a function, independently of its representation (NK-model or otherwise) can be quite useful and contributing. While in previously discussed examples Mate Choice is pretty much an instinctive reply to one stimuli or cumulative stimuli, functions have a number of implications. Firstly, there is a stricter definition of each stage of the processes of evaluation and choice. When evaluating a particular male: i) the female's sensory system assesses certain traits, building an evaluation context; ii) the stimuli coming from each sense is processed on that context through possibly complex preference interactions that combine stimuli; iii) an overall attractiveness value is computed. Having evaluated multiple males, comparisons can be made and choice may result from such comparisons, or by using a threshold. Secondly, from an engineering perspective, there's a clearer view of Mate Choice as a procedure or operator, implying an input that is processed to produce an output. Thirdly, assumptions can be made distinctively for each stage rather than globally, which may prove useful, simpler, and more detailed.

Focusing on sensory systems first, Lerena's model [178] relies on an individual-based encoding which distinguishes itself from previous static systems. While static systems assume that the whole population (or at least females) shares the same sensors, and that they remain immutable through the evolution process, dynamic systems allow for a bigger flexibility. Variation among individuals may help account for those with sensory deficits (blindness etc.), or biasing of some sensors over others. Also, their continuous adaptation may reflect more complex phenomena such as the discarding of non-discriminating sensors. At a first analysis, such diversity may seem counterproductive. Arguably, not making use of as many sensors as possible may represent an undesirable handicap, however, that may not be so. Variation and adaptation introduce an important competition among sensor biases, allowing for the selection of relevant ones, the reduction of context size by discarding non-relevant ones as well as adjusting to population conditions. From an optimization perspective, self-adaptive individual-based sensors are sure to be useful for the above reasons and more. Establishing proper evaluation contexts for Mate Choice can be a demanding task. Individuals should sense relevant and informative knowledge on candidate partners, which may often be difficult to determine. Researchers sometimes have to rely on their knowledge and may find it useful to round up a set of potentially relevant features, leaving it for the evolutionary process to select through competition which are more contributing or provide evolutionary advantage.

Processing the stimuli coming from multiple sensors into an attractiveness value is for sure the core of designing a Mate Choice operator. After all, independently of the dimensions or what stimuli are being sensed, this step determines the ruling laws of Mate Choice, or how such stimuli are processed together. On an alternative perspective, these rules map into a preferences landscape, with interaction complexity playing a role in determining the ruggedness of that landscape. In Lerena's model [178], static NK-tables are used, which for each context record the weight, or contribution, that each particular ornament has on a global aggregation function. For the purpose of studying complexity and dimensions, keeping interactions as static weighted functions makes sense for comparison purposes, however, such assumptions are somewhat limiting. After all, recombination and mutation are only allowed on sensory systems, while their evaluation mechanism is copied. The drifting process along the preferences landscaped is therefore limited, on the one hand benefiting from reshaping in the preferences vectors but on the other hand being bounded to initial conditions of the NK-tables. Of course, individual-level adaptive NK-tables are possible, either by mapping the tables to a vector representation or by applying tailored recombination operators. Table sizes may present a challenge but nonetheless, such an approach may be fruitful, independently of the application being a Natural/Artificial System, or an optimization-focused Evolutionary Algorithm.

However, even if relying on adaptive laws, NK-models impose a few assumptions worth discussing. For instance, even if weights fall under evolutionary pressure, the attractiveness value is always the result of an aggregation function. Different mathematical functions may be applied, from very simple to very complex, but in the end they remain static and limited. Their role is enormous as they regulate explicitly how preferences are allowed to interact. The impact of choosing an appropriate function is certainly meaningful. Additionally, contexts are limited to qualitative ornamentation, or in other words, to traits either being expressed or not. However, tail length, color brightness among others are quantitative traits, whose expression can grow or shrink or evolve in any direction to a certain extent. While contexts where ornament expression is binary may be suitable for studying complexity and dimensions, they impose a strong limitation. For the purpose of applying Mate Choice to Evolutionary Algorithms, the two discussed points may hold particular significance. They impose, firstly, that information assessed as ornaments is qualitative rather than quantitative and, secondly, that the use of that information is subject to a predefined process, which may be limiting to inner-population competition.

The discussion above focused mostly on Lerena's model [178], however it can be easily expanded to many models of Mate Choice. Ideally, such limitations should be kept to a minimum, both for the purpose of modeling Mate Choice as an unbounded mechanism but also for a more complete search of preferences and phenotypic landscapes. Focusing on viewing Mate Choice for Evolutionary Algorithms as a procedure is helpful for the purpose and can result in important contributions. A Mate Choice approach where evaluation is coded as a hardwired computation procedure, where programming instructions are followed step by step until an output is produced is viable. That code would determine the underlying laws of Mate Choice, defining what type of individual to give preference to under certain contexts, provided as input. Arguably, given that the operations taking place are well defined and deal with multiple data types, then the qualitative and quantitative character of Mate Choice can be modeled simultaneously. Moreover, the operations taking place within a procedure need not be limited to weighted functions, logical operators or any other type, given that they respect the data types involved. Regarding adaptability and the inner workings of the procedure, there are many alternatives within Evolutionary Algorithms that support the encoding and evolution of code blocks.

Following this reasoning, techniques for the encoding of computer programs as genotypes are suitable choices for the representation and evolution of mating preferences as evaluation functions. Genetic Programming [165] (different variants are available such as Linear Genetic Programming [32], Multi Expression Programming [214], or Cartesian Genetic Programming [202]), Gene Expression Programming [44] or Grammatical Evolution [246], are some of the potential candidates for such a task. As a rule of thumb, such representations require only the definition of a terminal (representing sensors) and non-terminal (acting as interactions) sets. Based on such sets, initialization mechanisms support the generation of evaluation functions that are able to evolve as part of the genotypes of each individual through the application of traditional operators. Overall, such representations can have plenty of benefits, while at the same time relying on less assumptions. Such assumptions are mostly related to what terminals to include, their data types and how to assess their value, and what non-terminals to allow, how they deal with particular data types and making sure that they produce feasible chromosomes, usable for calculating an attractiveness value that is meaningful for comparisons between mating candidates.

As an overview, modeling Mate Choice as a procedure can contribute with the following benefits: i) determining a set of potential qualitative and quantitative sensors as terminals; ii) allowing through initialization and reproduction the emulation of several phenomena such as the activation of multiple sensors simultaneously, or preference preexistence and dormancy; iii) determining a set of potentially useful operators for the representation of genetic interactions on a preferences level; iv) emulating multicomponency and gene interactions through the role of operators; v) representing multiple dimensions as well as different levels of complexity on an individual level; vi) allowing for the evolution, through inheritance and traditional operators, of both dimensions and complexity; vii) supporting the evolution of meaningful interactions between sensors in nontrivial ways; viii) accounting for the representation and adaptation of both Wallacean and Fisherian preferences side-by-side as a generic model. As final remarks on the subject, it's relevant to point out that the evolution of Mate Choice through evaluation functions is bounded by the terminal and non-terminal sets. Also, it may be difficult to interpreter and understand complex preferences, even if they could be studied in isolation within a particular evaluation context, or studied through their impact on male traits. Moreover, assessing the utility of certain traits can also be difficult, and thus distinguishing between choice for good-sense or for good-taste can be challenging.

3.3 Effects of Adaptive Mate Choice

The impacts of Mate Choice on Natural Systems have been thoroughly discussed in the previous chapter. So far on the current chapter, how to model Mate Choice has been extensively introduced, a discussion that is probably relevant both for the purpose of developing Natural/Artificial Systems and Evolutionary Algorithms. Starting with very simple setups, which have nonetheless proven to be relevant for various reasons, means to model complex, multidimensional mating preferences have been discussed. In addition, a view of Mate Choice as computational procedures has been discussed as

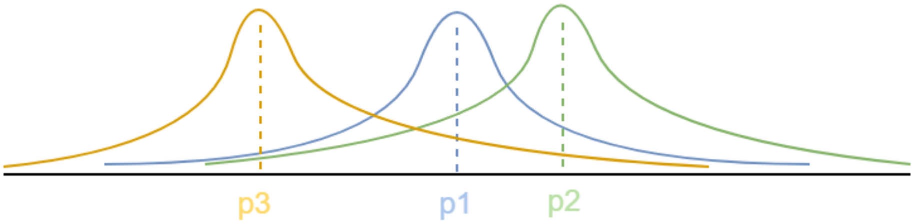

Figure 3.5: Illustration of three individual mating preferences in a multidimensional system. Each color corresponds to a different dimension and p to each dimension's point of most attractiveness.

an approach with good overall potential. Despite the discussion in the context of building goal-oriented Evolutionary Algorithms, the question of whether or not to introduce Mate Choice as a selection process remains to be fully answered.

It may be too soon to answer this question with confidence, and the answer may be all but straightforward. From a purely theoretical perspective it definitely makes sense. One of the most appealing features of Evolutionary Algorithms is their ability to discover solutions for optimization problems while requiring little problem-specific knowledge or interaction from users. Still, it's often found that problem-specific methods (although usually costly to develop) add value to the algorithm. Adaptive Mate Choice may be seen as a means to evolve selection methods that profit from problem-specific knowledge while putting much less strain on manual development. In more detail, mating preferences may be seen as adaptive heuristics that improve selection by continuously incorporating knowledge on the search process, by means of self-adaptation. Through that knowledge, adaptive mating preferences are able to hold information on the fitness landscape and, through achievements or misadventures (much like any other trait subject to evolution) help guide future adaptations.

Such a behavior is likely to bring forth benefits, as it gives the algorithm a selection mechanism capable of adapting to particular scenarios. From a more practical point of view, the overhead may or may not be worth it. Reaching a conclusion is difficult, however, from the perspective of Evolutionary Algorithms as a process of search and optimization, it's relevant to take a closer look at how Mate Choice can impact evolution through the adaptive phenotypic landscape as well as better assess the intertwined roles of Sexual Selection and Natural Selection. In the following subsections, effects on the search process of an Evolutionary Algorithm and potential advantages brought by Mate Choice are going to be discussed.

3.3.1 Walking the Search Space

Analysis of phenotypic landscape (also known as adaptive landscape or fitness landscape) has long been a useful exercise for better understanding the workings of Evolutionary Algorithms. On a typical scenario, the landscape is established by external factors, mostly by the nature of the optimization problem being tackled, and simply represents the search space which the algorithm has to explore and exploit in its search for a potential solution. The means by which an algorithm walks that landscape can be very insightful for multiple ends, including understanding the impact of specific operators. The introduction and studying of Mate Choice can also benefit from such an analysis, in a way to sum and illustrate what may be expected from integrating self-adaptive mating preferences. Similarly to other self-adaptive approaches, an intermediate landscape, which has sometimes been referred as preferences landscape [200], will be used as a tool for a simpler and phased analysis. Moreover, in order to ease the connection between the effects of Natural and Sexual Selection, a landscape of reproductive success will also be used as an illustrative tool. The following subsections will cover this analysis step by step and offer insight of potential impacts of Mate Choice on the algorithm's adaptive walk through the search space.

Preferences Landscape

Multidimensional landscapes have always proven challenging to visualize, requiring some type of transformation in order to fit them in a number of dimensions appropriate for drawing. For the upcoming discussion, such visualizations were kept as simple as possible through a number of plots. In those plots, the y axis represents the preference strength, or measure of attractiveness. The x axis is shared by multiple dimensions, and color has been used to distinguish between such dimensions. With that being said, the x axis represents, for each dimension, the distribution of attractiveness among possible sensory signals (or trait expressions). Figure 3.5 shows such an example, where p_1, p_2 and p_3 represent each the point of most attractiveness for each preference on their respective dimension. As can be seen, Gaussian approximate functions have been used but for illustrative purposes only, whereas they may actually take any other format. Still, this choice perfectly serves its purpose on this section.

Figure 3.5, representing the mating preferences of a single individual, shows a rather clean example, where each preference is well organized around a single peak, and is assessed in strict independence from other preferences as well as from the current state of the population. Still, if they are pictured in their full multidimensional character, then the preferences landscape is far from smooth, in fact it can be rather irregular, specially as the number of dimensions increases. If the mating preferences of a whole population are considered at the same time, then the effect is largely increased, as all preferences are overlapped in a population-wide landscape that is potentially highly irregular. In a simple linear scenario, for each preference dimension, the overall attractiveness distribution is the result of summing the heights of the preference functions of all females, producing one or multiple basins of attractiveness through the aggregate dimension landscape. Over the multidimensional space, this landscape will take a rough character and will have an important role in reproductive success. After all, much like within a fitness landscape, individuals that, through their features, are placed near peaks in the landscape will be favored by Mate Choice more often and thus will have a reproductive advantage.

The example above works for all purposes like a static fitness landscape, and much like such landscapes its tortuousness can be increased. For instance, in each dimension, preferences may express different functions, with multiple peaks or even tending to infinity in the limit. However, by moving away from that basic example, important differences will arise, which make the behavior of a preferences landscape quite singular. Firstly, its important to remember that mating preferences are genetically encoded and thus every individual in the population is likely to have its own landscape, so that the aggregate is likely to look rather chaotic (disregarding potential runaway processes or genetic takeover at this point). Moreover, preferences are subject to descent with modification and possibly genetic drift, so that when an individual produces offspring, their mating preferences may be slightly different, and those of its grandchildren may be even further different. The effect can be visualized in Figure 3.6. Consider this

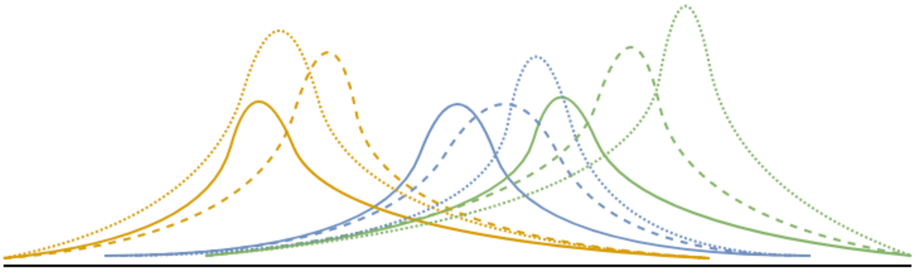

Figure 3.6: Illustration of mating preferences passed on from parent to offspring over generations. First generation - solid lines; second generation - dashed lines; third generation - dotted lines.

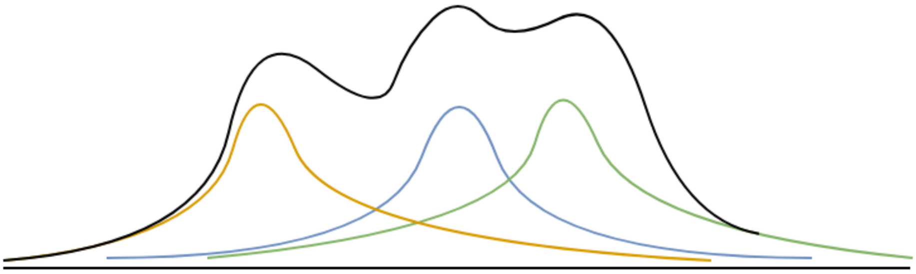

Figure 3.7: Illustration of a linear aggregate of multiple mating preferences.

effect on an aggregate population-level landscape and unlike the stability of a fitness landscape, the preference landscape is more like a tempestuous sea where waves come and go, higher or lower, over time [200].

Given that Evolutionary Algorithms seldom account for perception or evaluation noise, the way that each particular trait is perceived by individuals is deterministic, meaning that all individuals share the same perception capabilities or inputs, and that they remain the same. In a way, it may not make sense to prevent individuals to access informative cues on potential mating partners. However, in what regards their contribution to the mating value or the way that each trait influences the context under which each other is evaluated, the story may not be so simple. Interactions between mating preferences have been previously discussed, and their impact on search in the preferences landscape is quite meaningful. For comparisons purposes, Figure 3.7 shows an example with linear interactions. The figure shows a cut of the landscape where $p_1 = p_2 = p_3$, so that for each point of the x axis, the aggregate attractiveness value is the sum of the height of the curves shown. The result is drawn in black and shows the global attractiveness landscape that individuals are to adapt to through Mate Choice, on a particular generation. Clearly, in this particular scenario, mating candidates that are more capable of abiding to p_1 or p_2 (or both), are going to attain a higher reproductive success.

In the example shown in Figure 3.7, Mate Choice is going to push traits into meeting all three of the expressed preferences and attempt to maximize the reproductive success associated with those traits. If for some reason, the traits have to be expressed in a very similar fashion ($p_1 = p_2 = p_3$), then it is likely also that Mate Choice is going

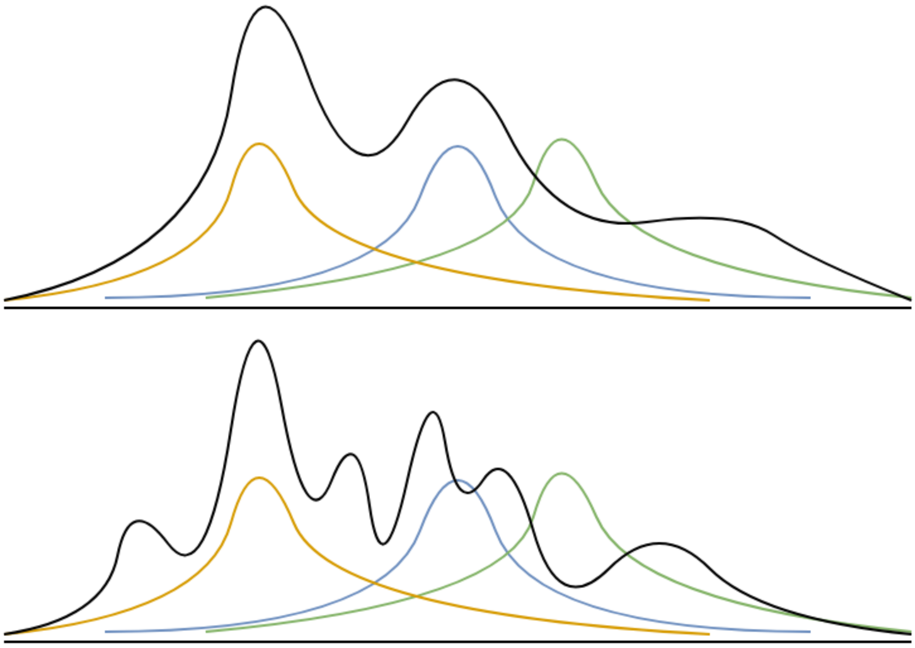

Figure 3.8: Illustration of a non-linear aggregate of multiple mating preferences. Top: lower complexity. Bottom: higher complexity

to push p_1 and p_2 preferentially for a higher profit, but when preference interactions are taken into consideration, the result may be much different. Figure 3.8 shows two illustrative examples of what may happen. Focusing on the top plot, and comparing it with the one in Figure 3.7, it's noticeable how the complex evaluation of mating candidates can deeply affect the expected reproductive value of the combined traits. In the presented example, p_3 which would normally have a lower contribution to the mating value ends up being very important while p_2 is neutral or borderline detrimental.

These bidirectional influences that preferences have on each other can have varying impacts on the preferences landscape. Firstly, genetically encoded preferences can change over time and, consequently, as evaluation contexts change, so does the mating value of a mating candidate. This is not news, however, what changes with complex preference interactions is that changes may be much more drastic: small, smooth changes on a particular trait or preference can result on significant changes between levels of attractiveness. This effect becomes more impactful as the complexity level rises, causing the landscape to become more rugged, as seen in the bottom plot in Figure 3.8. In a way, it can be said that complexity allows for a tunneling effect between levels of attractiveness that would otherwise be distant. Secondly, depending on the approach, preference interactions may be established as assumptions, initialized but kept static, or be subjected to evolution. If mating preferences are being modeled as procedures, then not only are interactions subject to evolution, but also how they are organized, ordered, and even the complexity level is evolving. This will have an effect on the constantly changing preferences landscape. Figure 3.9 shows a possible illustration of what it may look like over time. In comparison to the previous metaphor, the adaptive preferences landscape is likely to look as the perfect storm, with ever chang-

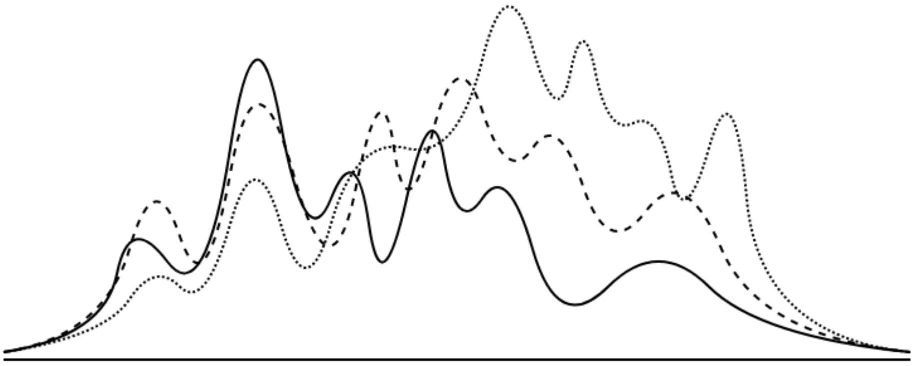

Figure 3.9: Illustration of attractiveness value resulting from complex interactions, passed on from parents to offspring

ing waves of varying amplitudes and lengths, moving on all directions with very little predictability.

Dimensions, Complexity and Contrast

The roles of component interactions in Mate Choice have been previously discussed to some extent, but further analysis can contribute to understanding their impact on the search process and to the preferences landscape specifically. Firstly, its important to understand that in a scenario where both preference dimensions and complex interactions are encoded in the genotype, such as when evolving Mate Choice functions, these characteristics are under evolutionary pressure as well. In more detail, given that there's some variation within the genetic pool of evolving mate evaluation functions, different dimension levels as well as context sizes and complexity levels will compete for fixation just as much as the preference interactions themselves. So, Sexual Selection related processes such as Fisherian runaway, sympatric speciation, and others, are dependent on such competition, whose effects are important to address and have previously been introduced by Lerena [178].

Expanding on the previous discussion on landscape ruggedness, let's consider the simple scenario of Figure 3.7, where complexity is minimum, and two mating candidates being evaluated by a female relying on the represented function. If these candidates are very close neighbors in the trait-space, their evaluation will show a high correlation, or in other words, their mate value will be very similar due to the smooth slopes in the preferences landscape. Arguably, increasing preference dimensions can contribute to individuals having an increased chance of perceiving differences among phenotypical neighboring mating candidates, simply by having more means for comparison [204]. On an Evolutionary Algorithm, adding to preference dimensions should however impose some evolutionary costs. Alternatively, complexity can play a part in providing higher contrast between closely related individuals, but not without consequences that need to be kept in mind.

It's been discussed that increasing component interaction in mate evaluation functions increases the ruggedness of its landscape, so that a higher number of interactions produce not only more peaks but also makes them more steep. As a consequence, when using non-linear preferences, comparing the evaluation of a particular trait in two competing mating candidates, on the same context, can show a higher difference. If the size of that context increases, so will the difference between mate values for that trait. If two competing mating candidates are up for comparison, and if they share most of their traits but have a small localized difference, mating preferences of higher complexity are less likely to attribute similar attractiveness to those traits. Overall, this should allow for a better contrast between otherwise neighboring (phenotypically similar) individuals. In a population-level view, this can have strong implications. If for instance a population is grouped in a particular trait-neighborhood, with little variation, complex preference landscapes can help increase the range of potential reproductive value for each individual.

Intuitively, based on this discussion, one may argue that in a population where there's variation between complexity levels, higher ones should be favored for a higher return in contrast. However, that benefit is highly dependent on the conditions presented by the evolving population. High ruggedness can surely evolve and spread through self-reinforcement, specially when trait variation is low, which would further increase the benefits that individuals with complex preferences have over those with simpler ones. However, increasing complexity indefinitely may add little value: while moving from low to high complexity may result in large improvements in contrast, moving from high to very high levels of complexity will provide only small improvements, which come with little overall benefit. Moreover, as variation between traits increases, the gap between high and low complexity is less evident. With individuals spreading over a larger range of the phenotypic landscape, less complex preferences are more likely to rate mate values appropriately, with little improvements coming from increasing the contrast.

Therefore, higher complexity levels may prove beneficial for distinguishing between individuals in populations where there's low variation on one or more traits, however, those benefits are less evident on other scenarios. Moving from a smooth landscape to a rugged one can often bring overall gain but only to a certain balance, whereas further adding ruggedness to a landscape can have undesirable implications such as choice inconsistency, which is a challenge for self-reinforcement. Two factors account for such a scenario. Firstly, as discussed previously, higher complexity will result in a less correlated landscape, meaning that small changes in traits can result in very large changes on attractiveness value. This is specially relevant if evaluation context is brought up. Secondly, recombination between highly complex preferences is more likely to be destructive, making it difficult to pass on preferences. These two factors make consistent choice difficult to maintain, which may for instance make it difficult over a few generations, to rank a set of mating candidates in the same way. Taking trait and preference mutation into consideration, the potential for such scenarios increases.

Lower complexity levels face less risks of inconsistent choice, which is likely to give them an edge in competition. So on the one hand, higher complexity may bring benefits on certain scenarios through higher contrast and therefore propagate through self-reinforcement. On the other hand, hindering choice consistency can make that difficult, allowing for simpler preferences to propagate and gain momentum unless there's a specific need for higher contrast between mating candidates. Arguably, after initialization of an Evolutionary Algorithm, assuming that the population has diversity and is able to maintain it for a few generations, conditions may in general be better for simpler Mate Choice mechanisms to propagate, possibly through Fisherian self-reinforcement. Moreover, this effect is likely to last longer in small complexity scenarios due to the larger size of the basins in the preference landscape, which may be beneficial for competition [178]. Basin size and the consequent larger number of Fisherian steps is important because as soon as a preference and the related trait is fixated, its relative evolutionary advantage burns out.

From the perspective of designing Evolutionary Algorithms, competition within dimension and complexity levels can bring various benefits. As it may seem, the competition is fixed towards takeover from less complex preferences, but complexity can still play an important role, specially if its given a chance to emerge (possibly through mutation) at times where less complexity can hinder the capacity of females to contrast between neighboring individuals in the trait-space. At that point, they may result in a runaway process. The relation between complexity and consistent choice is at the bottom of its behavior, and so it is also very influenced by recombination and mutation, which on the one hand can truly have a larger effect on highly complex mating preferences but can for sure also present opportunities. Higher complexity has been shown to emerge in situations where there is evaluation noise, or that determinism can't be assured in the evaluation of traits. In Evolutionary Algorithms that may sometimes be significant. Of course, the forces described in this discussion on contrast are only a part of what effects the whole dimensionality and complexity of preferences.

Phenotypic Landscape

Similarly to preferences landscapes, phenotypic landscapes can often be multidimensional. That depends on the problem being targeted and the corresponding representation. For the purpose of simplification, the following discussion will focus on unidimensional scenarios, without loss of generalization, and multidimensionality will be discussed only when relevant. In those cases, the visualization approach followed in the plots for preference landscapes also applies. In summary, traits or preferences in multiple dimensions will be represented on a common x axis and the y axis will represent strength through height in each respective dimension. While in this case the inner-workings of multiple preferences are not in focus, color will be used to distinguish between forces, yellow corresponding to fitness (Natural Selection) and red corresponding to attractiveness (Mate Choice).

The interplay between Natural and Sexual forces is challenging to understand, specially when their relation with phenotypes is taken into account. Figure 3.10 shows a straightforward scenario where fitness, preferences, and traits are well defined on one dimension, and their distributions are also well delimited. The scenario shows therefore a landscape where maximum fitness can be achieved by the trait taking value f, and the return diminishes as the trait distances itself from f. The presence of that trait in the population is distributed around t at that particular point in the evolution process, and hasn't been fixated so that there is variation, loosely represented by w. Finally, the population has developed a mating preference for individuals whose trait is distributed around p, which in this scenario makes the preference to be pointing the trait in the opposite direction from fitness.

As Figure 3.10 shows, selection has a double action on the distribution of traits. Survival will give advantage to individuals whose trait is closer to f thus drifting the distribution closer. Mate Choice on the other hand will favour individuals whose trait are closer to p, making the distribution shift again in its direction. In this case, as fitness has a stronger pull than attractiveness, in the end t will move towards f. However, as survival cuts off those individuals who are not fit enough and Mate Choice cuts off those who are not attractive enough, w is bound to reduce generation after generation. If at some point $w = 0$, then the trait has been fixated in the population and, for being

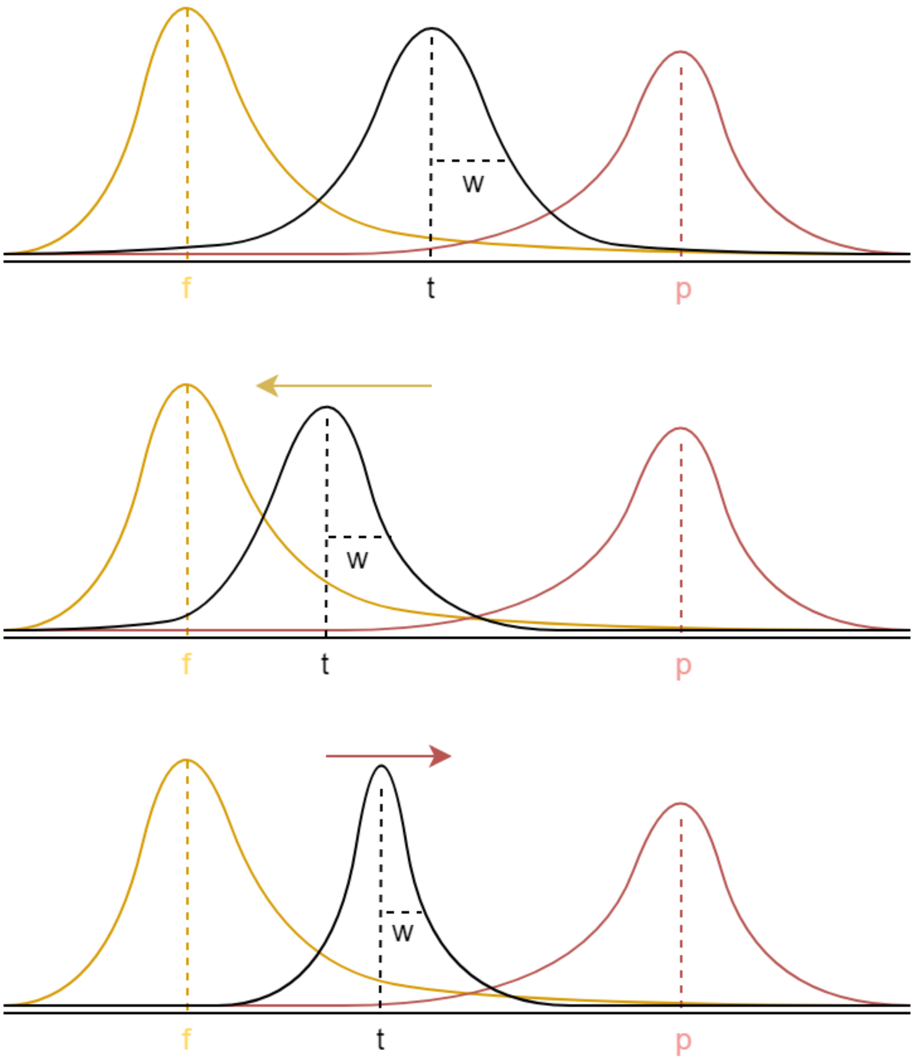

Figure 3.10: Example of interaction between Natural and Sexual Selection forces over a trait.

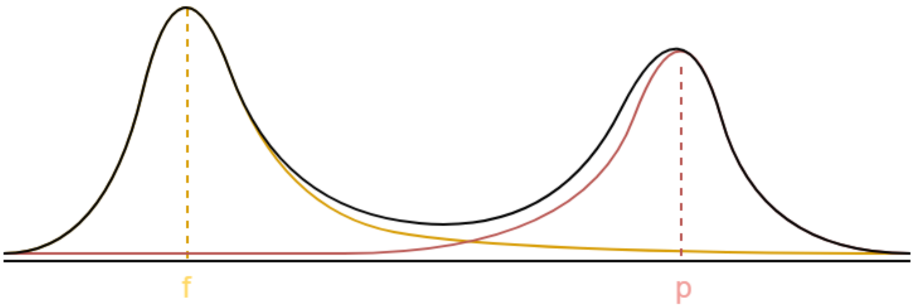

Figure 3.11: Aggregation of Natural and Sexual Selection forces.

no longer a distinguishing factor, it's role in selection is no longer significant. The fixated trait t in this case isn't either on f nor p, but on an equilibrium point that can only change in the presence of variation in traits, preferences, or fitness.

The model aims at demonstrating the effects of preferences and survival on the distribution of traits, and for that purpose assumes that there's an established interlink between the existing distribution of traits and preferences. The meaning of this assumption is that all females share a fairly similar preference which remains static during evolution. If that was not the case, then the behavior would be subject to the feedback loop between preferences and traits (making it less clear). If this assumption is removed from the model, various scenarios can emerge: i) the pull from natural selection may successfully fixate the trait at f, eventually fixating p as well; ii) p may slide quite fast toward t for favoring population density and the advantage of producing offspring that are within a popular part of the phenotypic space; p may develop enough strength through self-reinforcement to drag t and start a runaway process. There are many variables that determine what the outcome will be: i) the cost of developing a preference for that trait; ii) the initial distribution of the preference for that trait; iii) the initial distribution of that trait in the population; iv) the pressure of survival on that trait or the cost to maintain it.

Figure 3.11 combines in the same dimension the landscapes imposed by viability and attractiveness on a single trait. Together, they can be seen to form a reproductive landscape [201] that includes both pressure imposed by Natural Selection and Sexual Selection. Even if only non-complex traits and preferences are considered, this landscape can express a very different profile from each of its parts alone. It helps explain some movements in the phenotypic landscape that may seem unnatural from a fitness-based view, for instance downhill movement on a fitness landscape can actually be hill climbing on the combined reproductive landscape. This is made possible by the process described in Figure 3.10 alone, under the right conditions, and can have quite interesting results. For instance, consider a scenario where there's a second, higher fitness peak further right in the landscape. If the population is gathered around the original local optima, crossing the valley between peaks would be a very difficult task due to low-fitness individuals being unable to compete for reproduction. However, the self-reinforcement of mating preferences through inheritance can produce a self-imposed reproductive peak that empowers low-fitness individuals, allowing the population to travel the phenotypic landscape more freely. If at some point exploring individuals reach the second higher peak, they can pull the remaining of the population there through new competitive advantage and genealogy. In a way, a reproductive landscape can explain how

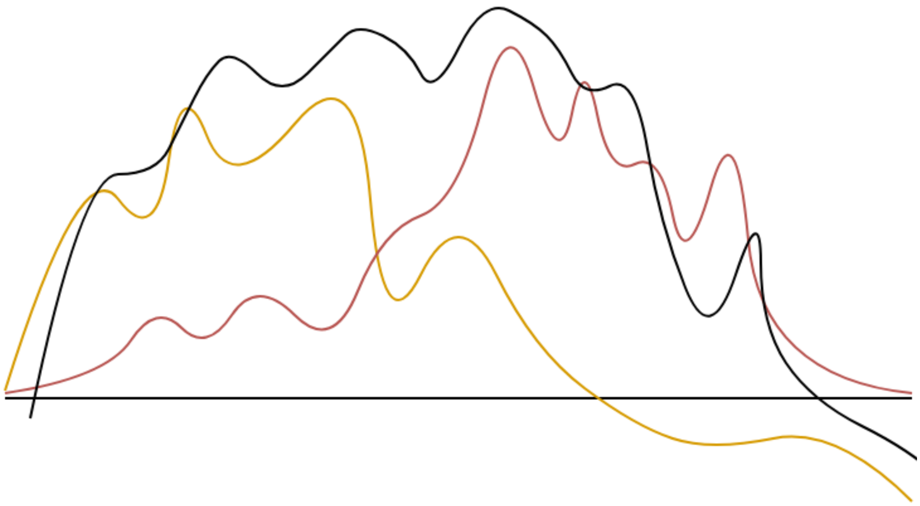

Figure 3.12: Aggregation of Natural and Sexual Selection forces, accounting for complexity.

Mate Choice allows for tunneling between peaks in a fitness landscape.

To further explore this tunneling effect, the roles of gender, as well as the interactions between evolving mate preferences and phenotypes need to be discussed. It has been previously discussed how Mate Choice can be modeled in Evolutionary Algorithms by applying different selection strategies for the selection of individuals for female and male roles. This distinction between selection mechanisms means that the reproductive landscape discussed above can be different for each gender. For instance, if females are selected using a fitness-based traditional operator, then in the scenario of Figure 3.11, they are bound to exploit the phenotypes around f. On the other hand, assuming that male mating candidates are selected randomly and compete based on attractiveness alone, then they have no force keeping them around f, but are rather compelled to try to match p which is imposed by female preference. This means that they are likely to be more able to wander, due to the adaptive nature of Mate Choice. In the end, males have a better chance of exploring the search space, finding new fitness peaks, and through reproduction pass on genes that are also inherited by females. These new phenotypic opportunities, if competitive, can pull the female population fast through the phenotypic space into new peaks.

This example suggests that females have an exploitative role while males have an exploratory one. While this can develop as a true behavior, it should be kept in mind that females have a say in exploration as well, either influencing males by being ever choosier, but also through the evolving evaluation functions, which encompasses sensory use, perception and choice. While not directly exploring the space of candidate solutions, they explore the preference landscape, which as demonstrated, as a direct impact on how search goes in the phenotypic landscape. If they happen to evolve a strategy that can better evaluate mating candidates, then through cheer competitive advantage, it is bound to propagate through both females and males, in this case allowing males to tunnel through the landscape into a place where they can contribute to the reproduction of better functioning females. The same principles apply to hermaphrodite

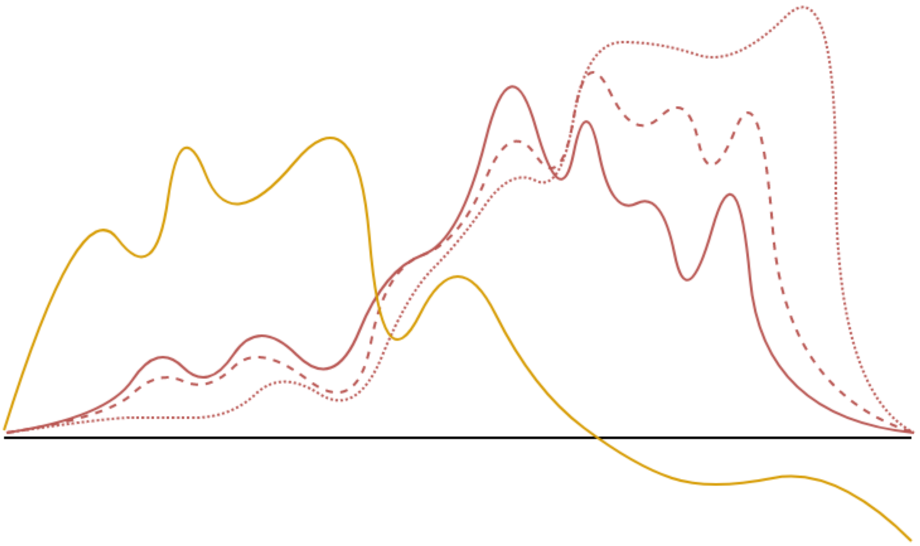

Figure 3.13: Illustration of the Evolution of Selection forces over time.

populations as well, where individuals are subject to the reproduction landscape as a whole. Interestingly, this may give way for the emergence of gender in populations with no external interference, as individuals climb to each peak, and preferences and traits fixate in the population.

Most of the relevant aspects of a walk through the phenotypic landscape have been addressed, in the scope of Mate Choice. However, so far they have been addressed on a single dimension with simple topographies. It is relevant therefore to expand the discussion into more complex scenarios. Figure 3.12 shows an example where non-linear multidimensional fitness and attractiveness functions have been mapped to share a single x axis. It should be noted that fitness and preferences don't necessarily exist on the same dimensions, however for simplification the model assumes that they depend on the same traits. The model shares most characteristics with previous illustrations but shows how complexity can make the behavior of an Evolutionary Algorithm with Mate Choice to be quite unpredictable. It shows also how it may be difficult to attribute the evolution of certain traits to Natural Selection or Sexual Selection.

For the purpose of the discussion, lets assume that a population is positioned on the left area of Figure 3.12. Hill climbing through Natural Selection can alone allow the population to reach the first local optima, possibly even escaping into the second local optima. However, unless there's some chance of mutation dragging the population further, the probability of reaching the global optima should be low. If Mate Choice is introduced, that reality may change considerably. Assuming for instance that as the population drifts from left to right in the phenotypic space of Figure 3.12, its individuals develop a mating preference for those that are most to the right (which gets self-reinforced in a Fisherian runaway process). This preference can maintain its momentum even if the whole population is within the second basin and continuously give preference to those individuals that are most to the right, even if they are less viable. At some point, if an individual escapes the basin, it will reach the global optima and pull the population with it. This effect is sometimes compared to that of a directional,

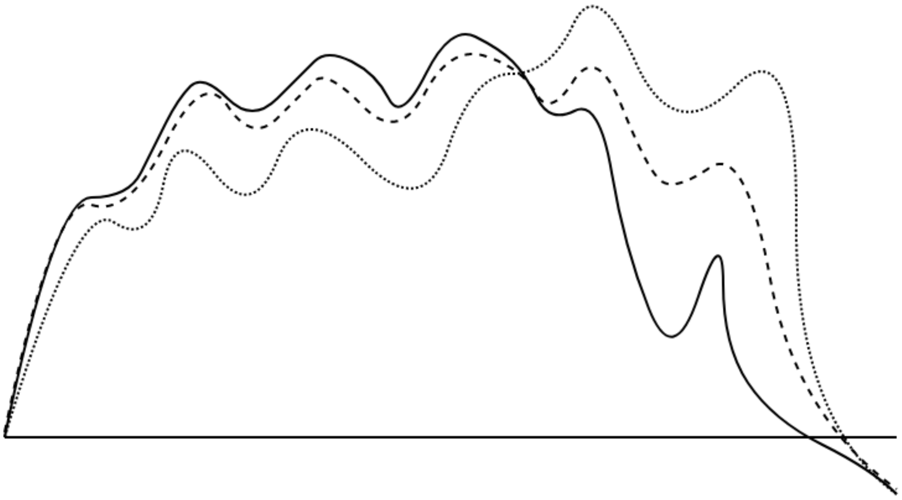

Figure 3.14: Illustration of reproductive success resulting from both Natural and Sexual Selection, passed on from parents to offspring

resistant, macro mutation, due to their similarities [199, 201]

It should be noted though that the process may not stop here, and the Fisherian process can continue to pull the population into an exaggeration of the features under sexual pressure, even if that pulls them away from global optima. In Figure 3.12 it is seen that the point of most success in the reproductive landscape doesn't share its location with the global optima but is further to the right. Also, Figure 3.13, shows the process of self-reinforcement, even to the point where preference is given to traits that are detrimental. Figure 3.14 shows how reproductive success can be associated with detrimental traits when Mate Choice takes preferences to extremes. In the end, even if there's a clear pull of Natural Selection pressure, Mate Choice can make the population drift through the phenotypic space impulsively [199, 201]. This drifting phenomena can sometimes pull the population toward global optima, but can also pull it into less rewarding parts of the search space. As shown by both figures, only Natural Selection can put a stop to this type of self-propelled exaggeration.

Its important to realize though that while a Fisherian runaway process evolving one or various traits may be stopping, another may be starting on other dimensions, on a different direction. Preferences and traits may be involved in more than one process at the same time. Also, the interlink between genes, the expression of preferences and of traits make such processes to be well intertwined (as well as with Natural Selection), which makes them able to influence each other. Powered by self-adaptive mating preferences, these effects can continuously push adaptive peaks in the reproductive landscape, in ways that can be perceived as chaotic. The storm-like character of the preferences landscape extends therefore to the reproductive landscape, potentially driving traits into multiple directions, sometimes in the same direction of Natural Selection, sometimes in opposite directions, sometimes changing directions during the evolutionary process. In all likelihood, and given means for variation in preferences and traits, populations are very unlikely to maintain stationary distributions in the search space, drifting towards their self-generated peaks [201]. These peaks are combined with those of Natural Selection, resulting in an adaptive landscape that can be unpredictable.

3.3.2 Potential Advantages of Mate Choice

As briefly discussed in the beginning of this chapter, Mate Choice can allow for Evolutionary Algorithms to self-adapt the way that individuals are selected and paired for reproduction, and as a product, take advantage from relevant knowledge regarding the search process that is progressively included in mating preferences. When discussing the effects of such a system, they come out as intricate, chaotic or anarchic. While its true that stochastic initialization can have a significant role, selection pressure sets structure and self-governance, in a way that is in fact organized, even if the resulting population dynamics are difficult to predict. The potential effects have been extensively discussed so far and several cues to potential advantages to the search process of Evolutionary Algorithms can be found scattered through that discussion. For the purpose of clarity, it makes sense to further present, in a more organized section, the most relevant potential advantages resulting from Mate Choice.

Miller and Todd have extensively discussed such potential advantages. While they rely on specific testing setups, it's reasonable to assume that such advantages can be generalized and found on many other systems that abide by the ground rules of self-adaptive Mate Choice. Miller [199] has succinctly listed them: i) increased accuracy when mapping from phenotype to fitness, therefore reducing the "error" caused by different forms of Natural Selection; ii) increasing the reproductive variance of populations by distinguishing between individuals with no survival-relevant (fitness) differences; iii) help populations escape from local optima through a directional stochastic process; iv) contribute to the emergence of complex innovations which may eventually contribute to fitness increasing; v) promote sympatric speciation, diversity and parallel evolutionary searches. Over the next few subsections, each will be briefly and individually discussed, relying mostly on Miller and Todd's studies.

Reducing the Error of Natural Selection

In a nutshell, an individual's evaluation by Natural Selection works by: i) mapping its genotype to a phenotype; ii) submitting that phenotype to evaluation on solving a target problem; iii) returning a proficiency value. For the purpose of selection, that value alone is used to compare the quality of genes between individuals. On simpler problems where the contribution of each gene can easily be mapped to fitness, or on target problems represented by smooth search landscapes, fitness alone can be very informative. However, when targeting tougher problems with complex genotype-phenotype mappings, scrutinizing the true value of each gene can be challenging. Of course, there are advantages in using deterministic fitness functions and there are ways to mitigate their problems by using fitness scaling or other methods. But in a way, when trying to assess the genetic quality associated with particular genes, fitness alone can be noisy, (for instance, by tagging genetically different individuals under the same, or closely similar, fitness values).

Fitness alone can be a very coarse grained measure of quality, too inaccurate for an efficient assessment of genetic quality. Mate Choice, can however contribute to reducing this effect, by selecting on phenotypic traits that while being different from those selected by Natural Selection, are correlated to fitness. Wallace's good sense Mate Choice extensively explores a direct linkage between fitness and ornamentation, but Fisherian good taste is rightfully capable of promoting the Sexual Selection of traits that are correlated to fitness as well. In nature, selection for symmetry might be a good example of a trait that correlates to fitness but is not a direct expression of aptitude

[201]. In Evolutionary Algorithms, the selection of ornamentation for their functional rather than beauty value can boost the potential for the emergence of more specific and informed selection strategies, specially if multiple information bits are available on mating candidates. In short, preference for aesthetic but useful criteria can help in the emergence of heuristics that guide evolution [199].

The process works by evolving Mate Choice strategies that reflect internally the potential consequences of reproducing with different kinds of mating candidates, so that their attractiveness match the expected fitness of the offspring. For instance, if a group of alleles has a beneficial effect on the fitness of an individual, and together influence the expression of an ornament, then mating preferences should evolve to favor that ornament. By doing so, not only can Mate Choice improve the precision involved in selection by particularly promoting those specific alleles, but it can also boost the evolution momentum in a certain direction. Moreover, while Natural Selection can penalize individuals not showing those alleles only if they have poor fitness (which may depend on other locus), Mate Choice can in turn penalize individuals on a more specific basis. The extent on which Mate Choice can do so is highly dependent on the assumptions of the system, such as what sensory systems are available and how signals can be combined. This process is of course linked to the previous discussion on contrasting between mating candidates and variation in reproductive success, and depends on choice consistency.

Increasing Contrast Between Similar Individuals

After the examination of Mate Choice as a means to reduce the error of evaluation functions, contrasting between similar individuals is a natural follow up topic, one that has been addressed previously when discussing the effects of Mate Choice, along with the main processes that make higher contrasting possible. Potential benefits come from the ability to convert small differences in male quality into large differences in reproductive success. This is achieved through a self-adaptive, flexible method for fitness scaling without the need for external assumptions. The evolving mating preferences rule how scaling is performed on an individual basis, which in turn are under evolutionary pressure to register appropriate differences in the ability of mating candidates. Mating preferences capable of contrasting between similar individuals in a way that give the resulting offspring an evolutionary advantage will themselves be inherited and benefit from that advantage to spread through the population.

As discussed, mating preferences should be able to incorporate information on the structure of the fitness landscape and hopefully provide better search means. Improving the ability to perceive differences between small fitness values should provide robustness and momentum, even when populations have began to converge to near-equal performance [201]. In those scenarios and in the absence of Mate Choice, small differences in fitness may be insufficient to successfully fuel evolutionary change. However, if individuals are allowed to do so, they certainly have the incentives to evolve means to be more selective or choosier and thus avoid population stagnation by promoting variance. Depending on the assumptions, on an extreme case where Natural Selection differences are minimum, preferences may discriminate based on differences in one locus alone. Such chances increase with the number of traits being evaluated, both assuming that differences in genes are perceptible in differences in traits, and granting the effects of complex evaluation.

Escaping Local Optima

In Evolutionary Algorithms, selection is the process that guides the population from lower to higher peaks in the fitness landscape while recombination and mutation are the engines that build and propose new candidate solutions for evaluation. Together, they explore the genetic pool (mutation may also introduce new genes), however their role is strongly subjected to the pressure of Natural Selection. Firstly, recombination can only access building blocks that are competitive as whole organisms and withstand selection, thus keeping genes that are immediately costly to the survival of individuals from contributing and potentially providing new better candidate solutions in the future. Secondly, while mutation can successfully introduce new building blocks, unless the resulting individual can compete immediately in selection, the most likely result is that such traits are deleted. There is a real struggle to maintain useless adaptations in hopes of accumulating them into useful ones. Either if they represent small changes or large disruptive steps, adaptations are bound by their immediate competitive success and as a consequence, so is exploration.

Mate Choice offers a mean of exploration by reducing the pressure of Natural Selection and influencing the impact of reproduction and mutation. The handover of selective power to mating preferences can allow for a directional Sexual Selection drift, powered by stochasticity, self-reinforcement, and runaway processes. Ultimately, this can cause the displacing of populations across the phenotypic space, even in directions that are potentially hindering to Natural Selection, as previously illustrated [200, 201]. In more detail, Mate Choice can cooperate with recombination and mutation in their task of building and proposing diverging candidate solutions by allowing them a higher frequency (by increasing their reproductive success if they abide by mating preferences) and allowing them to be maintained over a few generations. This contributes to the opportunity of increasing viability through the combination of multiple variation operations. Even if they are hindering on their own, they may be beneficial in accumulation. Natural Selection may then select for and improve on those solutions.

Gender has been shown to play an important role in exploration and the search for new optima in Mate Choice, by assuring a reduced risk in the process. While long periods of stasis are unproductive for optimization algorithms, blindly moving through the search space may also be undesirable. Mate Choice offers a balance. If for some reason, such as sensory bias or genetic drift in preferences causes a runaway process, as females are the active choosers, males will be more exposed to change. So males may be pulled from adaptive peaks in order to remain attractive to females, consequently looking for new opportunities in the phenotypic space as a byproduct. Females on the other hand remain closer to adaptive peaks due to the lack of male choosiness. If new adaptive peaks are not reached by males, not much is lost, an equilibrium should be found between mating preferences and male dimorphism, and new runaway processes may still happen. However, if new traits with survival value are found, then the whole population may tunnel through the phenotypic space through the effects of self-reinforcement. In summary, the population will have had jumped into a new optima in their search effort that Natural Selection can further exploit [201]. This should promote rapid evolutionary steps, much like the process described in the theory of punctuated equilibria [84]. This division of labor between genders can be be fruitful [286].

The effect of mating preferences can in some terms be comparable with the effect of mutation. As described, they share a capability for escaping local optima by introducing new genetic material that, possibly more often than not, simply produces deleterious traits, but sometimes can produce new viable evolutionary opportunities. They have nonetheless important differences, on top of what has been discussed. The most important may be that mutation is non-directional, causing variation as a diffuse mesh around the location of the population on the phenotypic space [286]. Mate Choice, on the other hand, should be able to reproduce stronger drifts in the search space through directional, self-reinforcing mating preferences. This difference gives them the opportunity to produce longer walks away from local peaks and therefore promote both sustainable innovation further away, and a stronger engine for speciation.

Emergence of Complex Innovations

As a necessary step in the already reviewed means for escaping local optima, the emergence of innovation has been almost sufficiently introduced. There are however a few particularities that justify being highlighted. Firstly, it has been previously described that drift or sensory bias can be responsible for the emergence of mating preferences that enforce new evolutionary paths. However, the same can be achieved through pre-existing mating preferences. In that case, their effect can stay dormant temporarily (for instance because there's lack of variability on the corresponding trait), and simply become relevant due to changes in the traits distribution in the population. In that case, innovation can emerge due to drift in ornamentation rather than on mating preferences. Secondly and following on the same discussion, innovation seems to benefit from a certain degree of neophilia coupled with Mate Choice. Without Mate Choice, innovating traits are treated just like any other, but innovations that emerge through Mate Choice do so through mating preferences that are liable for their initial maintenance (as previously discussed). They are therefore maintained not because their are useful but because they are boosted by Mate Choice.

As previously explained, the retaining of innovations through self-reinforcement gives them an edge that is unlikely in mutation generated innovations. Whereas deleterious novelties are likely to be selected against immediately or on a few generations, novel traits emerging through Mate Choice can accumulate and thus produce complex innovations. The taste of females for new ornaments (neophilia) should have a ruling role in the process. Much like mutation rates determine the amount of innovations that are introduced and proposed for evaluation [100], the rate of neophilia in a population determines the rate of innovations allowed to be introduced by Mate Choice. Not only that but it also determines the degree of cumulative innovations that are allowed to build up complex innovations [286, 201]. This rate is induced by the population on itself and is subject to self-adaptation, being capable of changing throughout the evolutionary process as a product of the distribution of both mating preferences and traits.

Mutation and Mate Choice have been shown to share some characteristics but also contrast in others. Arguably, both processes together can achieve best results, by being capable of producing both short-term micro-evolution, and long-term macro-evolution innovations [286, 201]. Their interactions may not be straightforward. In a standard scenario where only mutation takes place, innovations can be directly linked to such operations, however when both mutation and Mate Choice act together, other processes can arise. Simple mutation-based innovations can still happen, but mutation on either mating preferences or traits can start new runaway processes. In those cases, ornaments may be built on and elaborated until a viability breakthrough is achieved. There is also a chance that this is achieved not by the affected trait directly but as a byproduct, such as indirect impact of an ornament on others, or on complex mating evaluation functions, or impact of ornaments on traits that have no Sexual Selection role [201].

Spontaneous Sympatric Speciation

In models of Natural Selection, speciation is usually credited to the character of the adaptive landscape. A rugged landscape can present multiple high fitness peaks with low fitness valleys in between, which as a metaphor can be seen as geographical barriers between habitats. Given an initial population that is distributed between these peaks, the landscape can alone enforce breeding within peaks. The reason is quite simply that interbreeding is more likely to produce individuals that will fall in the lower fitness valleys and are therefore less viable. This alone can account for competitive advantage arising from sympatric speciation [71], or reproductive isolation. Methods for preventing cross-breeding and hybridization are therefore a natural outcome [286].

In Evolutionary Algorithms, standard models rely on a global process for selection, which by themselves have a low grip on hybridization. Given a population split between two adaptive peaks, selection is likely to pair individuals from either peak blindly, possibly producing individuals in low-fitness valleys that will in turn have a small chance in being selected. The effort for interbreeding is a burden on Evolutionary Algorithms and therefore various methods have been progressively introduced to mitigate such pointless crossovers. Niching methods, restricted or assortative mating, distributed or spatial models, among others, have been introduced to guide selection towards taking the best profit possible from speciation for the exploitation of different peaks in the phenotype space [199]. While these methods produce the desired effect, they ignore the potential of Mate Choice as a nature-inspired, self-adaptive process for sympatric speciation, with less need for external assumptions. Considering the above example of a population split apart, mating preferences in each of them can reinforce mating within each sub-population rather than between them. Even in a united population, competing runaway processes can arise at the same time, pushing parts of the population to drift in different directions.

In that scenario, diverging mating preferences will compete for momentum, pointing in different directions. If an equilibrium is maintained so that neither is reabsorbed, then the population may split and through self-reinforcement maintain itself in isolation. Individuals that try to abide by both will probably struggle to stay in the middle, in what may be seen as a low-reproduction valley in the preferences landscape. Mate Choice will work against such individuals, thus further promoting the splitting of the population. In a different scenario where Mate Choice or other stochastic methods pushes part of the population into a new high fitness peak of the phenotypic space, mating preferences can speed up the effects of Natural Selection in the process of splitting part of the population into that new peak, given that a subset of the females has or develops a preference for individuals in that new phenotypic space. In both scenarios, mating preferences have a ruling position in the emergence and maintenance of sympatric speciation.

In a way, much like traditional methods for speciation, Mate Choice introduces a two step selection and pairing mechanism, and thus avoids the impacts of a global selection mechanism. However, contrary to the aforementioned mechanisms, Mate Choice maintains an adaptive character and a relatively high degree of autonomy, thus being able to produce different behaviors and adapt to population and landscape dynamics. It may happen that splitting sub-populations drift back together in response to insufficient evolutionary gains and as an attempt for individuals to improve their reproductive rates [288]. The likelihood of such a process is also dependent on the characteristics of the phenotype and preferences landscape. Complexity and dimensions for once have an impact on sympatric speciation as they impact the ruggedness and character of the preferences landscape.

Arguably, complex preferences are more likely to promote speciation, as small changes in preferences can represent large changes in the attractiveness value of mating candidates. Such scaling can contribute to the reproductive isolation of males and through self-reinforcement contribute to that of females as well [178]. Furthermore, such an effect can both emerge through preference variation or trait variation. Still, spontaneous sympatric speciation has been shown to emerge as well in non-complex and quite distinct scenarios [288, 200, 201].

Chapter 4

State of The Art

Models of Mate Choice can be found in the literature as early as in the 1970's, sometimes for the purpose of modeling and studying the dynamics of natural populations but also with the goal of improving the search proprieties of Evolutionary Algorithms. While the previous chapter introduced a general model of Mate Choice to which most approaches can be easily linked to, the literature is replete with approaches that in some way or another deviate from that model, as will be shown. Because different operators will at least need to rely on a meaningful representation, this is somewhat expected, but the spectrum of ideas applied for Mate Choice goes much further than that. In fact, studies in the literature may diverge in many ways. Some design choices are linked to problem dependent characteristics but others are the result of different interpretations of Mate Choice theory. For instance, different authors may apply diverging assumptions or operators to mimic non-incestuous behaviors, gender attribution, or differences in mutation rates between genders. On the one hand, this provides a broad range of ideas to explore but on the other hand it shows some frailties: i) the knowledge and interpretation of theoretic ideas and how to integrate them in useful ways is still on a very early stage; ii) there is a wide range of problems that have been used for benchmarking, making it difficult to compare between approaches; iii) while the set of studies related to Mate Choice is not small, their design choices and applications are sparse and comparative studies are very rare to come by. These conditions make it very hard to truly assess the impact of Mate Choice in the research field.

Besides such differences, some authors choose to follow Mendelian ideas of genetic encoding and inheritance closely, while others rely on higher-level assumptions to determine the rules of Mate Choice. As a result, Fisherian Mate Choice can sometimes be found in the literature, but Wallacean models much more common. From an engineering perspective, Wallacean good sense has many favorable arguments, as the contributions of sensible choice are easier to understand and link to results. Mating preferences, as the core of the operators, are what influence their behaviors, and like any other design choice, there's a large range of setups found in the literature. Some operators rely on fixed population-level choices, others may rely on externally determined rules to adapt preferences in-run, part of such control may fall under evolutionary pressure for a sense of self-adaptive behavior and, finally, some instances where mating preferences can be said to be mostly under evolutionary pressure can also be found. Of course, stating that mating preferences are fully under evolutionary pressure without some external assumptions is challenging. The following subsections will however illustrate how far or how close research has reached.

Some additional remarks regarding the set of studies addressed should be made. The collection of papers has been divided into two groups. Related Work includes studies that while not being categorized as Mate Choice in its strict sense, are related in behavior and have been important for inspiration. For that reason, these studies are very often found to be the source for other relevant studies and are cited often. Studies on Mate Choice in Evolutionary Algorithms have been organized as a best possible effort in a set of categories. This is however not bullet proof as some studies cover more than one category or rely on hybrid operators. In these cases the studies are fully described but included in the subsection that seems to be the most relevant. Also, not all studies reviewed have a clear focus on Mate Choice, sometimes even imposing Mate Choice as a byproduct of their target approach. Because different authors reference the first and second parents in recombination through different names, hereafter they will be referred to by their female and male roles. Overall, the descriptions will focus on the design choices of the operators more than attempting on a comparative study (for the aforementioned reasons), as a basis to show how diversely Mate Choice can be interpreted and designed.

4.1 Related Work

Many applications of Mate Choice aim at finding and maintaining multiple local optima in multimodal functions, or alternatively at speeding up the process of finding the global optima in unimodal functions. The relation between Mate Choice and niching methods is therefore a closely related one. Not all niching methods are relevant for the study of Mate Choice. Some share very little with Mate Choice although their historical relevance may be great, but others share important ideas, inspiration and methods. The following subsections will cover Fitness Sharing, Restricted Mating and Restricted Competition, as well as Crowding methods. Their relevance for Mate Choice will be briefly discussed, in a case by case basis.

4.1.1 Fitness Sharing

Holland [131, 132] was, early in the history of Evolutionary Algorithms, interested in niching methods, techniques that would be useful for the scaling of individual's fitness in relation to others in their neighborhood. Following his ideas, high density areas of the search landscape, where lots of individuals share high similarity, would contribute more positively if the fitness was scaled down in proportion to density, rather than attributing the maximum fitness possible to each individual. For this purpose, either genotypic or phenotypic metrics may apply to measure the proximity of individuals and a neophilic character is promoted through the competitive benefit of individuals that are more isolated in the search space rather than crowded on a space that is unlikely to provide further innovation. Through this process, the population aims at stability and exploration, rather than convergence and exploitation of a single search neighborhood. Algorithms that induce these dynamics are often called sharing methods, due to making individuals in a population to share their fitness with others in their proximity.

Sharing functions, as put by Goldberg [111], regard fitness as a finite resource that should be distributed among individuals in the same niche and over all niches, with niches being delimited by groups of similar individuals. Petrowski [224] on the other hand suggested that fitness in each niche be taken by the strongest individual, in a winner-takes-all fashion. Mauldin [191] had an alternative proposal, where instead of sharing resources between individuals by whatsoever rules, individuals would only be allowed in the population if their genotype distanced by n bits from others already there, hence promoting uniqueness. In this method, pressure would be decreased throughout the evolution process.

Goldberg and Richardson [112] developed a sharing function that based on a pre-established threshold, determines if two individuals are similar or dissimilar. Sharing is achieved by reducing each individual's fitness in relation to the number of similar individuals in the population, while dissimilar individuals aren't impacted. They suggest that phenotypic or genotypic measures can be applied and report maintaining speciation on multimodal functions. A later study [69, 110] compared euclidean (phenotypic) and hamming (genotypic) distances on the same set of problems, showing advantages on using the phenotypic measure. Also, restricted mating is used and successfully contributes to the prevention of destructive crossovers. While fitness sharing is not a mating strategy by design, it's niching character is possibly the root of early interest of the research community in Mate Choice as an engineering, goal oriented strategy, rather than a method of interest for the study of natural populations.

4.1.2 Restricted Mating

Unlike fitness sharing methods, operations restrictive of mating do share some characteristics with Mate Choice. As a general description, such strategies assess the pairing of individuals for mating and, according to a certain metric or rule, determine if those individuals are restricted from mating or allowed to reproduce. This shouldn't be mixed up with female Mate Choice as an active effort to choose a mating partner, but as a more high level approach that emulates behaviors often found in nature such as the prevention of incestuous reproduction. Within restricted mating, two global approaches can be found in the literature, either similarity-based restrictions (based on a genotypic or phenotypic measure) or ancestry-based restrictions. These topics will be covered separately.

Similarity-based Restriction

Booker [30, 31] proposed a method aiming at preventing destructive recombination by restricting mating between dissimilar individuals. By allowing the pairing of parents only if they are sufficiently similar to each other, the method promoted the exploitation of fitness peaks while discouraging mating between individuals whose offspring would likely fall into low fitness valleys. By doing so, speciation is reportedly maintained on multiple fitness peaks, with individuals crowding and mating in isolation in each peak. The approach was tested on a task of message classification where classifiers can only pair if they are relevant to the same messages. In order to ensure proper maintenance of species and niches, a crowding mechanism is employed where densely populated areas of the search space will see their weakest classifiers periodically deleted through a sharing method.

Eshelman and Schaffe [86, 87, 88] have studied an incest prevention technique that inhibits mating between individuals whose hamming distance is below a certain threshold. The approach randomly selects pairs of individuals consecutively until two parents that meet the criteria come up. At this point, offspring are generated, which will substitute the worst individuals in the population. Soft restarts are also employed in order to introduce new genetic material in the population when it gets stuck in a local optima that prevents new non-incestuous pairs of parents to be selected. The threshold at this point may also be relaxed to allow for a higher rate of successful pairings. This technique has been applied to function optimization, one-max, and traveling salesman problems, showing an ability to increase the productivity of the crossover operator while preserving fast convergence in the population. This threshold based incest prevention technique has been shown to postpone loss of alleles almost indefinitely in certain conditions [255].

Ancestry-based restriction

Craighurst and Martin [53] have also addressed the issue of incest prevention by disallowing mating between individuals that are too similar. In their study, instead of relying in a genotypic or phenotypic metric to measure similarity between individuals, they rely on their ancestry tree. As individuals store information on their lineage, the approach is able to measure an ancestry distance between two subjects by searching for a common ancestor. Reproduction is prevented between individuals whose distance to a common ancestor (in generations) is bellow an established threshold, thus encouraging crossover between individuals that are less likely to share genetic material, reportedly helping maintain diversity in the population through a broader exploration nature. The authors report performance gains when compared to a traditional Genetic Algorithm on traveling salesman problems.

Fernandes et al. [96] applied a similar approach (non-incest Genetic Algorithm) with a steady-state population of varying size to four peaks and royal road problems, showing both similar behaviors and gains in performance when compared to a standard Genetic Algorithm. The varying population size allows for offspring and parents to coexist and compete in the same population. A later study by Fernandes et al. [93, 94] proposed a follow-up approach where the incest control threshold adapts dynamically as a response to the average diversity found in the population. An external rule determines the direction in which the threshold is adapted: if population diversity decreases, then the threshold shifts in order to promote dissimilar mating; if population diversity increases, the threshold is less restrictive on which individuals can be paired. The algorithm takes upon itself to adapt its own behavior without external intervention, although doing so under the directions of a pre-established rule. When compared with a standard Genetic Algorithm, non-adaptive non-incest Genetic Algorithm, and both positive and negative assortative mating, the adaptive threshold method proves to be competitive, specially when tested on multimodal and deceptive optimization problems, and also when using smaller populations. When compared with the top performing negative assortative mating approach, results are reportedly more consistent from run to run, specially on harder problems.

The discussed approach was later tested by Fernandes et al. [90, 91, 185] on dynamic problems , although two modifications were proposed as a better suit to the effort: the varying size population was adjusted and now employs a replacement strategy where new offspring replace the n worst individuals in the population; the initial mating threshold was relaxed, thus allowing for more similar individuals to pair. In tracking the extrema of a set of dynamic adaptive functions, the approach performed competitively with a standard Genetic Algorithm, standard steady-state Genetic Algorithm, negative and positive assortative mating and two tailored random migration strategies from the literature [91]. In other published papers, a comparison is made between static and dynamic environments [185], and a dynamic knapsack problem is also targeted [90]. In the knapsack problem, the approach performed as well as a standard Genetic Algorithm, with the lack of difference being related to the problem being less hard to tackle, thus mitigating potential advantages. Overall, the approach seems to outperform others on more difficult instances of the problem and to scale particularly well as the size of the dynamic function grows, specially on deceptive problems. On the other hand, the algorithm seems to react better to a low extrema change rate but struggles to keep up on higher rates. On this topic, negative assortative mating seems to respond quicker to deep changes while positive assortative mating responds well to fast, small changes. Regarding its behavior, it's argued that the adaptive operator contributes to a higher population diversity, and while making slow fitness gains in the beginning, it follows the optimum closer and more consistently. Overall, the operator seems to profit from its ability to emulate negative assortative mating (which seems appropriate for deceptive functions) and from adapting its pressure according to the state of the search process and as a reaction to changes.

Ting et al. [285] integrated tabu search into a mating strategy by adding two attributes to each individual's genotype: a clan id, and a tabu list of clan ids with whose individuals mating is forbidden. At each selection step, two individuals are selected for the roles of female and male through traditional selection methods, at which point two criteria are checked for reproduction to go through. Firstly, a potential offspring is produced and if its fitness is better than the best found in the population, then the offspring is introduced in the population. Secondly, if the first criteria isn't met and if neither of the selected parent's clan id is featured in each others tabu list, mating is also allowed. If neither criteria is met, mating is restricted and a few tries are made to select a new and appropriate male. In a last case scenario, after a limit number of tries is reached, the selected parents are simply mutated and reintroduced in the population. If a successful mating pair is found, their tabu lists are updated to include each others clan id, using a first-in-first-out approach in case the list is full. Their offspring will, apart from the remaining genetic material, also inherit the tabu list from one of the parents. As a result, each individual can keep track, through its own tabu list, of its own ancestry line (either a patrilinear or a matrilinear one, depending on the inheritance assumptions). The authors argue that by restricting mating between individuals that share ancestry, diversity is promoted through outbreeding, a rule whose enforcing pressure can be relaxed through the maximum size of the tabu list. In a way, the tabu list is an adaptive component, as it is inherited and adapts through pre-estabished rules. A comparison is made between the two-criteria mating strategy coupled with self-adaptive mutation, and conventional approaches (Genetic Algorithms, tabu search, and a Genetic Algorithm that runs tabu search for local search) on a traveling salesman problem, with results showing improvements in solution quality and convergence speed.

Al-Madi and Khader [5], while aiming at studying aspects of social interactions suggest, a restricted mating approach on top of a distributed model of evolution. By itself, the distributed nodes restrict mating within the sub-populations in each node, while still allowing migration and the consequent injection of genetic material. Additionally, mating is inhibited between genders, and parents and offspring. In order to achieve this, each individual keeps record of their immediate ancestry (its discussed adding a second level to inhibit mating with parents and grand-parents) and is attributed a gender at initialization. The study presents only early stage experiments on a knapsack instance.

4.1.3 Restricted Competition

Goldberg et al. [57] bring restrictions to the selection of individuals competing in a binary tournament selection. Whereas a traditional approach would see two individuals randomly selected in the population, the proposed approach selects one individual randomly and the second one in a restricted manner. Individuals are randomly selected until one that is sufficiently similar to the first one comes up (genotypic similarity bellow a pre-established threshold). The competitor may not however be the same. If no such individual can be found after a few tries, the first individual wins the tournament by absence of opposition and proceeds without being subjected to reproduction. Mahfound [188] has also tested restricted competition, successfully finding all peaks on a test function. As a follow-up, restricted mating is enforced, so that parents mate only if they are satisfyingly similar, otherwise moving on to mutation. The combination of both restricted competition and mating aims at reducing destructive crossover and consistently maintains the distribution of the population over the previously found peaks.

While restricted competition has not been attempted very often, it shares strong resemblances with restricted mating as well as with crowding mechanisms. The main differences are that restricted competition imposes selection rules upfront rather than after the pairing of individuals, such as with restricted mating, or at replacement, such as with crowding methods. Nonetheless, the elitist nature of the operator is maintained, successfully influencing the reproduction, or replacement, rates of individuals according to their proprieties in comparison with others.

4.1.4 Crowding

De Jong [68] was among the researchers first introducing the concepts of niching and crowding, having suggested replacement operators that would introduce new individuals in the population in substitution of the most similar one. Such methods are inspired by nature's geographical barriers and aim at maintaining diversity while searching multiple parts of the search space simultaneously by avoiding convergence. While their relation with Mate Choice is not straightforward, the mechanisms used to compare between individuals have been regarded as relevant, and often cited in Mate Choice studies. The mechanism introduced by De Jong [68] was inspired not by nature's mating dynamics but rather by the competition between individuals of the same ecological environment for a limited amount of resources. This effect is bound to be more prominent within the same niche or population with closely similar individuals rather than between dissimilar individuals or different niches. Through competition, stronger individuals remain while weaker ones are crowded out by lack of access to resources, thus maintaining the size of the population in balance with the amount of available resources.

In Evolutionary Algorithms, this allows for a replacement strategy that can hopefully better contribute to diversity, and that may be relevant to the study of Mate Choice because of how selection for replacement can often be akin in strategy with selection for mating. For instance, De Jong's crowding strategy [68], applied on a steady state Genetic Algorithm, worked by producing offspring through a standard operator and then randomly selecting a set of replacing candidates, from which the most similar (according to hamming distance) to the new offspring is selected for replacement. The aim was at maintaining diversity, which was achieved to some extent, although convergence reportedly still happens due to drift.

Cedeño and Vemuri [46] suggest an approach that accounts for both similarity and fitness, in a worst-of-the-closest operator. They rely on positive assortative mating to select individuals as males to pair with traditionally selected females, but focus on the role of a replacement strategy that consists of multiple steps: first, multiple groups of individuals are randomly selected from the population; secondly, the individual from each group that is most similar to the offspring being inserted in the population moves to a second selection pool; thirdly, the worst performing individual in that pool is substituted by the newly produced offspring. The authors report some ability to maintain the population spread over various peaks but don't show how much that may be related to the composite replacement strategy or rather to the assortative mating operator.

Culberson [56] employs a variation of a replacement strategy that tries to take the best profit from the crossover operator. The proposed approach restricts mating in order to promote the pairing of individuals with similar fitness. Each pair, instead of reproducing once, does so *n* times and group the corresponding *n* pairs of offspring in an intermediate population. Two alternatives are then considered to replace the parents: i) keep the fittest pair of offspring (fitness of the pair is the fitness of the best individual in the pair); ii) keep the fittest pair only if they are better than the pair of parents. As a result, and because no mutation is applied, the algorithm maintains and reorganizes the genetic pool, promoting fit individuals to mate with fit individuals and unfit to mate with unfit ones, thus contributing to the emergence of two sub-populations that become more and more unlikely of mating between them. The replacement strategy contributes actively to the effect by being elitist, and so does the means by which pair fitness is calculated. Harik's [125] method relies on random parent selection and as two offspring are produced, a replacement pool is gathered also randomly from the population. Each offspring is compared to the individual in the pool that is his most similar (by phenotypic measure) and the fittest of the two is maintained. The author reports being able to reasonably maintain presence of the population among all peaks in a set of multimodal functions, and regards that the generations span where that behavior is possible is exponentially related to the size of the replacement pool.

4.2 Mate Choice in Evolutionary Algorithms

The topics covered in the previous section represent an interesting collection, both on an Evolutionary Algorithms context and specifically for Mate Choice. On top of knowledge specific to each study, they hint at the engineering perspective that is often present in Mate Choice strategies. This chapter will show how broad such strategies can be and how they are inspired by Mate Choice theory, or Sexual Selection as a whole, in different ways and on different levels. At this point, it's important to take notice that suggesting that all the approaches discussed in this chapter are indeed means to introduce Mate Choice in Evolutionary Algorithms might be stretching the truth. However, because of their parallelism with different aspects of Sexual Selection, a full review would feel incomplete without mentioning their contributions, even if only for contrasting purposes. Briefly expanding on this remark, not all approaches in the literature are centered on mating preferences, gene-centered evolution or female choice, which are arguably the core of Mate Choice theory, specially if following Fisherian rather than Wallacean ideas. Still, from an engineering perspective, there are many ways to introduce behaviors that are related to Mate Choice or Sexual Selection (as has been already shown in the previous section), and that can often help achieve goals while maintaining a relative simplicity.

A good number of authors rely purely on external rules to determine the behavior of individuals along a run, rather than depending on a feedback loop for self-adaptation. For instance, some studies focus on gender dynamics, such as the alleged exploring role of males versus the exploiting role of females, and suggest achieving such behaviors by using different selection pressures. Gender determination procedures alone may also have enough impact to impose such behaviors, as well as other. Some focus on population wide rules for choosing mating partners, which promote certain behaviors. Others try to evaluate genotypic or phenotypic information on mating candidates, or to combine different metrics, but approaches that rely solely on fitness based operators can also be found to successfully control selection pressure or the pairing of individuals. Furthermore, some authors make an attempt at generalizable methods while others try to make the best use of problem specific knowledge, whether they are tackling unimodal, multimodal, multi-criteria, or constrained functions, among others.

Despite the differences between some of these approaches with both the Wallacean and Fisherian genetic models discussed previously, one can't but see an implicit relation. Even without imposing a direct fitness cost on certain features under Mate Choice pressure, many times there are assumptions that aim at maintaining an healthy population and are therefore purely Wallacean as they contribute to the good of the species (costs are sometimes implicit). Selecting for dissimilar individuals as an attempt to maintain high diversity is an example of such a scenario. A different example is that of using fitness as part of the attractiveness value. Choosing for individuals that show good fitness through their attractiveness can be a way of introducing choice for good sense. If part of the Mate Choice strategy falls under evolutionary pressure, the same parallelism is maintained. Depending on the relation between the evaluated features in mating candidates and fitness, there are instances where a behavior of good taste for good sense is present. If age of mating candidates (in generations), is assessed as an indication of how many survival steps it has overcome, female preference for older individuals may develop due to its implicit benefit. As can be seen, depending on the external assumptions and how Mate Choice is designed, Wallacean ideals can be appealing. Still, there are also scenarios of Fisherian self-reinforcement and also instances where it's remarkably difficult to say for sure if certain features impose or not fitness costs. The following subsections will cover a collection of studies related with Mate Choice in Evolutionary Algorithms in an organized and comprehensible way.

4.2.1 Fitness based evaluation

Alleson [7] has suggested that a traditional selection strategy is akin to a model where all individuals have a mating preference for the fittest individual in the population. A scenario is described where such a mating preference might be evolved, by splitting the population in deciles according to fitness, and having each individual's preferred decile encoded in the genotype. During Mate Choice, the corresponding gene is used to guide the selection of mating partners. Inheritance is also discussed as having various potential behaviors, including inheriting from one parent or combining the preferences of both parents. While results are not presented for any application, a discussion of future work involves the integration of phenotypic features other than fitness into attractiveness evaluation. The author suggest that such a model would be more intuitive and closer to natural behavior, while allowing for problem specific indicators such as angles, measures, lengths, etc. to be included. This example is a simple, yet purposeful illustration of how fitness can be used as a mating preference. However, fitness based selection has been used as a component on very different approaches

Bandyopadhyay et al. [19, 20] implemented a two genders model where each individual's sex is determined by a combination of two genes. If both are zero, then the individual is a female, otherwise it's a male. While selection for a mating pool is done from both sub-populations combined, using a traditional fitness based method, pairing is afterwards done randomly and with no repetition, between females and males in the mating pool. Eventually, one of the genders may run out of individuals, at which point all the remaining individuals will pair with the fittest one remaining (even though they have the same gender). At initialization, one sub-population is populated randomly (in one study its the females while on the other is the males, coming nonetheless to the same end) but the other one is generated in a way that attempts to maximize the hamming distance to the previous one. Their composition as well as the size of each sub-population may however change during reproduction, as two offspring will have their gender attributed through inheritance. Each parent contributes with a a bit, meaning that gender will depend on whether the male parent contributes with a zero or a one. This may result in the production of two females, two males, or one male and one female. The approach was tested on various binary function optimization problems [19] as well as on pattern classification problems [19, 20] (including multidimensional problems), reaching improved efficiency when compared to a standard Genetic Algorithm. Selection in this case is ruled by fitness, similarly to other standard approaches, however as discussed by the authors, the initialization strategy was an important contribution which, aided by the two genders mating strategy, introduced dynamics that helped balance exploration and exploitation.

Chakraborty and Chakraborty [47] suggest two approaches for the pairing of mating partners, either according to their fitness or according to their age similarity. Their setup selects individuals from the population and into a parent's pool using standard operators, after which pairs are selected randomly. If using the fitness based method, the normalized fitness difference between the two individuals is first measured and transformed through a function following a normal distribution. The function returns a higher mating probability if individuals have similar fitness, and decreases as their difference increases. The width of the function is controlled by a second function that depends on the current generation number. The mating probability between similar individuals is therefore more likely in the beginning of each run in order to promote exploration (in each niche) of the search space and increasingly narrow by the end of the run in order to impose convergence. A randomly generated number is used to determine if two individuals reproduce together according to their mating probability. Alternatively, the age based function measures the average age of two individuals against the average population age. In this case, new or mutated individuals are attributed age 0 which increases from generation to generation if individuals survive. The approach is built to give a higher mating probability to individuals whose age is greater than average, in order to prevent new individuals from fully taking over the search process, thus promoting exploration, while at the same time relying more on survival proven individuals. The two approaches are tested separately against a standard Genetic Algorithm, with and without linear fitness scaling, on unimodal and multimodal maximization problems. Results show that both approaches contribute to a better exploration of the search space and that the fitness based approach achieved the best solutions. The authors suggest coupling the approaches together as well as with others, and discuss the tuning of parameters in order to achieve higher exploitation on unimodal functions and exploration on multimodal ones.

Vrajitoru [301, 302] discusses a model with four genders: males and females can mate with the opposite sex or any of the two other; self-fertilizing individuals can mate with any individual including themselves; hermaphrodites can mate with any individual other than themselves. Other relevant rules apply to the model: if males or females can't find an appropriate mate at a given generation, sex changes can occur in order to escape situations where all individuals have converged to one of these two genders;

also, if one of the selected parents is a male or a female (from among the four choices), resulting offspring can either be a male or a female (heterosexual individuals act as a loosely coupled group). Gender is nonetheless inherited from parents to offspring as part of the genotype. Initial experiments using fitness proportionate selection and constrained pairing show that convergence to a single gender occurs fast and often to self-fertilizing individuals. This may be the effect of that gender being the only one able to self-reinforce by choosing individuals of the same gender, thus reaching a higher competitive advantage. Further tests compared the following setups coupled with fitness proportionate selection: self-fertilizing only; four genders; hetero only (male/female); hermaphrodites only. On a set of standard and deceptive optimization functions, best performance was achieved most times by hetero or hermaphrodite setups. The adaptive four gender scheme is almost never the best, which suggests that avoiding self-fertilization can contribute positively. It's also suggested that hetero strategies can be a better fit to large populations whereas non-partitioning hermaphrodite populations have an advantage if they are small.

The study is further expanded by introducing social mating restrictions. During selection, one individual is selected for the role of female through a fitness proportionate method and the male is selected from her neighborhood, with either first ordering the population by fitness, or maintaining it disordered; Ordering promotes the pairing of individuals with similar fitness while the alternative promotes the pairing of individuals that were introduced in the population at the same step or closely, which benefits shared ancestry. The analysis shows that such design choices have a greater impact on solution quality than the previous reproduction models. It's also suggested that as the size of the population increases, differences between mating schemes become less and less relevant. A later study by Vrajitoru [303] expanded on the topic with two main experiments using the four genders described above. The first experiment, including no Natural Selection (random selection) shows that in the short term, sexual differentiation features disappear and over the long term, hermaphrodite individuals are chosen against as well. Simple asexual reproduction seems to prevail and dominate the population through cheer competitiveness. The introduction of Natural Selection shows that the sexual features of high fitness individuals tend to dominate the population and are not always the same ones that are found in the setup with no Natural Selection. The interaction of both forces seems to contribute for individuals with low probabilistic expectations of survival to remain present in the population.

Zho et al. [327] describe a Genetic Algorithm with a diploid population organized in two genders. Much like other traits, in this case gender is determined through an *AND* operator between both chromosomes, specifically on the last bit or the last three bits, depending on problem dependent representations. In their approach, restrictions are imposed through a reproductive age threshold (measured in generations), below which males can't be matched to females and can only reproduce asexually. During their mature age, females and males are ordered according to fitness and matched through their rank, meaning that possibly not all females are allowed to mate. New offspring are generated through crossover followed by mutation, which has a higher rate in males, promoting exploration and exploitation in males and females respectively. The best performing offspring will go through a replace-worst strategy to enter the population, which may have a dynamic size as a result of individuals being excluded when they reach a given age. The approach was tested on the minimization of five functions. Reportedly, the approach converges to the global optima on the whole test set and does so faster than a multi-species Genetic Algorithm used for comparison. The authors discuss that the behavior is a result of a broader diversity.

Tahera et al. [281] discuss two approaches for gender assignment in Genetic Algorithms. During initialization, gender is attributed to meet a pre-established male-female ratio and, when new offspring are spawn, an adaptive assignment approach attributes gender based on population densities, meaning that if the population count of one gender is low, that gender will be assigned in order to balance the population. Otherwise gender is attributed randomly. A second strategy attributes gender to individuals at each generation, by ordering individuals according to fitness and attributing a female gender to the fittest half and male gender to the bottom half. Independently of the strategy, selection of parents is done in each gender with the same fitness based operator, so that the only restriction is that male and female pairs have to be formed, arguably promoting diversity. The approaches were compared to a standard Genetic Algorithm and a constant gender assignment strategy (one offspring is female and the other is male), and random assignment, on the design of pressure valves. Results suggest performance gains with both the proposed methods. A different study by the same authors [282] using the adaptive gender assignment introduced a few other design choices. When reproduction occurs, the two resulting offspring compete and only the fittest one is introduced in the new population. Also, reproduction contributes to building half of the new population, while the remaining half consists of the top 50% of the previous population. Mutation rates are also different for males and females, with males being given a higher exploratory character through a higher probability of mutation. The new approach is applied on the design of tension strings and compared to a standard Genetic Algorithm, an alternative gender-based Genetic Algorithm [79] with standard and higher mutation rates for males, and adaptive gender assignment with standard mutation. Results achieved by the approach are reportedly competitive, mostly through the introduction of population diversity.

Sodsee et al. [274, 275] apply a gender based Genetic Algorithm where sex determination is accomplished through an extra gene in the representation. Initialization is made so that the corresponding sub-populations have a balanced size and inheritance aims at maintaining that balance. During selection, individuals are selected through a fitness proportionate method from the whole population and placed on a mating pool, from which females and males are randomly selected and paired without replacement. Reproduction takes place as long as there are two genders in the mating pool and a crossover probability determines their ability to reproduce. Alternatively to reproduction, individuals may suffer mutation with different probabilities and operators. Males are mutated on a higher rate in order to promote exploration. Afterwards, offspring compete with the previous population for a spot. The approach is applied to multi-objective functions as well as to a computer network design application. The authors report finding pareto-optimal solutions on the first and non-dominated solutions on the latter more efficiently than a standard approach. Despite the approach being generalizable, it seems to struggle with premature convergence on some runs.

Cheng et al. [49] introduce a scheme with simple individually encoded mating preferences. Using a two genders population, they suggest that females encode a preferred fitness value and that, after a female is selected through a standard operator, the pairing male is selected in order to best match the female's preference. After reproduction, the offspring are attributed a gender based on a replacement strategy that maintains the sex ratio stable, and females inherit their mother's mating preference. Preferences are then adapted through a function that biases it towards the best fitness value found so far. The approach is therefore not purely self-adaptive, but is rather influenced by a directional adaptation mechanism. The authors report performance improvements when compared with a standard Genetic Algorithm on most instances of a set of unimodal and multimodal functions for maximization.

Nazmul and Chetty [207] also develop a fitness based approach for Mate Choice. They propose organizing the population into three clusters labeled best, average, and worst. Individuals are attributed to each cluster according to their fitness and in a way that ensures that all three clusters are populated, which is achieved by adjusting the limits of each cluster as a response to the population. This is done before each selection phase, at which point three mating candidates groups are also established, one for each of the clusters and equally labeled. A preference matrix controls how these mating candidates groups are populated, by registering for each cluster a preference weight linking to all three clusters. By using the preference matrix, the mating candidates set of each particular cluster will be filled with individuals in accordance to the weights. The most preferred cluster will contribute with many candidates, the second preferred group with an average number of candidates and the least preferred group with only a few. After all three groups have been built, selection can begin.

All individuals in the population are given a chance to reproduce as a female, and depending on the cluster that they belong to, they will choose a mating partner from the corresponding candidates pool. In this scenario, each mating partner is randomly selected from within the pool. The preferences matrix ensures that each mating pool keeps a selection of individuals sampled in a way that works best for each cluster, by dynamically adapting to successful reproduction. At each generation, the success of each pairing is considered by assessing if the offspring are better than at least one of the parents, and if the success rates are not in accordance with the weights in the matrix, they are rotated (this is a lightweight way of changing the sampling priority). The authors discuss potential benefits brought by this approach on diversity maintenance, favoring fit individuals while providing a fair chance to less fit ones, and reducing the chance for takeover. The approach is compared to tournament selection and roulette wheel selection on a large set of unimodal and multimodal functions. Arguably, the approach is able to dynamically adapt selection pressure by using feedback, to adjust the contributions of each cluster to mating candidate pools while ensuring that they all get a chance to contribute. Overall, the strategy has beneficial effects in convergence speeds.

4.2.2 Selection pressure

Rejeb and Abuelhaija [240] discuss a two genders approach for Genetic Algorithms. They suggest ordering the first population according to fitness and attributing a gender tag (male or female) in an alternating way. The gender tag is encoded as part of the genotype, so that during reproduction, a male and a female are always bred, assuring the gender balance in the population. Pairing is done using traditional fitness operators, although ensuring that mating only happens between a female and a male. The approach is applied first on multimodal function optimization but also on network partitioning problems. When compared to a Genetic Algorithm with no genders on each test set, the gender based setup finds better performing solutions while requiring fewer generations. While the approach is purely fitness based by design, the focus on the comparative study was more on the impact of gender attribution and the splitting of the population into two subgroups, specially regarding the selection pressure of individuals.

Sánchez-Velazco and Bullinaria [253, 254] studied a Genetic Algorithm with two genders, with selection methods applied independently, favoring competition between males and co-operation between females. The population is divided at initialization, randomly generating individuals for both genders. Two operators are then applied, selecting one individual from each gender. The male selection operator, favors competition in fitness, therefore traditional operators can be used. Female selection is done in order to favor co-operation within the population. The co-operative fitness of each female is calculated as a weighted function accounting for three factors: competitive fitness is the standard fitness measure; fertility is determined through a triangular function centered around the age of maximum fertility (measured in generations) and with a given width that also sets the lifespan of individuals; female contribution is measured as the fitness difference between her last male offspring and her potential male partner. After selection, two offspring are produced, one of each gender, and relying on independent crossover points. Special inheritance rules apply: the male offspring inherits the head of the chromosome coming from the mother and the tail of the father's chromosome; the female offspring, using a different crossover point, inherits all its genes from the mother, although inverting the first half. Reparations may be required at this point and standard mutation applies, with a higher probability on males than on females, for a higher exploratory character. Interestingly, the study proposes a composite evaluation metric for females. However the focus is on introducing different selection pressures to promote different behaviors between genders.

The approach was first applied on a traveling salesman problem and compared to a standard Genetic Algorithm [253]. On a second study, traveling salesman instances were also tackled, as well as two test functions for global maximization [254]. Overall, the authors discuss that the approach contributes to avoiding stagnation and helps maintain diversity, reportedly contributing to overcoming standard Genetic Algorithms on all test functions. The linkage between problems and parameters is also discussed, and the higher design complexity is weighted against a higher freedom of behavior. The co-operative fitness weights are discussed as being able to improve the competitive fitness and diversity of females. A technical report by Deslauriers [70] includes a parametric study comparing the proposed approach with a standard GA, using roulette wheel, tournament selection, or a biased tournament operator for the selection of individuals from each gender. Co-operative fitness is used for female selection nonetheless. The report suggests that gender based evolution is not always beneficial, depending on the context. It is argued that while elite individuals benefit from the setup, reaching closer to optimal values, the population as a whole rarely improves. The author is looking more into the system for its natural evolution aspects than for the sake of optimization.

Wagner and Affenzeller [304] study the application of different traditional methods for the selection of female and male parents. The argument made is that male vigor and female choice can be broadly mimicked by traditional methods and its control of selection pressure. Using an instance of the traveling salesman problem, the authors study how the average selection pressure can be adjusted by choosing different selection schemes for each parent. They suggest using random selection for females and a higher pressure method such as a fitness based roulette wheel for the selection of male parents. Nonetheless, their study includes all possible combinations of random, roulette wheel, linear ranking and tournament operators of different sizes. They show that it's possible to have some control, which should be adapted to the design and problem at hand.

An alternative study authored by Affenzeller and Wagner [3] also relies on traditional methods for the selection of parents. However, in this case, their replacement strategy shows two possible behaviors. They require new offspring to go through a replace-worst strategy until a pre-established percentage of the population is renewed. The offspring that have not been accepted are then randomly sampled to fill the remaining spots in the new population, successfully replacing all individuals from the previous generation. The authors argue that this is similar to having individuals tryout multiple partners until one or more offspring are successfully accepted in the new population. It's discussed that such a mechanism is a self-adaptive way of adjusting the selection pressure to the characteristics of the population. Fewer individuals are produced when fitness gains are easy and more reproductive steps are necessary when the population finds it difficult to make performance gains. In the first scenario, there's a better chance that more individuals will find their offspring in the following generation. The approach is tested on various n-dimensional test functions and results show that the approach is able to find the optima even on highly multimodal instances. The authors finally argue that the approach is capable of generalization to any representation.

Snijders [273] relied on a two genders Genetic Algorithm to tackle NK-landscape problems. Individuals are generated randomly and attributed a gender so that the population remains balanced with half females and half males. During selection, a tournament operator is used on both males and females although with different tournament sizes. Males are selected through a larger tournament, promoting exploitation, while female selection uses a smaller tournament, thus giving a higher chance for exploration. Mutation on the other hand is higher for males, thus also promoting exploration. A balance between exploration and exploitation is aimed for males. While mutation generates new individuals, selection keeps a high pressure on new mutations, promoting profitable mutations but deleting hindering mutations fast. Results show slight performance improvements when compared to a baseline approach.

Drezner and Drezner [79] describe a Genetic Algorithm with two genders, male and female, randomly attributed to the initial population so that the ratio is balanced. The first parent is selected randomly from the population but the second parent is selected from the subset corresponding to the opposite gender (also randomly). After recombination, offspring are attributed a gender randomly, therefore gender ratio is dynamic and doesn't have to remain balanced. During the experiments, the authors report not coming across situations where only one gender prevails. The approach is tested against a standard Genetic Algorithm with no genders on four problems: the Golf Scramble problem, a distance-dependent Unreliable Multifacility Location Problem, a Network Design Problem, and a Quadratic Assignment Problem. Overall, the results were improved on all instances, and the population average diversity measured through hamming distance was seen to be maintained higher throughout the evolution process.

Ansótegui et al. [14, 284] consider the use of a population with two genders for the problem of automatically configuring solvers through the tuning of their parameters. They rely on a tree-based representation to maintain a specific structure between the evolving variables, and different selection strategies for each gender. The population is separated into competitive and non-competitive groups, which are regarded as females and males respectively. During selection, the fittest 10% of females are selected for reproduction and 70% of males are selected for mating. Each male is then randomly assigned to a female and their offspring is randomly attributed a gender. Elimination of individuals that have been active for three generations keeps the size of the population from bloating. Reproduction is done through problem-specific operators. Reportedly, the approach produces gains in configuration time when compared with other approaches, including a standard Genetic Algorithm. It's argued that the approach can reduce the need for testing a lot of bad configurations. The authors discuss that this may be the result of boldly selecting for the fittest individuals while relying on non-competitive individuals to provide gene diversity to the search effort.

Ramezani and Lofti [236] suggest attributing female or male genders randomly during population initialization in a half-half ratio. During selection, females all have one chance to reproduce and for each one, a male partner is selected using a traditional selection mechanism. Furthermore, pairings where the female and male share one of the progenitors or are themselves related through parenthood are restricted from mating. New offspring are attributed a random gender and, following mutation, are added to the population. After each reproduction phase, the population is ordered by fitness and its initial size is enforced by removing the bottom individuals. As a mechanism to avoid deadlocks caused by the domination of one gender over the other, when necessary, new randomly generated individuals are introduced in the population. The approach is tested against a standard Genetic Algorithm on a large set of optimization problems, showing performance gains on all instances.

Xu et al. [320] suggest applying a two gender approach for constraint satisfaction problems. In their model, at each generation individuals are randomly divided into males and females, with males competing for n elitism spots for reproduction and females sharing the same probability for mating. Offspring are generated by pairing elite males with randomly selected females. Tested on a Traveling Salesman problem, balanced incomplete Block Design and Langford problems, the approach improves performance when compared with a standard Genetic Algorithm. The approach is then introduced in a setup where increasingly complex instances of the problems are tackled, with the population of each run being initialized with the best individuals from the previous one. Results back up the potential benefit of coupling such strategies by showing that their combination can successfully solve the proposed problems.

4.2.3 Assortative Mating

Assortative mating promotes the selection of the most similar (positive assortative mating) or the most dissimilar (negative assortative mating) mating candidate. Arguably, this is the model most found in the literature. In its basic form it relies on a simple external rule, which can nonetheless impose complex behaviors. Some authors build on its simplicity by allowing for part of the parameters or assumptions involved to be encoded in an individual-level approach. Like other models, the impacts highly dependent on initial conditions and the topology of the search space. For instance, positive assortative mating can lead to rapid convergence in the population and loss of diversity. On the other hand, it may promote niching or speciation through exploitation of multiple areas in the search space. Negative assortative mating is better regarded for its contributions to maintaining diversity but can also result on non-productive crossover operations. In the end, design choices on assortative mating may be worst or better suited depending on the target problem.

Ratford et al. [237] introduce an attempt at capturing both the behaviors of positive and negative assortative mating. For doing so, they suggest modeling attractiveness as a triangular function, limited in $[0,1]$ and with a pre-established center. During evaluation, the hamming distance of each mating candidate to the active female is measured and normalized, and thereafter fed as input to the function. The output will determine the attraction value. In this case, the center of the function is set manually and adjusts the behavior of the algorithm. By setting it closer to the top extreme, negative assortative mating is valued, while the inverse behavior can be reached by setting the center closer to the bottom extreme. As a result of the triangular function, not only is the preference for negative or positive assortative mating modeled, but also a sense of contrast through the steepness of the function. The authors also propose substituting the triangular function with a skewed bell curve for a more detailed control of its behavior.

As a follow-up, it's suggested that the center of the function dynamically adapts at each generation, initially favoring mating between similar individuals but progressively shifting into mating between dissimilar ones. Regarding selection of individuals, three approaches are discussed: in tournament selection, a female is selected and so is a set of mating candidates, from which the most attractive will play the role of male; in marriage selection, after the female is selected, individuals are picked randomly from the population until one is found to be more attractive than the first one (which acts as a threshold); in courtship selection, an individual from the population and a threshold are selected randomly, and if that individual's attractiveness is above the threshold, then it will be selected as a pair, otherwise the process is repeated. In the later scenarios, if no pair is found for a few tries, the most attractive individual evaluated so far is chosen. The Mate Choice approach is coupled with three algorithms: traditional Genetic Algorithm; a crowding algorithm; and a spatial reproduction algorithm. In all cases the female is selected according to each algorithm and the male through Mate Choice. The mix of setups is tested on a large number of multimodal problems using binary coded representations. Results suggest that the combination of crowding with Mate Choice produces quite poor quality solutions while coupling Mate Choice with spatial reproduction performed better than either approach alone. Furthermore, Mate Choice improved the Genetic Algorithm's ability to locate and maintain multiple optima.

In a complementary study [238], a broader set of mating strategies were considered. Firstly, two seduction functions, triangular (not the same as the one above) and bell shaped functions, whose depth and center are manually controlled, are compared between them, with no significant differences being pointed out. Secondly, three means to determine an individuals attractiveness value were proposed: using the seduction function alone; averaging the seduction function with a normalized fitness; multiplying the seduction function by a rank based normalized fitness. On preliminary tests, using seduction alone performed better than the other composite approaches. Preliminary testing on the use of a phenotypic metric (euclidean) distance and genotypic metric (hamming) showed that their performance may be problem specific and are thus inconclusive. Still, both performed better than a building block metric. The three aforementioned selection operators (tournament, marriage, and courtship) were also compared, with courtship consistently outperforming the other two. The setup combining the best design choices was compared on a set of optimization functions, outperforming traditional Genetic Algorithms persistently. An additional setup was tested, where Mate Choice is coupled with an incest prevention threshold, below which attractiveness for a particular individual is reduced to zero. While preliminary results showed it to be contributing, an extended study suggests that it may work as an intrinsic part of Mate Choice with implications hard to isolate.

De et al. [65] propose three approaches for positive assortative mating selection. The first one selects the fittest individual as female and the individual in the population whose hamming distance is minimum but not zero as a male partner. The second method works similarly on the first selection step but then selects as the next female the individual whose hamming distance is minimum but not zero to the previous male. The new male is selected by the same means as in the first operation. In the third approach, the first female will be the fittest individual in the population and the male will be the second fittest, and so. In all methods, individuals are allowed to mate only once and are thus removed from the population. The authors suggest that while hamming distance is a good genotypic measure, fitness is an appropriate phenotypic measure. The three approaches were compared to a standard Genetic Algorithm and to Eshelman and

Schaffe's non-incest approach [86, 87, 88] in a test set including function optimization problems, a task of choosing parameters for a multi-layer perceptron, and a problem involving the extraction of object regions from noisy images using neural networks. Results show general improvements when compared to a standard Genetic Algorithm. When compared to the non-incest approach, the first method performs sometimes worst while the third method is consistently better. As a conclusion, for the particular scenarios tested, fitness-based pairing seems to outperform hamming distance based pairing.

Fernandes et al. [95] have also tested the usefulness of assortative mating as a selection method. In their approach, an individual is selected for the role of female using a traditional fitness-based selection operator and a set of mating candidates is also selected through fitness. Each of the mating candidates is then evaluated according to its hamming distance to the female and the most fitting one is selected for the role of male. Two approaches are considered: positive assortative mating favors the most similar mating candidate; negative assortative mating favors the most dissimilar one. On a vector quantization problem, similarity was measured using a squared euclidean distance. The approaches were compared to an iterative search method and Genetic Algorithms employing the iterative method. While the iterative approach reportedly found the optima on some instances of the problem, other approaches came very close.

The positive assortative mating approach produced results similar to those of a standard Genetic Algorithm while the negative approach outperformed both, specially on more difficult instances. The negative approach seems to become stuck in local optima less often, increasing its chances of finding the global optima. The size of the set of mating candidates was also discussed. It's suggested that boosting the selection pressure by increasing the set size is beneficial for negative assortative mating, due to promoting the pairing of dissimilar individuals which results on an exploratory behavior. When coupled with a population of varying size, as tested by Fernandes and Rosa [89, 92], the aforementioned algorithm outperformed a standard Genetic Algorithm with both variants. Tested in a royal road problem, the negative approach achieved the best results, most likely due to its increased aptitude to escape local optima.

In two publications, Huang [135, 136] applied negative and positive assortative mating to royal road problems, relying on hamming distance to measure the distance between a female parent and each remaining individual in the population, for the role of male. Initially, it's suggested selecting the mating candidate whose distance is higher or lower, in a tournament fashion, but it is also suggested to attribute a selection probability proportional or inversely proportional to hamming distance. Using Markov chain analysis, it's demonstrated that on this particular scenario, dissimilar mating produces a higher population diversity than similar mating and contributes positively to finding a single top performing solution, an effect which becomes more significant for performance as the mutation rate is lowered or as the objective function becomes more complex. Nonetheless, it's also shown that dissimilar mating can result on a higher rate of destructive crossovers, disrupting building blocks and causing potential decreases in the population's average fitness. Similarity mating is shown to avoid such concerns.

Ishibushi and Shibata [140, 141, 142, 143, 144] couple a mating strategy with traditional algorithms for multi-objective optimization. Their initial approach [143] selects an individual for the role of female as well as a set of mating candidates using a binary tournament operator. Afterwards, mating candidates are evaluated based on either phenotypic or genotypic (hamming or euclidean) distance to the female and the most similar or most dissimilar is selected for the male role. On follow-up studies [140, 141], the same operator and comparisons between the two choices are also included. The approach is tested on multiple problems such as multi-objective Knapsack, permutation

Flowshop Scheduling, Onemax and Zeromax problems. An analysis shows that preference for dissimilar mates improved performance on smaller instances of the Knapsack problem while a preference for similar individuals was more valuable for larger instances. Moreover, negative assortative mating seems to have contributed to diversity in the population, and positive assortative mating to an increased convergence speed [143]. The effect seems nonetheless to be highly dependent on the problem. Complementary experiments suggest that positive assortative mating can also contribute to the maintenance of diversity without compromising convergence [141].

The size of the tournament operator has also been studied, with experiments showing that a higher selection pressure can promote a decrease in the similarity between mating partners, which may be counter-intuitive (potentially due to pairing individuals in multiple peaks) but that slows convergence speed [140]. Overall, such effects can be seen as positive or negative, depending on the target problem. An alternative mating scheme was also proposed, aiming at better balancing diversity and convergence speed [142]. The operator works by building two pools, one for the role of female and one for the role of male, using binary tournament selection for choosing candidates. For female selection, the center vector of the first pool is calculated and the most distant candidate is selected. For the role of male, the candidate in the second pool that is most similar to the female is chosen. The method therefore suggests selecting a pair that within is closely similar but as distant as possible from a sample's center, aiming therefore at means for convergence but exploration at the same time. The authors argue that the methodology can be compared to attributing a combined fitness value to pairs, promoting those that are extreme when compared to others [142].

A version where the female is selected either as the most distant candidate or the most similar candidate to the pool's center was later studied, as well as the selection of the male for negative or positive assortative mating [140]. The authors argue for the flexibility of the system to adapt to any search space through the control of the size of the pools as well as the metric used for the selection of each gender. Achieving both convergence speed and diversity shows to be a highly difficult task, where design choices have a strong impact and are very dependent on the problem and other factors. An adaptive strategy for the method was also presented [144] focusing on two strategies: focusing on convergence in the beginning of the run and diversity later; focusing first on diversity and later on convergence. This is achieved by adjusting the candidate pool sizes to emphasize the desired strategy. Arguably, the method shows potential for a better control of diversity and convergence, with results consistently improving in NSGA-II [141, 144]. Overall, they report benefits from combining extreme females with similar males, mostly because of its positive effect on diversity, rather than convergence speed. Regarding hamming and euclidean distances, it's discussed that they perform better or worst depending on the problem and design choices.

Ochoa and Jaffe [209] conducted experiments with both positive and negative assortative mating on a knapsack problem with moving extremes. Their approach selects individuals for the role of female as well as for the set of mating candidates using traditional fitness-based methods, and also compares haploid to diploid representations. Apart from suggesting that haploid representations worked better than diploid, reported results show that negative assortative mating performed better on the target problem than a standard Genetic Algorithm, which in turn performed better than positive assortative mating. Interestingly, the study also focuses on the relation between each approach and mutation rates, and observes that when moving from negative to positive assortative mating, mutation gains a much more important role in the maintenance of population diversity, which is directly impacted by the mating strategy.

Further analysis by the same authors [208, 209] on the dynamics between assortative mating and mutation rates, for the goal of maintaining population diversity was later published. The authors discuss a mutation rate threshold over which building blocks in genotypes are destroyed at a faster degree than they are reproduced. Results suggest that the threshold is higher on positive approaches and lower on negative ones. It's argued that mating with similar individuals promotes the consistency of the genetic pool, whereas the opposite can be rather destructive. As a suggestion, mutation rates should be considered while taking that into consideration in order to achieve a balance between mutation and assortative mating strategies.

García-Martínez et al. [108] have studied the application of assortative mating as defined by Fernandes et al. [92] on the selection of mating partners in a multi-start local search method used to enhance particular solutions. When an individual is chosen for local search, it takes the female role and a set of male mating partners is selected. For that purpose, assortative mating is performed multiple times, each with a set of randomly selected mating candidates. Recombination takes place through a multi-parent uniform crossover operator, relying on all selected parents and producing one offspring. If the new individual is better than its mother, it takes its place in the population. The approach was tested on a large number of target problems such as Onemax, Maxcut as well as deceptive function, having shown to be capable of outperforming other traditional local search procedures on most instances.

A more ambitious study by García-Martínez et al. [182] explored multiple selection operators to be applied with parent centric crossover operators. Initially, the authors tested three scenarios: i) selecting the female parent through uniform fertility selection (individuals have a higher chance of being selected if they had fewer chances to reproduce in the past) and selecting the male parent through negative assortative mating [92], coupled with a replace-worst strategy; random selection of both parents with roles randomly attributed, using a crowding replacement strategy; selecting the best parent as a female and a set of random male parents, and using a multi-parent crossover operator to reproduce a set of offspring, from which the best two compete with two random individuals in the population for their spot. The authors then suggest introducing a gender determination technique instead of allowing the whole population to be eligible for either role. The proposed method relies on two thresholds: individuals whose fitness is over the first threshold are put in the female group; individuals whose fitness is over the second threshold are put in the males groups; the approach allows individuals to belong simultaneously to both groups. Arguably by tuning each threshold, accuracy and reliability can be balanced, as can the exploratory or exploitative character of the evolution process. It's also discussed adapting between both behaviors dynamically, focusing on exploration for the first generations and then shifting the behavior towards being more exploitative.

Experiments on a test set of optimization functions shows that the gender differentiation technique improved results on the three considered approaches, and that the adaptive setup performed more robustly than focusing on exploration or exploitation alone. García-Martínez and Lozano continued to study the application of their adaptive strategy on further publications [106], using the first selection mechanism described above. They suggest using a low number of females when tackling unimodal problems, for a better accuracy and exploitation, and higher number in multimodal problems for a better exploration. The approach was used on a large set of optimization functions showing varying behavior depending on the characteristics of the target problem. An extensive analysis of the algorithm's behavior is included in a later study [107] where comparisons are made with multiple optimization algorithms as well as between different parameter setups. Conclusions are in-line with previous studies and contributions were made regarding design options when focusing on this approach.

Raghuwanshi and Kakde [235] describe a Genetic Algorithm with species and genders. After initialization of the population, gender determination is done as follows: each individual is given a number of trial opportunities to mate; at each opportunity, four partners are randomly selected from the population and parent-centric multi-parent recombination [126] is performed to generate offspring; if the offspring is better than its first parent, it takes its place; the process is repeated until all individuals have had their share of opportunities to mate. At this point, those individuals more successful than average are labeled as females and the others as males. Success in this case is measured not by fitness but by the ability of producing offspring that are better than the first parent. Therefore, during the described process, every time an offspring takes the place of its parent, a counter for that spot is incremented, for later comparison. After gender determination, species are organized around each female, and males are attributed the species of their closest female, according to euclidean distance. A later study [234] showed how the number of trial opportunities given to each individual to show its fertility influenced the outcome by either promoting the very elite ones to females (through a large number of trials) which has been shown to be beneficial for unimodal functions, or relaxing the pressure (through a smaller number of trials) which benefits behavior on multimodal functions.

During reproduction, each female selects a number of mating partners randomly from its species and parent-centric multi-parent recombination takes place. Two possible operators are applied, one more focused on exploration and the other on exploitation. Which operator is applied is determined through a voting system encompassing all contributing parents. Each individual's vote is encoded as an extra gene in their genotype. Alternatively, exploration is endorsed in the first generations and the strategy is shifted to exploitation towards the end [234]. If a female has no males in its species, it's bound to reproduce asexually relying on mutation only. New offspring compete with their parents for a place in their own species and, if they successfully replace a parent, the counter attributed to that species is incremented. If a species shows poor performance, it is absorbed temporarily by the closest one (in euclidean space) with all new members acting as males. This composite approach was tested on the minimization of a set of unimodal and multimodal functions and compared to state of the art Genetic Algorithms and Evolutionary Strategies [124, 182], with results showing that while being able to successfully find the global optima, its performance was only competitive in some instances, while performing worst on the others.

A different species assignment strategy was proposed by Patel et al. [222], relying on a k-means clustering algorithm [187] to distribute the location of species in the search space, before the evolution process can begin. After the step where females and males are assigned to a species, here referred momentarily as cluster, the mean of the cluster is calculated based on its inhabitants, and the female is updated according to that mean. Males are then reassigned to their closest females (which may have changed due to females having new locations), and the process is repeated until the females stop moving. The approach aims at ensuring that females are well distributed in the search space for a more contributing role in the evolution process. Tests were performed on unimodal and multimodal functions and compared to previous results [235]. The k-means strategy shows improvements in regards to the number of function evaluations required to find the optima. The authors link this behavior to better distributed and separated species, improvements in diversity and to the self-adaptive nature of the species assignment algorithm, which automatically detects the number of clusters and initial position of centroids depending on the target function and its characteristics.

Gálan et al. [104] study a mating strategy with different mating preferences and evaluation metrics. Their operator starts by selecting a set of individuals randomly from the population, from which the fittest one is given the role of female and the remaining the roles of mating candidates. The candidates are then ordered according to one of two criteria: fitness or euclidean distance from the female. Their rank is regarded as a mating index and three selection strategies are analyzed: selecting the lowest index (fittest or most similar); selecting the highest index (less fit or most dissimilar); and a self-adaptive scenario where each individual encodes a mating index, allowing females to choose the mating candidate corresponding to their encoded mating index. Experiments are conducted also on the size of the candidates pool and index span. Regarding the self-adaptive scenario, encoded mating indexes are initialized randomly and inherited as part of the chromosome through crossover. Mutation is applied specifically, allowing for the increase, decrease, or reset of the index. All approaches are tested on the optimization of unimodal and multimodal functions, and on a transverse analysis results show a great dependence of performance on the candidates pool size and the preferred mating index. In detail, the higher the rate of multimodality, the higher the mating index should be. The self-adaptive approach, while achieving good results on unimodal functions, showed a high dependence on the candidate pool size on multimodal ones. Regarding the distance metrics used, results are comparable for a good part of the test set. As future work, the authors discuss controlling the mating index on a population level or in a deterministic manner, as well as allowing for the encoding of the mating pool size for a self-adaptive control.

Jung et al. [152] employ a global mating strategy for a two gender population where all mating pairs are determined simultaneously using an Hungarian method [166]. They describe three approaches: the first one attempts to minimize the sum of distances between all mating pairs; the second one aims at maximizing that same sum; the third one pairs individuals randomly. During selection, as a consequence of the Hungarian method, all females mate once with a male, producing also a male and a female offspring. For testing, they tackle a Traveling Salesman problem using a quotient swap distance as a phenotypic distance between individuals, and a Graph Bisection problem for which they rely on quotient hamming distance. On both scenarios, the authors discuss that the first approach has a strong impact on diversity, causing it to drastically fall, which accounts for it performing worst than the other two approaches. Through the analysis of these experiments and the character of the search spaces, the authors propose an approach where the selection method changes in a deterministic way at a pre-established generation, so that the benefits of positive and negative assortative mating (as a global operator) can be better balanced.

In a follow-up study [153, 154], the authors suggest choosing the selection method for the next generation based on a voting scheme. For that purpose, the authors use two thresholds to establish three voting intentions (over the higher threshold corresponds to the first approach, below the lower threshold corresponds to the second method, and in between corresponds to random pairing). After each reproduction step, a vote is cast whose value is determined through a function that captures a ratio of distances between parents, offspring, and within each gender (parent and offspring). As an exception, if the distance within each gender is zero, the vote goes to the second method. The authors argue that such an approach allows the population to adaptively choose the most profiting strategy based on its own constitution and feedback, towards a better balancing between exploration and exploitation. When compared to their previous approach, results show improvements.

4.2.4 Composite attractiveness

This section covers approaches where evaluation of mating candidates is done through a number of chained rules, such as if-else rules, or attractiveness functions that focus on the combination of multiple metrics, such as weighted functions. More exotic approaches for composite attractiveness can nonetheless exist, such as the application of sub-populations to finding all the peaks in multimodal functions, explored by Ryan [249]. The approach considers a number of sub-populations equally spaced in the search space. Individuals are initialized and belong to one or multiple sub-populations, depending on their distance to the center of each sub-population. Within each sub-population individuals are evaluated with a weighted product accounting for global fitness and distance to the center. Therefore, individuals have multiple evaluations that are dependent and relevant for each particular sub-population that they belong to.

Moreover, each individual carries an extra gene that determines their preference for outbreeding. During selection, a random sub-population is chosen from which an individual for the role of female is selected probabilistically, according to inner-population fitness. The female's preference for outbreeding is checked against a pre-established threshold, if it is below the threshold then it inbreeds, otherwise it will outbreed. The second parent is selected through the same means according to the female's breeding choice. The additional gene is passed on in reproduction through the same means as other genes and the fitness values of offspring are attributed through the same means as before. Four approaches are considered for selection: always inbreeding, with or without replacement; control inbreeding through self-adaptation, with or without replacement. Results suggest an increased performance by the self-adaptive method when compared to others, and also to a standard Genetic Algorithm, and other niching methods from the literature on tougher instances of the problem.

Matsui [190] proposes combining both fitness and negative assortative mating in a mating evaluation metric. After an individual has been selected for the role of female, a mating partner is selected from the population so that it maximizes a weighted function that combines the candidate's fitness and hamming distance to the female. Therefore, the strategy favors mating with high fitness, dissimilar partners. The method was tested in combination with a replacement strategy where new offspring replace their parents. As a result of both strategies, the approach improved results when compared with a standard algorithm in Royal Road problems and Knapsack with moving extremes, arguably as a result of its increased aptitude to maintain population diversity.

Jassadapakorn and Chongstitvatana [149] propose the following method for mate choice: an individual for the role of female is selected through traditional fitness based methods, and a set of mating candidates is selected randomly; mating candidates are evaluated through the product of their fitness with their hamming distance to the female. The contribution of the hamming distance is however transformed through a power function. While dissimilar candidates are always favored, the contrast between distances can be increased by upping the value of the power constant. A constant of value 0 will correspond to a linear function while higher values will increase the attractiveness impact of the hamming distance. The authors propose selecting the constant from an integer interval dynamically and according to its own contribution to the evolutionary process. Initially, the contribution of each possible value for the power constant is set to 0 and therefore, the value used in each selection step is set randomly. At the end of each generation, the success of each reproductive step is measured by comparing the fitness of each offspring pair to that of their parents and, if at least one offspring performs better than the worst performing parent, the contribution counter of the constant used on that selection step is incremented. In the next generation, constant values will be chosen following the distribution of contributions. As a result, the use of each constant value is dynamically set from generation to generation and the preference for dissimilar individuals is adapted.

The approach is applied to Onemax instances, a deceptive function and a multimodal function. Results for the Onemax problem show a tendency for low constant values, thus less preference for dissimilarity, which causes faster convergence. On the deceptive problem there's an initial preference for low constant values which later changes to higher values in an attempt to escape local optima by promoting diversity. On the multimodal problem, there's a preference for higher constant values in order to promote exploration over the whole run. When compared to manually set values, the system is able to dynamically go toward optimal values, showing therefore generalization properties. Overall, performance was competitive on the test set. The same authors [150] suggested a different approach where constant values, rather than being dynamically used for selection, are used to control a sub-population each. The performance of each sub-population, in regards of their best performing individual, is controlled and poorly performing ones are dropped periodically in order to focus computational effort on the better performing ones. Results and conclusions regarding behavior and preferred values was in agreement with the aforementioned discussion.

Fry et al. [103] study the application of Mate Choice in a model using a Genetic Programming representation. They suggest selecting an individual for the female role using a standard fitness based approach and evaluating a set of mating candidates to find a pair. Individuals are evaluated based on fitness and edit distance to the female, so that similar individuals are penalized. Therefore, individuals that share no edit similarities with the female are attributed an attractive value equal to their fitness, while those that are increasingly similar are penalized proportionally. Two metrics for measuring similarity are considered: relative distance measures how different two specific trees are; absolute distance measures how different any two trees are. Moreover, self-adaptation was introduced as a mean to decide which operator to apply for the selection of males, either tournament selection or Mate Choice.

Two setups were tested: in a population-level approach, the use of each operator is reinforced from one generation to the next one based on how they succeed to produce offspring that are fitter than their parents; in an individual-level approach, individuals encode which operator should be applied, with adaptation relying on inheritance and mutation. All possible setups combining the above possibilities were tested on Symbolic Regression tasks and a Max function where the goal is to produce the maximum value possible within a maximum tree depth. The approaches were compared between them and with a standard Koza [165] approach. The authors report that between the two metrics tested for similarity, relative edit distance performed better overall, arguably due to its better ability to contrast on smaller differences, which is beneficial as trees converge and become more similar. The Mate Choice approach is able to accelerate evolution and enhance Genetic Programming performance. Regarding self-adaptation, the authors find it to be valuable, helping balancing exploration and exploitation as a response to population dynamics over each run. The individual level approach using the relative edit distance was the overall best performing setup.

Zhang et al. [324] present a scheme where individuals are evaluated through multiple steps. Firstly, they are evaluated on their performance on the target function, then their fitness is adjusted through a weighted function that accounts for the fitness of their parents. This process is inspired by the Baldwin effect [18] and improves the fitness of individuals whose parents have a higher fitness, while reducing the fitness on individuals whose parents have a worse fitness. Secondly, sharing is applied to adjust fitness values of individuals in the same niche. Individuals are randomly attributed a gender at initialization or after reproduction. Selection takes place in two stages: the top performing individuals in the female and male groups are directly selected through elitism and paired by rank; tournament selection is then applied on the remaining individuals in each population separately and females and males are paired randomly.

Crossover and mutation rates are also adapted deterministically, gradually reducing throughout the generations. When two individuals have been paired, their crossover rate is also influenced in accordance with their hamming distance, in a bid to promote mating between similar individuals. The approach is tested on a set of optimization functions. The authors argue that such an approach adaptively adjusts the role of the reproduction operator, to bring up cooperation and competition through different means, while the Baldwin effect promotes polymorphism. Compared to standard Genetic Algorithms and to an adaptive Genetic Algorithm [278], the algorithm reaches better results, showing ability to tackle high dimension problems while helping avoid premature convergence. A second study by Zhang et al. [325] compares the approach with various state of the art particle swarm optimization algorithms and argues that the approach can find optimal or close to optimal solutions, maintaining a competitive performance.

Varnamkhasti and Lee [148, 294] and Varnamkhasti and Vali [293] suggest a strategy for gender determination that at each generation attributes male or female genders in a sequential and alternating way, in an unsorted population. Also, at each generation, the order of attribution is switched. The authors compare this methodology with a similar one but on a fitness sorted population, random attribution, and splitting the population halfway. The authors consider their approach to bring advantages, probably related with attributing sibling offspring to different genders [148]. During selection, a female is selected through tournament selection, a set of mating candidates is randomly selected, each one is assessed using hamming distance to the female and the most dissimilar one is selected for mating. However, if two or more candidates draw, the fittest one is given the opportunity, and if there are still draws, the candidate with highest number of active genes is preferred. If all three criteria fail to differentiate between candidates, a random one is selected. Reproduction then takes place, with one study focusing on experiments with fuzzy crossover and mutation operators and varying probabilities [148]. It is argued that this negative assortative strategy with additional rules contributes positively to maintaining diversity and avoiding premature convergence. The approach is tested on a multidimensional 0/1 Knapsack problem and shows performance improvements on a standard Genetic Algorithm.

4.2.5 Genetically encoded preferences

Miller [199] as well as Miller and Todd [288] describe an option for adding Mate Choice to Evolutionary Algorithms as a generalizable approach. They describe that after a parent has been selected for the role of female, an additional step must take place so that each female (and potential mating partners) has a chance to sample multiple potential partners and choose the most attractive based on its own preferences, perhaps stochastically, and perhaps mutually. The authors propose representing preferences as probability-of-mating functions, which span over the entire n-dimensional phenotype space, giving each location and therefore all individuals, a probability of mating or attractiveness level. A probability-of-mating function can therefore be seen as an extra dimension where peaks correspond to ideal partners and low peaks correspond to unattractive ones. Mating preferences can be encoded as a set of genes that control the parameters of the probability-of-mating function, built in relation to a sexual reference position in the phenotype space, which can be determined in one of four ways: i) identical to the individual's phenotype location; ii) the phenotypic location of a parent; iii) the average of all phenotypic locations of the population; iv) an absolute position in the phenotype space. Which strategy to use can also be determined genetically on an individual-level. Given this reference position, the function can be built as a radially symmetric function with a given width, either around it for non-directional preferences or offset by a given vector for directional preferences. The strategies to determine the sexual reference position have been extensively discussed [288].

Miller and Todd have strongly advocated for the role of Mate Choice in Nature, its impact, characteristics and benefits, and have lengthily discussed how Mate Choice can be critical in speeding optimization, avoiding local optima, developing important new evolutionary innovations, increasing parallel search, niching and speciation [201]. They have also argued for their approach to be a better alternative than other established methods in optimization, while maintaining a closer metaphor to nature. Some of these methods include positive assortative mating for niching and speciation, negative assortative mating for outbreeding, balancing the two, selective breeding, promotion of novelty or aesthetic Sexual Selection [199]. Todd and Miller coupled their ideas with a Genetic Algorithm to study the evolutionary dynamics of populations. They present a simulation where individuals are placed in a two-dimensional space and are solely represented by their coordinates, thus evaluating mating candidates based on those coordinates as well [288]. In a following study, Miller and Todd [200] rely on parent-relative directional preferences (with an offset). Their individuals encode their own 2D coordinates, two genes to determine the direction of the offset, and one gene for the length of the offset vector. An additional gene determines the width of the basin of attraction and therefore the pickiness of individuals when choosing a partner.

Two scenarios are considered, one where there's Natural Selection and one where only Mate Choice occurs. During selection, an individual is selected for the female role through a traditional fitness-based method or randomly, depending on the scenario. A mating candidate is selected through the same means, and both the female and the mating candidate evaluate each other through their personally built probability-of-mating function. The female in this case uses its directional preference offset while the male candidate does not. The pair's probability of mating is the result of the product of both evaluation results. If they end up pairing, reproduction occurs, otherwise a different mating candidate is selected for a few tries, after which a different female is chosen. During reproduction, offspring are produced through crossover and mutation. In a scenario with Sexual Selection alone, the authors initialize the population in the same location and with directional vectors pointing in the same direction. They observe that phenotypes follow the direction of the vectors in an attempt to better adapt to such preferences. They also observe that preferences are able to diverge from their initial configuration, causing the phenotypes to move in other directions, which through self-reinforcement, results in drifting in the population. This produces an arms-race between phenotypes and preferences.

In a scenario with both Natural and Sexual selection, fitness is given so that individuals in the south-west corner have maximum fitness and those at the north-east corner have the lowest fitness. A first test where mating preferences point towards north-east shows the population moving through Sexual Selection, but eventually Natural Selection takes its toll and promotes those individuals that are fitter for survival. The mating preference vectors adapt to these phenotypes through self-reinforcement.

When the population is grouped in the south-west corner, peaking the fitness function, preferences may again drift and pull the population in a runaway process, showing the ongoing tug-of-war between the two forces. In a second test where mating preferences initially point toward south-west, both forces reinforce each other's effect and the population moves with increased momentum towards the optimum. Eventually they will reach the described scenario where individuals are packed around the function's peak and mating preferences may drift and pull the population through mutation. The authors conclude that Sexual Selection is capable of a strong role in evolution even in the presence of strong and consistent Natural Selection pressure. A later study by Todd and Miller [286] further contributed to testing. Applying Sexual Selection alone, individuals are initialized in the center of the simulation space and directional mating preferences are initialized in random directions. Results show that the average location of the population wanders through the simulation space with individuals moving towards Mate Choice peaks, which shift unpredictably from time to time, causing the population to follow. Mating preferences and traits seem in an arms race for adaptation.

A simulation where preferences are non-directional causes the population to jiggle around its initial location. In the previous scenario but with both Natural and Sexual selection (fitness function peak is in the center of the simulation space), the interplay between the two forces is visible, with Natural Selection pushing the population towards the peak and Sexual Selection making it drift towards its own desire. This causes the population to diverge from the peak, in an effort to escape and explore the search space. The authors compare the effect with other induced behaviors for escaping local optima. Finally, in a scenario with only Sexual Selection and non-directional mating preferences, mating partners are chosen according to each female's sexual reference position and choosiness. The scenario shows the ability for sympatric speciation, with a slower but steadier movement of the population that potentiates splitting. The same behavior can be observed with directional preferences, but the authors show that in order to achieve this, they had to double the amount of genes encoding traits and preferences, so that they could slow the effects of mutation. Experiments with the sexual reference position being determined by the individual's own phenotype or by an absolute position that is inherited through the genotype, and in a scenario with no Natural Selection, speciation was observed. The effect was seen to increase with the mutation rate [288].

Ventrella [295, 298] developed a virtual ecosystem that simulates a 2D pond that is inhabited by a population of swimmers. These agents encode a genotype that represents their morphology and control. Their phenotype is focused on producing locomotion, and apart from having perception systems, these agents are capable of two mindsets: foraging for food and pursuing mating partners. Depending on their energy level, they will engage in one of the two tasks. Individuals are not explicitly evaluated, but their ability to survive and reproduce dictates their success since how much their reproduce is linked to how much energy they can dispense. Crossover and mutation ensure the inheritance and variation of genes from parents to offspring. Among other experiments, Ventrella [295] adds an extra gene to the genotypic representation that is initialized randomly to represent a color. This gene represents each individual's mating preference, meaning that when looking at other individuals as potential mating partners, they will be more attracted to the one most composed by body parts with their preferred color. While this aesthetic feature has no fitness cost associated to maintain, the authors observe a mean of sympatric speciation, with individuals splitting into smaller populations that promote reproduction with different colors and that only occasionally are capable of interbreeding. These sub-populations show a loop between their traits and preferences so that individuals prefer to mate with others of the same predominant color as themselves.

Ventrella [296, 297, 298] later expanded the virtual ecosystem so that body parts can accommodate more complex formats, thus producing more complex morphology (such as parts of different size and formats) and behaviors. A preliminary study [296] using the aforementioned color based preference would prefer mating partners with more massive parts, because of their higher color area. The authors discussed that while it was expected that such a scenario would have a negative impact on locomotion and therefore on hunting and mating abilities, efficiency proved to be similar to experiments without such preferences. This suggests a linkage between evolved colors and high performing individuals. Further experiments [297, 298] used different mating preferences, this time acting as population-based choices rather than individually encoded: color (same or different); size (big or small); movement (hyper or still); length (long or short); shape (straight or crooked). Reported results show that depending on the mating preference chosen, the corresponding characteristic spreads through the population and has an impact on the locomotion pattern followed by agents. In this case, there's a cost or genetic link between the preferred feature and the survival ability of each individual. Their struggle for attractiveness impacts their struggle for effectiveness. In some cases, strategies emerged that took advantage of attraction or being available to many individuals, rather than efficiently tracking for food, while others balanced both behaviors. A scenario where the preference was skewed to individuals remaining still has arguably produced polymorphism, with some agents maximizing attraction and saving energy for reproduction and others moving very fast and acting as breeders.

Jaffe [147] studied a gene-controlled model with different mating strategies on a multi-agent simulation where individual behavior is determined by the genotype. The simulation allows for different kinds of phenotypic interactions that are ruled by diploid chromosomes and alleles activated randomly. Regarding reproduction through Sexual Selection, various genes are relevant: one gene determines the gender of the individual, two establish the sex determination mechanism for offspring, one gene controls the level of attraction of females towards males, and other control the age for reproduction as well as the size of the mating candidates pool to be assessed by females. An additional gene determines the Mate Choice criteria to be applied by females: random; high attractiveness as determined by the aforementioned gene; younger or older males; dissortative mating; good genes for survival; handicaps. The last two are determined by survivability related genes. Depending on the gender, different genes will be activated. During selection, females that are allowed to reproduce look for a male of the same species, analyzing a pool of gene-defined size, using its own strategy and judgment. During reproduction, standard inheritance rules apply. Two types of experiments were performed: isolated populations were tested, each using a different selection criteria; a global population where all strategies are initially uniformly distributed. The author discusses among other things that individuals whose phenotype is influenced by a large number of genes are likely to produce good signaling attributes for gene quality, and that Mate Choice strategies are expected to be sophisticated and assess multiple signals concurrently, potentially reflecting good genes or similarity. Also, it's argued that results are favored by a higher degree of positive assortative mating.

Lerena [177] explored the encoding of complex preferences, by simulating the evolution of a population with two different degrees of complexity competing against each other. The system relies on Mate Choice alone and introduces varying levels of cognitive and evaluation noise, as a strategy to study complex evaluation of mating candidates in natural populations. The genotype used in the simulations encodes binary traits and binary preferences for each trait, and also a NK-table, which is a function defined over N-dimensions of preference vector, with K interactions within them. During evaluation, while the preference vector determines how traits are perceived, the NK-table determines their combined attractiveness value. During reproduction, each individual has a chance to take the role of female and is presented with a candidates pool, randomly drawn from the population. Evaluation is done through a XOR operator between the female's preference vector and the candidate's trait vector, with the resulting intermediate vector being used as input for the NK-table, which returns the respective attractiveness value. The most attractive candidate is finally selected for reproduction. Crossover is applied by switching chromosomes as no intra-chromosomal changes are permitted. Still, mutation may take place within the traits and preferences chromosomes. Over the evolutionary process, NK-tables are inherited but are immutable and represent the rules of evaluation. Overall, the study suggests that high perception noise or high rates of mutation give evolutionary advantage to simpler preferences, while the opposite is true. Regarding evaluation noise, high levels favor complex preferences, with the reverse happening for low levels. An extensive study later explored the complexity of mating preferences and their response to perception and evaluation noise, as well as mutation levels [178], extensively discussing implications on natural and artificial systems.

Beck et al. [25], while focusing mostly on biological behavior, developed simulations with a very large population (10.000 individuals) using Genetic Algorithms with genotype-encoded mating preferences. Individuals encode a set of genes for survival purposes but also 10 genes, each corresponding to an age and encoding the probability or preference of mating with a candidate with that age. Each individual therefore has an age propriety that increases at each generation from 1 to 10. The population is partitioned in half between males and females and during selection, all females have a chance to reproduce. For each female, candidate males are selected consecutively until one is accepted or a number of trials is reached, at which point a random candidate is accepted. Mating candidates are selected randomly and are evaluated according to their age and the mating preferences of the female. When a male is accepted as a mating partner, reproduction occurs and produces four males and four females. After all offspring have been generated, a two step survival procedure takes place. First, individuals in the population are evaluated through a combination of fitness and age, stochastically removing a subset according to their probability of survival. Individuals that have reached the age limit are also removed. New offspring go through the same process but relative to fitness alone, at which point random surviving offspring are selected to be included in the population until its size is back at 5.000 individuals of each gender.

Simulations shows that, while there is no direct link between fitness and age, there's a bias towards preferring older males as age is a good honest indicator of good genes. Also, if survival pressure is increased, that preference is reinforced, while the opposite behavior is observed if pressure is loosened, which allows females to be less picky with their mates without risking the survival of their offspring. Despite the preference for older males, very old males are unlikely to be selected for because they are unlikely to exits in high numbers. They are however very likely to have passed on their genes at this point. The authors also discuss that low juvenile mortality and high adult mortality are a pressuring contribution to female preference, as older male give better proof of gene quality. If the pressure is inverted, the behavior shifts for a preference to young to middle aged individuals as old age becomes a less contrasting characteristic for quality. Additional effects of preference for older males include a stronger pressure in males for survival and less deterioration with age, as well as reducing the impact of age independent factors in evolution.

Omori et al. [215] explore a self-adaptive approach for Mate Choice on a 2-dimensional search space. Their model relies on two gender sub-populations and pre-selects females and males for reproduction based on fitness. After pre-selection, each female gets a chance to choose a mating partner from a candidates set randomly drawn from the pre-selected males. Males exhibit a vector of n traits on the 2-dimensional phenotypic trait. During evaluation of a particular male, the difference between each of its traits and the population's average is calculated, thus producing a relative vector of differences. Females will measure the similarity between that vector and a vector encoded as their own mating preferences, using a cosine function to determine their attractiveness for that male. The male candidate that produces the smaller similarity between those vectors is chosen as a mating partner. In other words, females evaluate how candidates distance themselves from the population's average on each trait, being able to adapt their preference closer or more distanced to individuals on each particular trait.

After reproduction, a male and a female are produced, thus allowing the exchange of genetic material between each gender's pool but afterwards, crossover is imposed within each gender, with individuals being selected randomly. Mutation also plays a part, with a higher rate for males in order to induce exploration and a lower one for females leading to more stability and potential in exploitation. Both operators affect traits and mating preferences. In a follow-up study [216], the idea was expanded into a parallel model where nodes run sub-populations that follow the aforementioned strategy independently, therefore allowing each node to diverge into different directions in the search space. Migration between nodes contributes to introduction of new genetic material that cause sudden bursts in evolution. Overall, four approaches were tested on flat and multimodal functions: standard Genetic Algorithm, parallel Genetic Algorithm, Mate Choice, and Parallel Mate Choice. Both of the latter, coupling Mate Choice with different rates of mutation allowed for a broader search and the escape of local optima, producing in the end better performance.

Smorokdina and Tauritz [272] and also Holdener [129] tested a self-adaptive approach for Mate Choice where individuals encode their own mate selection function. Unlike an evaluation function, a selection function takes as input the whole population as potential mating candidates and returns the one that is chosen as the best choice. The function is encoded using a Genetic Programming tree, where the terminal set has a solo item, which is the set of individuals in the population. The non-terminal set on the other hand contains a large set of operations that sub-divide or join parts of the input, based on multiple criteria. Such operations may include among others, fitness based selection, similarity based competitions etc. By combining such operations in a tree, each individual is capable of reducing the list of mating candidates to one, through a complex selection method. During selection, the individual for female role is picked through traditional means, and uses its selection function to choose a mating partner from the remaining of the population. During reproduction, two inheritance methods are considered for the selection function: if the fitness of the offspring is higher than those of the parents, and the improvement is steeper than the slope of maximum plot in the previous generation, then the offspring inherits the selection function of the female; otherwise its selection function is the result of recombination of both parents, with a chance of mutation. The approach was tested against a standard Genetic Algorithm on a test set including Onemax, SAT, and a variation of DTRAP functions. While performing better on the first two scenarios, the approach arguably failed to capture the deceptive nature of DTRAP. The authors suggest that performance may be highly dependent on the non-terminal set which was not fit for deceptive problems, restricting the features that can be assessed in mating candidates.

Holdener [129] also proposes an approach where individuals encode mating preferences as a vector of desired features. Each allele in this preference vector is linked to a locus in the candidate solution and is initialized in $[0,1]$, representing how much the individual wants its partner to encode a 1 in the corresponding locus (binary representation). The proposed model gives each individual a chance to reproduce as a female and choose a mating partner. When doing so, a mating candidate is selected randomly, evaluated by how much it meets the preferences, and a probability of selection is set. If it gets selected (through dice rolling), a second step takes place where the male evaluates the female and likewise may or may not accept it as a partner. If both agree, reproduction takes place, otherwise another male candidate is selected. Feature evaluation is done through a weighted function that takes into account preferences, traits, and how important it is that they match. Inheritance of preferences is done following certain rules: offspring inherit preferences in a way that they match the traits inherited from each parent; the new solution is evaluated and fitness compared to each parent; if the offspring's fitness is higher than that of a parent, then its mating choice was positive and both the parent's and offspring's preferences are reinforced for the selected traits; if offspring fitness is worst than a parent, preferences are penalized; the procedure affects both parents. The approach is compared along with a replace-worst strategy to a standard Genetic Algorithm on DTRAP. Performance was improved or remained competitive on all instances, while requiring less parameters. Holdener and Tauritz [130] discuss a similar approach, although selection is done using Gale and Shapley's operator for the stable roommates problem [105] which promotes the best overall pairing possible between males and females, according to preferences. For the purpose, each individual acts as a female and as a male once, and has to evaluate all others, in this case with preferences ranging in $[-1,1]$. After pairing, inheritance and preference tuning takes place as before. Results on DTRAP show competitiveness with a traditional Genetic Algorithm.

In a later study by Guntly and Tauritz [114], a similar approach is used, although, preferences are initialized to the opposite value of the encoded traits in each individual. Selection of females is done randomly, as is the selection of the mating candidates pool. A population level setup is also discussed, where two centralized preference vectors are maintained and updated for the whole population, instead of requiring all individuals to encode their own. The first vector stores how much any individual with an allele of 0 will want the corresponding allele to be 1, while the second vector encodes how much any individual with an allele of 1 will want the corresponding allele to be 1 as well. When evaluating mating candidates, individuals will look up their own alleles and consult the appropriate vector for preferences. The remaining of the evaluation process remains the same and the vector is updated at each selection step through the same feedback process discussed before, linking offspring performance to that of their parents. The approaches were coupled with a restricted replacement strategy and compared to a standard Genetic Algorithm and an assortative mating approach on DTRAP, NK-landscapes and Maxsat functions. Overall, the individual based encoding of mating preference was the most successful, although assortative mating preformed better on NK-landscapes. The centralized approach was regarded by the authors as competitive.

4.2.6 Multi-criteria evaluation

Alleson [7], while discussing ideas for a multi-function application of Genetic Algorithms addresses genders as sub-populations but also Mate Choice. It's discussed that genders can be used to tackle multiple functions, for instance females targeting one problem and males targeting another. In the proposed approach reproduction is allowed only between genders, which are attributed randomly after reproduction or through a means to maintain a stable sex ratio. Ronald [244] also discussed the topic and introduced a selection model relying on two fitness functions: while individuals are selected for the role of female through a regular fitness function, they are selected for the role of male partner through an alternative fitness function. This secondary function was referred to as seduction function, and although its outcome is not dependent on the individual acting as female, it allows the evaluation of the population based on features that are different and only indirectly relevant to their fitness value. For instance, on a Royal Road problem, seduction may be measured based on unitation features [242] (ex: number of ones represented). Reported results were poor but potential applications to multi-objective scenarios were discussed. These ideas would later be expanded to suit scenarios with multiple evaluation criteria.

Ryan [247] tackles a network sorting problem with two goals in mind: efficiency and solution size. For the purpose, he relies on two sub-populations, each focusing on optimizing one of the objectives, rather than balancing both on a common evaluation function. Individuals are divided into the two groups and during selection one from each is selected probabilistically, thus putting pressure on both goals simultaneously. The author reports that the model made individuals more likely to converge on an optimal solution while avoiding the effort of weighting the importance of each objective in a function. An expansion of the proposed strategy was discussed by Ryan [248], with sub-populations each tackling a particular objective in multi-criteria optimization. The author describes the previous behavior as a form of outbreeding and suggests introducing and balancing inbreeding as well. During outbreeding an individual from a sub-population will mate with a selected mate from another sub-population and during inbreeding the mate will be selected from the same sub-population. As a first approach, he experiments with multiple population level probabilities of inbreeding, although the results are inconclusive on an optimal rate.

The study moves on to test self-adaptive approaches, where each individual encodes its own preference regarding the strategy. During selection, three potential behaviors are tested: all individuals mate according to a population wide average probability; individuals in each sub-population mate according to their own sub-population's average probability; individuals mate according to their own encoded probability. In all approaches, preferences are initialized randomly and passed on through inheritance. All approaches were tested on a range of population sizes and on a set of multi-criteria functions, with the individual approach achieving best results, both over the average strategies and the fixed rate approaches. Further experiments were conducted, employing three alternative mate restriction behaviors: a free choice model, after the first individual and the mating candidate have been selected accordingly (inbreeding or outbreeding), allows mating only if the candidate agrees on the strategy, otherwise the candidate is redrawn; an influential partner model follows the same steps but has the breeding probability of the candidate influenced by that of the female parent through a geometric mean; an opinion reinforcement model behaves as the individual-based model but uses feedback on the quality of the offspring to reinforce their inbreeding probability in order to promote successful behavior. Among these three behaviors, only the last one achieved competitive results when compared to individual-based selection, suggesting that allowing evolution to adapt the breeding preference produces advantages.

Lis and Eiben [180] suggest using a multi-gender population to tackle the concurrent minimization of multiple functions (multi-criteria optimization). They tackle the problem by adding an extra gene to the individual's representation, encoding a particular gender. Each possible gender corresponds to a criteria and to the respective evaluation function. Therefore, during evaluation individuals are evaluated on a particular evaluation function alone, according to their own gender gene. For reproduction, one individual from each gender is selected proportionally to their fitness rank within their own gender and a multi-parent crossover operator is applied, after which the offspring will inherit the gender of the parent that provided the most genes. The authors argue that results back up the approach's abilities to find pareto-optimal solutions and to prevent the population from converging to positions optimal to a specific criterion, by relying on multiple evaluation functions. A later study by Bonissone and Subbu [29] proposed alternative means for gender determination in this setup, although applied to a flexible manufacturing problem. The authors suggest having offspring inherit the gender corresponding to the criteria in which they perform better, thus requiring their evaluation on all criteria. Additionally, they study random gender attribution.

Kowalczok and Bialaszewksi [161, 162] apply a multi-gender Genetic Algorithm in a multi-objective scenario. For that purpose, they suggest organizing the evaluation criteria into sets and creating a gender by attributing individuals to each set. This is accomplished by evaluating each individual on each criteria, producing a profit vector and attributing individuals to genders based on their sub-pareto multi-objective ranking. The same method is used to determine the gender of newly bred offspring. However, within each gender, ranking is done through stochastic remainder choice. During selection, individuals are selected and paired so that inbreeding is restricted, thus promoting pairing of individuals that specialize on different criteria. An alternative approach [27, 163, 164] organizes genders in a hierarchical tree that is used for ranking purposes. In detail, while genders are likewise determined by sets of criteria, virtual genders are formed in a upper level joining those of the lower level. Multiple levels repeat this step until a solo virtual gender is found as the tree root. In this case, individuals are not attributed a gender but are rather fed as input to the tree, which not only ranks individuals within each gender but also returns a global rank as output. This is an alternative to pareto assessment. Because individuals are not attributed a gender but are evaluated on each one and globally, the previous mating restrictions no longer apply. Both variants are tested on a set of multi-objective functions, both impacting the dimension of the objective space, helping contrasting between otherwise similar individuals. This ability ultimately contributes to promoting search in the right direction, through a more detailed ordering. Moreover, gender attribution and mating restrictions contributed to diversity and resilience to initial conditions.

Drezewski and Siwik [75, 77, 78] and Drezewski and Cetnarawicz [76] explore Mate Choice in a co-evolutionary multi-agent system for multi-objective problems. The model is distributed into nodes that are organized in a torus topology, allowing the migration of individuals between neighboring nodes. Also, both the environment and the individuals can maintain resources, that are distributed or shared through different means, depending on the study. When individuals have enough resources, they can broadcast a call for reproduction or answer to other calls, after which different mating strategies may apply. An initial approach [75, 77] relies on gender groups, one for each criteria in the multi-objective function, with each individual being randomly attributed a gender. During evaluation, individuals are assessed on the criteria corresponding to their gender and receive resources accordingly. During mating, they are limited to pairing with those of other genders. If multiple candidates answer a call for reproduction, choice is made proportionally to their resources, reproduction occurs, new offspring inherit part of their parent's resources, and are inserted in the population if they dominate one or more individuals, which in turn are eliminated. The model was tested against classical, non agent-based approaches. While it failed to outperform all other approaches on the test set, it is argued that diversity improves and that the model should be further studied.

An alternative approach [78] relies on two genders, attributed randomly during initialization. During evaluation, individuals are evaluated on all criteria and resources are transferred between individuals, from pareto-dominated individuals to dominating ones. During reproduction, individuals are restricted to pairing with the opposite gender and do so according to individual preferences which are encoded in their genotype. These preferences are represented as a vector of weights, each corresponding to one criteria, and evaluation of mating candidates is done as a weighted function combining weights and the performance of each candidate on each particular criteria. While genes and resources are passed on from parents to offspring, preferences and gender are initialized randomly. Like the previous approach, non agent-based approaches performed better but the proposed model is arguably faster and advantageous when strict processing restrictions apply. A third approach [76], for multimodal optimization, attributes a female or male gender to individuals and resources proportionally to fitness. In this setup, females have a higher cost for reproduction and different strategies apply: females have a preference for males that are more similar to them according to euclidean distance; males look for females within their neighborhood. When tested against standard multi-agent systems, and a deterministic crowding method, results show the ability to form and maintain niches in local optima basins of attraction.

4.2.7 Complementary selection

Dolin et al. [72] developed a selection strategy specially fit for problems whose fitness is a composite aggregate of multiple test cases. Their operator tries to improve the reproduction of offspring by pairing individuals that complement each others weaknesses. To do so, they propose choosing an individual for the female role through a traditional method, and consider the remaining individuals as potential partners. In order to select the one that best complements the female, the vectors of scores of both the female and each mating candidate are compared, and for each test case the maximum value is kept. The resulting vector is used to measure the attractiveness of each mating candidate, which can be calculated traditionally (sum or weighted average etc.). Ties are solved by selecting the fittest candidate. The authors argue in favor of the generalization character of the approach, which is independent of data types, representations, or performance measures, requiring only a way to determine which score is best. The approach is compared to fitness proportionate selection and tournament selection on three problems of Genetic Programming representation: Boolean 6-multiplexer, intertwined Spirals Classification, and Sunspot Prediction. The complementary phenotype selection operator shows performance gains across the whole test set, with further experiments suggesting that gains are not the result of higher selection pressure but that indeed complementarity is favorable.

Hinterding and Michalewicz [128] propose an approach for constrained optimization problems which alters the evaluation function for it to return not only the fitness value but also information on each individual's violated constraints and the extent of such violations. This information is used both in the selection of individuals for the female role but also for Mate Choice. Individuals are selected as females through a binary tournament that prioritizes feasible individuals and fitness (if both are feasible). If both participants are unfeasible, the one with less violated constraints is selected, or if there's a tie, the one that has less extensive violations is selected. Regarding the selection of males, two mating candidates are selected randomly from the population and feasibility is preferred. However, when both candidates are unfeasible and satisfy an equal number of constraints, they are assessed on how much they complement the female. In other words, the one that together with the female violates less constraints is chosen as a mating partner. The approach tries to promote complementary parents in an attempt to produce offspring that satisfy more constraints than each parent individually. Reproduction takes place through crossover and self-adaptive mutation, with a parameter for mutation being encoded in each individual and activated on feasible individuals. The setup is tested on a set of constrained numerical optimization problems and compared to a state of the art approach for constrained optimization, achieving competitive results. The authors emphasize that the approach penalizes unfeasible individuals without the need for a penalty function, while always seeking to optimize or build feasible individuals from unfeasible ones. For that purpose, the algorithm allows for unfeasible individuals to remain in the population and contribute with potentially useful genes, which promotes exploration of the search space.

4.2.8 Co-evolutionary approaches

Hillis [309] applies a positive assortative mating strategy to a problem of minimization of sorting networks, using a problem specific metric to measure similarity. By relying on a binomial approximation of the Gaussian distribution, Hillis aims at measuring the displacement between individuals in the search space and favors mating between close neighbors. Reported results show competitiveness with a collection of state of the art search algorithms, although with no improvements. Interestingly, the study also suggests the co-evolution of test cases and candidate solutions as two independent sub-populations (a host-parasite model). While candidate solutions are evaluated on their performance on the evolving test cases, the latter are evaluated by how poorly a candidate performs on them. In a way, the approach evolves not only a population of individuals but also how to evaluate them. Results from this approach are reportedly superior to all but the best of the results found in the literature at the time for Sorting Network problems. Also, the co-evolutionary approach reportedly produces increasingly complex tests in order to surpass increasingly competitive candidate solutions.

Ochoa and Jaffe [210] performed a set of simulations using Hamilton's model for host-parasite interactions [121]. The authors introduce a Mate Choice mechanism (Hamilton relied on random selection), among other features. Various strategies are considered: asexual hosts self-replicate; hermaphrodite hosts select a partner from a mating pool either randomly, favoring the most similar, or favoring the most dissimilar. The mating pool is sampled randomly from the population, either diploid or haploid representations are used, and reproduction is achieved through uniform crossover and mutation, or just mutation in asexual hosts. The simulation, much like any host-parasite model, enforces a co-evolutionary arms race where hosts and parasites evolve simultaneously, in what can be seen as an adaptive fitness landscape that is ever changing. In experiments where all reproduction strategies are competing, asexual individuals quickly takeover the population. However, in experiments where all individuals follow a particular strategy, the asexual population is outperformed by both random and negative assortative mating, when using a haploid representation. With a diploid representation, random selection is disfavored but negative assortative mating remains the best performing approach. Overall, negative assortative mating performs best by accelerating the evolution of defensive alleles against multiple parasite types.

4.2.9 Offspring competition

Aicklin and Bull [4] tackle two constrained optimization problems, nurse scheduling and tenant selection, by resorting on a hierarchical pyramidal distributed model. Within their intricate scheme, they populate nodes that are higher in the pyramid through selection of parents from lower nodes. For that purpose, they have tested an approach where an individual for the role of female is selected from a pre-selected sub-population and a set of mating candidates is selected from another appropriate sub-population. In a potential reference to certain forms of sperm competition, the female reproduces with each candidate once and the offspring that achieves the better fitness value is maintained while the others are discarded. The authors report a beneficial behavior as a result of post recombination selection.

Castro et al. [67] discuss a gender based algorithm where individuals carry a randomly initialized gene for gender determination. Their selection operator behaves by picking a female individual and a set of male mating candidates from each respective group, using fitness proportionate selection. Then, they suggest simulating reproduction between the female and each mating candidate and evaluating the prospect offspring. The attractiveness value of each candidate results from combining their own and their offspring's fitness values. The candidate that is regarded as most attractive is selected and reproduction takes place. The approach is compared to a standard Genetic Algorithm and tested on function optimization. Reportedly, it converges faster to the global optimum, although runs where the evolution process gets stuck in local optima are not taken into account.

Snijders [273] introduced an approach where paired individuals reproduce multiple times, thus producing a high number of offspring. A competitive arena is set between the generated offspring and the top performing two are kept, in a potential analogy of egg competition in some species. Interestingly, competing offspring are not evaluated on the fitness function used for survival, but rather on an alternative metric that assesses only part of the genotype. This approach also achieved slightly better results than a baseline approach but performed worst than the genders based technique discussed previously. Both, nonetheless, performed worst than a frequency dependent selection method.

4.2.10 Distributed and cellular mating

Holland formulated Echo [131, 132, 133, 151] as a simulation tool for ecological systems, where agents interact with each other and with the environment. The system consists of a geographical model, divided into sites or nodes. Each node produces resources over time, which may be consumed by agents that inhabit that node. Agents can take multiple actions and interact with other agents, with their behavior being outlined by a set of user defined rules and the resources that they own [203]. Echo doesn't explicitly evaluate individuals but those that can't maintain enough resources are bound to perish, while those that adapt better to the environment (and to other agents) will have a higher chance of accessing resources and reproducing. At each time-step and at each site, agents are randomly selected and given a chance to interact with others. If they have enough resources, that action may be either asexual reproduction through cloning or mating with a geographically close agent. Offspring inherit both genetic material and resources from their parents. Bedau uses a similar agent-based model [26]. Simulations like Echo often depend on location to determine which individuals are available for mating with females. Additionally, distributed approaches such as island models or cellular models also impose restrictions on mating, often to those in the same neighborhood.

A tag-based restriction policy is explored by Spears [277] for the goal of finding and maintaining all peaks in functions with multiple optima. Initially, a strategy where each individual has a k-bit tag and mating is restricted to individuals with the same tag is described. Another approach where a fitness sharing technique distributes fitness within individuals with the same tag, reportedly maintains most of the peaks on certain functions but sometimes loses presence in lower peaks. More interestingly, an extension to the approach suggests organizing individuals in a cellular model, using a ring topology where mating is restricted by both tags and neighborhood (two neighbors by individual), which successfully favors the maintenance of all peaks. The author reports results comparable to Godlberg's algorithm [112] without the need of computing distances between individuals, instead relying on tags for partitioning. On the other hand, it is questionable how much search can be accomplished with such restrictive operators, or how much of the results are a direct impact of initial conditions.

Unemi and Nagayoshi [291] study a training strategy for real life robot teams, with robots being controlled each by their own neural network. Their approach includes evolution as a coarse grained adaptation mechanism but agents also learn throughout their life span as a local search method. Their representation uses a chromosome for neural net weights and a second chromosome with learning related parameters. While both adapt through evolution, the genes are not changed throughout the life of each agent to incorporate what they learn while tackling their objective task. Fitness, however, is influenced by their overall behavior and determines their reproductive success. After having been evaluated, individuals gather fitness information on closely located peers and define a mating strategy according to their fitness in relation to others. If an agent's fitness is in the top third of the neighborhood, it maintains its behavior. If its on the second third, it gets information on the genetic code of a random individual from the top third. If its on the bottom third, the agents right out replace their genetic code with a mutated version of a randomly selected agent from the upper third. Individuals in the second third ultimately incorporate knowledge through traditional reproductive operators on both chromosomes. The approach was tested on a sweeping task, and multiple parameter setups tested, including varying mating pool sizes, lifespan length, among others. Overall, results show that the approach works sufficiently well even if the mating pool is very small. The size of the pool also seems to influence the optimal lifespan of individuals.

Smith and Tailor [271] presented a framework for evolving multi-agent systems for optimization. Among other actions, the system allows each agent to determine when they want to mate, how they advertise their intention, and how they choose their mating partner. The following functionalities are implemented as a base for the mating mechanism: agents can advertise their interest to mate with other agents; they determine the information that they display to potential partners; agents can hold information on agents that have shown interest to mate; they can compare between agents based on such information. At each action cycle in the system, agents seeking to mate check their list of candidate partners and, if it's smaller than a given threshold, they promote themselves as available to a random agent. When agents receive a signal for mating, they reply with their own interest in mating. At the moment that an individual has a full list of candidates, it will sort its interest using its own evaluation metric and the provided information. On a first scenario, Smith and Tailor [271] tackled a Onemax problem, where individuals promote the number of active genes to potential partners and evaluate candidates on fitness. The candidate with higher fitness is selected as a mating partner, giving place to crossover, mutation, and for a new offspring to be inserted in the system. Results show that the approach can successfully solve the proposed problem.

The same strategy was applied by Smith et al. [268, 269] on a more complex problem where agents compete on a dynamic economy where they need to allocate workers with the aim of maximizing profit. This time, while individuals still advertise the number of active genes and are selected accordingly, that information is not used as a fitness function, only for candidate evaluation purposes. In this scenario, the approach achieved better results than randomly selecting mating partners. Smith and Bonacina [270] applied the system to two multimodal functions with the goal of finding all local optima. For that purpose, they change the mating strategy so that mating candidates are only accepted into the list of each individual if their distance (phenotypic or genotypic) is lower than a given threshold. This restrictive mating strategy that promotes positive assortative mating is reliant on a pre-defined threshold on euclidean or hamming distance, therefore individuals advertise information on they phenotypic or genotypic composition. Results were favorable, with the approach successfully finding all optima. It should be noted the parallelism between the Onemax approach and a tournament selection operator while operating in a decentralized way. Regarding the second approach, the authors discuss the ability to control selection pressure through the size of the candidates pools and the number of individuals reached by advertisement. Regarding the third approach, they report being able to control the niching pressure through the threshold value. Different parameter settings and metrics are also analyzed [270].

Lee and Antonsson [172] propose a selection strategy for a steady state cellular Genetic Algorithm. In such a model, individuals are organized similarly to nodes in a topology (ring, torus, etc.), usually mating with those in their neighborhood. The author's approach propose reorganizing the location of individuals through a reinforcement learning strategy based on the reproductive success of individuals. In order to do so, the authors suggest selecting an individual for the female role and then using a stochastic method based on a Gaussian distribution centered on the female, to select a mating partner from among the neighbors. As a result, females have a higher preference for those closely located in the topology, depending on the width of the Gaussian distribution. In the first generation, individuals are sorted using the Manhattan distance between them, therefore promoting similarity, however, in order to self-organize the distribution of individuals, the authors describe a methodology that rewards mating partners that produce good offspring and penalizes the pairings that do not, by either moving them closer or further to the individual acting as female.

This is achieved through the following steps: after a female has been selected, two or more individuals are selected for the role of male; reproduction happens between the female and each male; offspring are compared and, if the farthest male produced a better offspring, the location of the males are swapped; also, if the best performing offspring is better than the female, it takes its place in the population. The authors argue that the approach contributes to an organization of the population that groups together individuals that reproduce with relative success and promotes mating between them.

The approach is tested against a standard cellular Genetic Algorithm and a standard Genetic Algorithm on finding the optima on unimodal and multimodal functions, as well as on Ising's model [145], which has been shown to require niching to solve [134]. Results show that the proposed method can outperform the standard Genetic Algorithm and converges faster to the optima than the cellular approach on all functions.

Wickramasinghe et al. [315] explore a system that aims at being a feasible fully decentralized approach with survival and selection happening independently in each node. The proposed system is a cellular GA where individuals are organized in a topology, communicating and passing information with their neighbors only. Without a centralized approach, individuals have limited knowledge on the proprieties of the population and therefore have to make decisions on their behavior locally. The authors describe each iteration of a node as a set of ordered steps. Firstly, gossiping rounds allow for the publishing and collection of information between neighbors. Based on collected knowledge, each node may make estimations on population size or other metrics as well as make decisions such as stopping evolution if the optimum has been found. Secondly, adaptation in each node happens, with parameters being adjusted in response to the data collected in the previous step. Thirdly, evolution happens. During each step and based on the parameters adapted in the previous step, each node computes its chances of survival and, if it successfully survives, its chances of reproduction. The same sigmoid function is used on both steps, defined through a center and a steepness variables, showing a linkage between survival and reproductive success. If the individual reproduces, it chooses a random neighbor that it has knowledge about and the resulting offspring is introduced as a new neighbor as well. This has the effect of maintaining relatives close to each other based on ancestry, which suggests a form of positive assortative mating. After reproduction, the iteration is over. The authors apply this model on multiple instances of the N Queens problem and report it to be feasible. Regarding selection, they discuss that maintaining offspring close to their parents was helpful for the gossiping algorithm to work properly but don't address its impact on solution quality or other metrics.

Chapter 5

Evolving Mate Evaluation Functions

Modeling Mate Choice has been discussed to be an intricate task. While Fisherian and Wallacen behaviors can be modeled with surprisingly simple representations and a few assumptions, the introduction of preference multicomponency and the implications under its veil introduce many challenges. Multi-dimensionality, complex interactions, pre-existent preferences, and other particularities have been debated as some of the most difficult barriers involved. This chapter will introduce a framework followed by two approaches relying on different assumptions – PIMP and CMP-GP. While both use Genetic Programming encodings, each offers its own potentials, with the second approach allowing for the explicit modeling of preference multicomponency and complexity through evaluation functions. In the previous chapter, many ways of modeling Mate Choice or specific behaviors related to Sexual Selection have been described. The approaches that will be introduced here, while sharing some characteristics with certain studies, are innovative and distinct in their core elements. This work is therefore of exploratory nature and will be carefully explained, both regarding the approach's inner workings but also their relationship with Natural Selection. Later, means to analyze behavioral and performance impacts will be addressed. For the purpose of clarity, problems that have traditionally been tackled through Evolutionary Algorithms will be used to illustrate and proof the use of these models.

5.1 General Framework

Following the loose classification used in the previous chapter, if one would describe the proposed model through the same means, it would be included among those that have genetically encoded preferences, sharing the bulk of its nature-inspired mechanisms, specially regarding inheritance. However, the representation of mate evaluation functions requires a broader view of Mate Choice, one that focuses not only on preferences as genes, but on a model that takes into consideration a perception system, an interpretation context for the reckoned traits, and how they are evaluated according to one's preferences into an attractiveness value. In Lerena's studies [176, 177, 178], a partial distinction can perhaps been seen, with the vector representing the perception system and context and the NK-table encoding the preferences and evaluation process for each particular context.

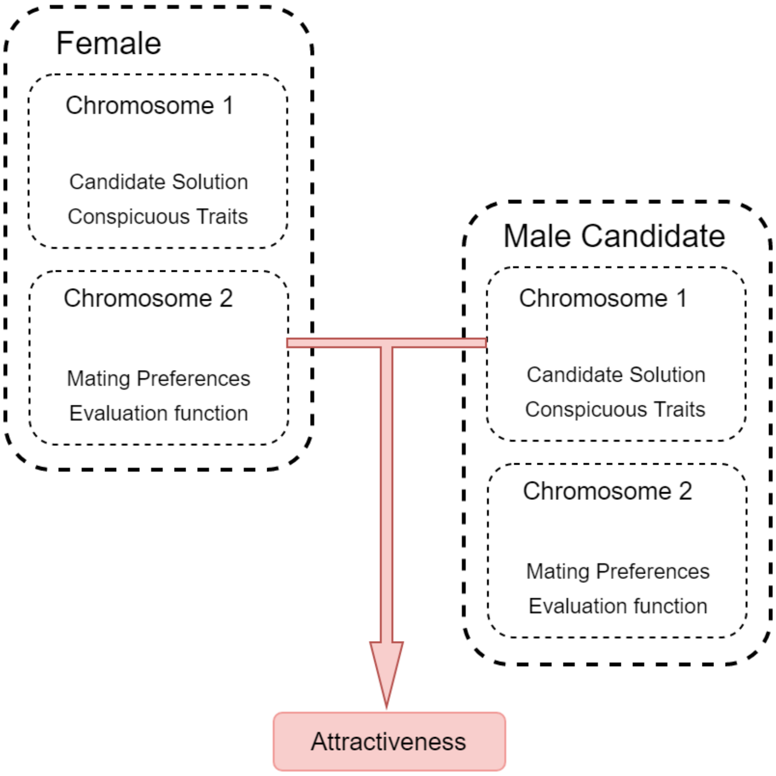

Figure 5.1: A general framework for Mate Choice with gene encoded preferences.

Figure 5.1 shows a scheme of the proposed model, focusing on representation and on the candidates evaluation process, and highlighting how each component is built and interacts with others. On the following subsections, details on conceptual choices for this general model will be introduced in an orderly fashion, starting with global assumptions and requirements and then outlining how to properly design mating evaluation functions using Genetic Programming trees. Two models for designing and encoding evaluation functions will be introduced, each with its own inspiration and characteristics. They can be said to share the same framework and its general outline but should nonetheless be seen as distinct, and representing different approaches on male candidates evaluation.

5.1.1 General Requirements and Assumptions

The introduction of complex preferences through Genetic Programming evaluation functions brings its own assumptions on representation, evaluation, and inheritance. However, with or without complexity, its important at this point to establish which are indeed the requirements and assumptions associated with the development of a general purpose framework for Mate Choice in Evolutionary Algorithms. Generally, this depends solely on the successful introduction of selection pressure resulting from genetically encoded mating preferences, and its influence on reproductive success. By itself, such a scheme should be able to mimic the theoretical behaviors discussed previously, at least to some extent (artificial populations and Evolutionary Algorithms are different from biological ones, having themselves certain assumptions and restrictions). With that in mind, many studies in the literature introduce assumptions that are unnecessary for the modeling of Mate Choice. The remainder of this subsection will aim at clarifying the requirements and assumptions needed for the spontaneous evolution of Mate Choice in Evolutionary Algorithms. The remainder subsections will then focus on the role of Genetic Programming in the introduction of complex mate evaluation functions.

Spontaneous Evolution of Mate Choice does not require:

Multiple Species
As an inner-process, Mate Choice does not depend on the concurrent initialization of multiple species in the same simulation. While from an engineering perspective it may seem useful to organize the population in distinctive species, its explicit impact on Mate Choice as a restrictive strategy is unnecessary for its emergence. Speciation may nonetheless occur as an effect of Mate Choice.

Natural Selection
Survival has at most an inhibiting relation with Mate Choice. Elaborate processes of Sexual Selection are in fact mostly dependent on the self-reinforcement of mating preferences. Open-ended systems giving rise to runaway Mate Choice are good illustrations of that matter. Nonetheless, the combination of Natural and Sexual selection is likely to be found together in Evolutionary Algorithms. Still, implicit agreements on the direction of their impact is likely the result of assumptions, design choices, or initial conditions being favorable, rather than a signal of Wallacean good sense.

Complicated components
While this study particularly focuses on the modeling of complex evaluation of mating candidates, that is not an absolute requirement. In fact, as shown by the two-locus and three-locus models, Mate Choice can take place with very simple representations. The proposed approach doesn't imply that evolved mating preferences will be complex, but rather allows for complexity to evolve as part of the Genetic Programming representation.

Gender determination
While gender differentiation is broadly present in natural population, it has been discussed previously that Mate Choice can emerge in simultaneous hermaphrodite populations without setbacks. The literature shows many strategies for gender determination, mainly establishing which individuals are available for selection for each role. However, allowing all individuals in the population to be selected for either role with no constraints will not hinder the process. Of course, female and male genders may casually emerge if there's an evolutionary edge in specializing on a particular strategy for being selected (being fit vs. being attractive).

Inheritance rules
Mate Choice abides by the same inheritance rules for preferences as any other trait, the genetic slice and splash that is commonly embodied by crossover operators. While in certain contexts it may be fruitful to design specific strategies, the traditional gene-level competition is the only requirement to ensure the self-organizing behavior of Mate Choice.

Self-knowledge
Despite the potential usefulness of incorporating self-related knowledge on the process of Mate Choice, its emergence is not dependent on doing so. Each individual's genetic composition, value or ancestry, among others, can hold important information, however Mate Choice may rely on the display of phenotypical ornaments and the raw sense of attractiveness to operate, in a closer resemblance with nature.

External rules
Guidance on how to choose a mating partner may range from very minimal, such as perception rules, to very conditional, such as enforcing the preference for a certain characteristic. While modeling Mate Choice will always be dependent on some kind of external condition or assumption, they can be kept surprisingly simple and limited.

Trait costs
In nature, the expression of ornaments and behaviors will always come with an associated cost (which may or may not impact fitness significantly). In artificial systems that cost may be explicitly set or be an implicit byproduct of certain preferences. In some cases, it's difficult to assess if a given preference-trait introduces costs, and how they relate to fitness (this could make them Wallacean or Fisherian). Independently of the scenario, spontaneous evolution of Mate Choice is safeguarded because cost is unnecessary for preferences for beauty's sake to kick off.

Polygamy
Like in nature, Evolutionary Algorithms don't have to impose polygamy to mimic Mate Choice. Despite potential impacts on the speed of preference reinforcement, resulting from the selection pressure imposed by female choice, the behaviors associated with Mate Choice are still bound to take place.

Spacial environments
In Evolutionary Algorithms, location is not always accounted for, although it can be simulated through reproductive barriers such as species, island or cellular models. While location can introduce behaviors that influence the outcome of Mate Choice, such as individuals placing themselves accordingly or the development of behaviors specific to certain geographical neighborhoods, in the absence of location individuals are still able to influence which ones will be the most attractive, and therefore affect the outcome of reproduction.

Spontaneous Evolution of Mate Choice requires:

Sexual Reproduction
As the engine of evolution, reproduction has of course a center role in the emergence of Mate Choice. As shown by Fisher-Darwin theory, there's a gene-centered character to Mate Choice, with multiple starting preferences and traits (stochastically generated for instance) competing on a gene level for reinforcement and proliferation. Moreover, self-reinforcement implies preferences selecting for themselves, which directly relies on sexual reproduction rather than duplication or mutation-only scenarios.

Perception capabilities
How individuals perceive each other is also central to Mate Choice. After all, which information is accessible and relevant for the evaluation of mating candidates will dictate on what grounds they can be judged. While this study focuses on complex preference

interactions, which implies a certain degree of perception capabilities, large dimensionality is not a requirement for the spontaneous evolution of Mate Choice. In fact, minimum capabilities are all that is needed for choice to be possible based on a certain preference.

Autonomy
Minimum levels of autonomy are required either on an individual level and on a genetic level. In what regards their reproduction, individuals should be able to choose their mating partner on their own accord, rather than relying on a centralized rule or population-level operator. Also, genes should be given the freedom of coupling with whichever other genes as they struggle for competition, in a non-biased, rule-free way.

Genetic Variation
Much like any process of evolution, diversity is key and the lack of variation puts a stop to any further evolutionary steps. In the event of stagnation, choice can't be said to be actually happening because all subjects will be similar and their reproductive success will not depend on Mate Choice. Expanding on the subject, lack of variation in mating preferences doesn't imply stagnation, as contrast between mating candidates and therefore choice is still possible. However, if all males look the same for all females, the process of Mate Choice is considered to be stopped (at least temporarily).

Genetically encoded preferences and traits in this study follow the coming assumptions:

Autonomous choice
Following the previous remarks on autonomy, individuals must choose who they mate with based on their own perception of mating candidates and on their genetically encoded mating preferences alone. They should attempt to make the best choice possible, on a purely selfish manner and with no regards for the good of the population or the evolutionary process. This is in-line with a selfish gene-centered view of competition.

Unbiased inheritance
Mating preferences should be subject to variation operators (crossover and mutation) like any other trait, allowing them to evolve strictly under evolutionary pressure and with no bias, such as having one gender pass on all the genes, or pre-establishing rules that dictate how preferences in offspring are inherited.

Reproductive success
Individuals, and therefore their genes, should be under scrutiny by both Natural Selection and Sexual Selection, making it so that their reproductive success is the result of their combined selective pressure. This way, Mate Choice introduces its own selection pressure but is under selection pressure itself. The interplay between the two forces makes it so that the reproductive success of individuals may depend as much on choosing appropriate mating partners, as on being highly attractive to others.

Traits as indicators
No explicit relations between traits and fitness are determined by external rules or other means. Still, this doesn't mean that the cost of maintaining a certain trait is zero. Rather, traits may implicitly affect fitness in both simple or complex ways, even if no assumptions are made. As a result, no Fisherian or Wallacean characters are enforced but both can emerge and co-exist on different traits (one being preferred for its usefulness and another for beauty's sake). Intricate scenarios can emerge, with traits acting

as honest, neutral or dishonest indicators of genetic quality, but not always in straightforward ways. For instance, traits that risk survival can still be indicative of good genes (Zahavi's handicap principle [322]).

Elaboration
The proposed model allows for different degrees of preference elaboration, with effects ranging from the perception system to the choice process itself. However, assumptions abstain from settling if complex preferences work better than simple ones. It's up for the evolutionary process to determine which will get a competitive edge.

With these general assumptions in mind, the remaining subsections will cover the most relevant steps in the evolutionary process, from representation of mating preferences, to evaluation of mating candidates and how evolution can impact them. Finally, some design choices that are important to the system are discussed. During this discussion, it's also important to keep in mind that Genetic Programming introduces its own restrictions and assumptions. This study includes a discussion on the impact of such assumption only to a reasonably short extent, with most setup picks (such as operators and parameter) following standard, classic choices.

5.1.2 Representation of Ornaments and Mating Preferences

The proposed model, as can be seen in Figure 5.1, relies on individuals encoding two chromosomes. The first chromosome represents a candidate solution to the problem at hand. Depending on the target problem, trees, binary arrays, real arrays, or others can be used for representation, with no additional assumptions being introduced by the proposed Mate Choice model. During evaluation, this chromosome is mapped into a phenotype that is evaluated to determine each individual's fitness value, for survival purposes. In addition to being under the direct pressure of Natural Selection, the first chromosome also encodes the traits that will be made available for Mate selection purposes. In many cases in the literature, this implies adding a number of genes to the chromosome, so that part of the chromosome is used to encode the candidate solution and part is used to encode ornaments, with no overlaps.

However, that is not an absolute requirement, as often the same genes can be mapped for both purposes (how to do so may be highly problem dependent). In either case, the effects of Mate Choice and potential costs of ornaments on fitness are assured through genetic linkage. However, on the second scenario, a stronger polygenic and pleiotropic character is enforced, with multiple traits (for survival or ornamentation) being influence by multiple overlapping genes. This results in a closer impact of sex traits on fitness, as the expression of certain ornaments may impact the overall performance of individuals through more than a genetic linkage. Overall, this chromosome will be directly impacted by both Natural and Sexual Selection, in a dynamic struggle to produce fit, attractive phenotypes.

The second chromosome represents mating preferences using Genetic Programming trees, which on an all-around perspective has some implications. For instance, in some scenarios this means that individuals may be composed of chromosomes with two different representations, one for their own candidate solutions and one for the evaluation of others. A two chromosome setup allows for a greater control regarding these design choices and offers a stricter regulation of variation operators, making it possible to apply different operators or different rates on each part of the genetic code and thus study their impact through a simpler process. Back to the representation of mating preferences, two possible approaches are considered: i) representing an ideal mating partner and relying on a comparison metric to evaluate the distance between that idealization and each mating candidate (PIMP); ii) representing an evaluation function that takes as input a set of observed characteristics and processes the interactions between them into an attractiveness value (CMP-GP).

Each approach will be extensively presented further on, but at this point it's important to mention some characteristics of each representation, specifically regarding their terminal and non-terminal sets. For instance, the PIMP requires that a Genetic Programming representation is possible for the target problem, so that both mating preferences and mating candidate phenotypes can be mapped to the same phenotypic space. It also requires that a distance metric is available for that phenotypic space. On the other hand, if targeting a scenario that traditionally uses a tree representation, then the same terminal and non-terminal sets can be used for the initialization of both chromosomes, without the need for additional design choices or assumptions. CMP-GP has no requirements on solution representations and distance metrics. However, it does require that individuals can extract and evaluate characteristics from their mating candidates. In this case, the terminal set will establish the evaluation of individual traits or ornaments, while the non-terminal set will provide a number of operators that map interactions between such individual signals into a complex evaluation function.

CMP-GP introduces therefore a Genetic Programming function as the second chromosome, which models complex interactions between preferences into a single attractiveness value. In the end, independently of the approach used, the terminal and non-terminal sets introduce additional assumptions, controlling how mating preferences evolve and how they should be interpreted. For instance, by changing the terminal pool or increasing the number of allowed operations between them, results and behaviors may change drastically. Finally, while this chromosome is not under the influence of Natural Selection, it's indirectly impacted by it. It is also under the influence of its own selection pressure, with the first chromosome acting as an indicator of encoded preferences, as described by Fisherian self-reinforcement.

5.1.3 Evaluation of Mating Candidates

As previously discussed, Figure 5.1 shows an overall framework for evaluation with three main components: perception, context interpretation, and a measure of attractiveness. Also, the complex character of evaluation of mating candidates has been extensively debated as well as its implications on the design of evaluation functions. In short, all components involved with evaluation will have a role to play in the modeling of complex evaluation functions, specifically in the way that traits are assessed and weighted into an attractiveness value. Over the design of each step in the evaluation process there's an aim to keep assumptions to a minimum, but at the same time to ensure a certain freedom for individuals to autonomously make decisions on the value of traits, their interactions and overall role.

Each of the two representation approaches has its own relation with the three components in evaluation. In PIMP, after a female has been selected, its second chromosome is mapped into the phenotype space, as is the first chromosome of a mating candidate. The similarity between the two is measured through a pre-established metric (for instance a sum function combining multiple factors) and the candidate that best resembles the mapped preferences (ideal mating partner) is favored in selection. The approach assumes therefore that: the perception system remains the same for the whole evolution process and over the whole population; the evaluation context is stable and course-grained, since the whole phenotype of the candidate is considered for evaluation; the measuring function of attractiveness is fixed, which keeps preference interactions partly non-adaptive. However, because the ideal mating partner is encoded as a tree, it is debatable how much interactions depend on the encoded preferences rather than on the metric used to combine factors.

CMP-GP evaluates mating candidates through a different process. Instead of comparing mating candidates to an idealization of a mating partner, it evaluates them through a complex function that encompasses multiple traits. The tree encoded in the second chromosome represents all three components in evaluation: the input to the tree establishes the perception system as well as the context under which traits are assessed; the chain of operators combining terminal nodes into an attractiveness value determines the interactions of each trait in the given context. None of the components is therefore fixed in the population nor through generations, keeping the whole of the evaluation process under evolution. During evaluation, each trait in the tree input is assessed independently and later combined through the chain of inner-tree operations, thus having its true contribution influenced by others in the context. In the end, the process is ruled by what terminals and non-terminals are made available for the construction of these mate evaluation functions. Despite its relevance, building these sets doesn't have to be perfect. It should be done with the best knowledge available but in the end, competitiveness will contribute to determining which sensors and interactions are valuable, harmful, or irrelevant.

5.1.4 Inheritance and Evolving Forces

After two parents have been selected, two offspring are generated by means of traditional reproductive operators. In the proposed model, operators are applied independently at each chromosome, with also independent probabilities. This decision not only allows for operators suitable for different representations to be applied, but also for different parameters to control the partial search process in each chromosome. After all, candidate solutions and mating preferences may produce different search spaces, with different dimensions and sizes, and best tackled through different strategies. Considering the two proposed approaches, PIMP should produce a preferences landscape similar to the phenotypic landscape but CMP-GP is very likely to result in an unpredictable preferences landscape. Still, even if the landscapes are the same, optimal parameters and design choices may be different for an adequate contribution to the global search effort.

Following traditional choices, thoroughly discussed by Koza [165], preferences may be subject to crossover, mutation, or replication. At each reproductive step, one operator is applied with exclusive probability, meaning that individuals may inherit a combination of both parent's preferences, a mutated version or and unchanged copy of the preferences of one of their parents (mutation and replication are likely to happen with a much smaller probability than crossover). As previously discussed, the operators are applied based on probability alone, unbounded by any external inheritance rules. Therefore, preferences are regarded as any other genetic block, being up to the selective forces to help shape traits and preferences through cheer competitiveness. Depending on the approach, this process can impact some or all parts of the process of evaluating mating candidates.

The representation and inheritance of mating preferences as an additional chromosome may raise questions regarding their true relevance in competition. The application of operators independently in each chromosome, for instance, may mean that for genes in the first chromosome to thrive in consecutive generations, they may as well simply adapt to the objective function. However, as thoroughly discusses, when Mate Choice is present, its impact can't be overseen. Surely the genetic flow is likely to be more complex and chaotic than the behavior of a standard selection system, but although the dynamics may look unpredictable and somewhat anarchic, they are not left entirely to chance. In fact, the system is quite autarchic, having Mate Choice as a self-governing force that is able to determine the population's trajectory in evolution. A way to illustrate this is through a simple analysis of cost associated with reproduction in Evolutionary Algorithms.

Consider a system with Natural Selection alone and a population where there's genetic and fitness variation. Because (most often) there's a limited number of slots for selection, genes that reduce chances to reproduce have an associated cost. In other words, individuals with lower fitness pay a higher cost to reproduce than elite ones, which get to reproduce often with low competitive effort. Moreover, there's a cost associated with the pairing of individuals, with those that end up paired with inferior individuals having to bear the cost of producing low fitness offspring. In summary, high end individuals pairing among themselves share the lowest cost possible and are thus favored in competition. The introduction of Mate Choice results in some changes. Firstly, the cost associated with pairing falls under the control of mating preferences, so that individuals with good senses or good taste have a lower cost of reproduction, since their offspring will not only likely be favored but also reinforce their choices (the attractive sons theory). Secondly, the cost usually associated with fitness becomes shared between being fit but also attractive, making it so that individuals that are very fit but non-attractive have a higher cost than before, and those that would have a higher cost based on low fitness have the chance to pay a lower cost by being attractive. Of course, these costs are adaptive due to the dynamics of Natural and Sexual Selection.

Therefore, in disregard of how mating preferences are encoded, the impact of evolving forces in both chromosomes is ensured through their implications in cost. Through their impact, the emergence of Mate Choice, rather than selecting random mates, is ensured through the generations not because it is explicitly enforced but because it is given the means to evolve. This would be akin to individuals in a location based system moving to certain locations not because they are guided there, nor because they offer better resources, but because they offer higher chances of being around and available when reproduction occurs. Neither approach holds objections on this analysis.

5.1.5 Design Choices

The previous subsections have introduced general concepts on the proposed model for Mate Choice. Two representations have been briefly introduced as well as particularities on how they can be used for evaluating mating candidates. Despite their differences, inheritance and evolving forces work through similar means and have been covered as well. The bulk of the framework has therefore been introduced, however, there are different design choices that should be briefly considered for discussion, as they surely influence the behavior of the Mate Choice algorithm. The following topics are relevant: initialization of mating preferences; variation operators; operators for the selection of females and mating candidates; probabilities and parameters associated with each operator. As previously mentioned, most choices have been kept to standard, well tried choices.

Regarding initialization, Koza's traditional Ramped Half-and-Half algorithm [165] is used, which combines both the Grow and Full algorithms with 50% chances. The Full algorithm always introduces non-terminal nodes until a maximum layer is reached, at which point a terminal node is introduced. The Grow method may introduce terminals or non-terminals at any point and therefore may produce unbalanced branches and not always reach a full sized tree. Moreover, the Ramped method stochastically selects a growth limit for each tree within an interval that is user defined. As a result, parameterization of the Ramped method controls the initial complexity and size of the represented trees, while at the same time ensuring that individuals are not all attributed preferences with the same dimensions and complexity. Unlike in Lerena's study on complexity [178], this model doesn't focus on that feature alone, allowing for a less restrained behavior. The initial composition of the trees is ruled, as previously discussed, by the terminal and non-terminal sets made available to the algorithm.

On the topic of selection, while the process for evaluating mating candidates has been introduced, preliminary steps until that operation can take place need further covering. For the purpose, a female and set of male mating candidates for her consideration need to be selected from the population. The way such individuals are selected can be quite relevant for the behavior of the population, specially regarding gender dynamics and the balance between Natural and Sexual Selection pressure. As discussed previously, simultaneous hermaphrodites offer an opportunity for all individuals to act as females and males without additional assumptions on gender, and at the same time making the whole gene pool available for both roles. Consequently, gender roles are emulated during selection, as often found in the literature. The model works by selecting a female through a traditional fitness based tournament operator and presenting that individual with a set of randomly selected mating candidates. The candidate that best matches the mating preferences of the female gets selected for the second spot.

These preliminary steps to Mate Choice offer some opportunities: all individuals are available to be selected as females as well as males; the tournament operator ensures that all individuals are subject to Natural Selection, so that fitter individuals have a higher chance of reproducing; the size of the tournament therefore controls survival pressure, but because it is associated with the selection of females, it also controls the degree of polygamy induced (a larger tournament increases the chances that only a small set of elite females are given many chances of reproduction, which contributes to female choosiness and the rapid spread of a few preferences); the selection of mating candidates through a random operator ensures that individuals can contribute by being attractive to others alone, rather than fit; the size of the candidates pool controls the competitiveness pressure between males (the larger the lek size, the higher the pressure on meeting female preference, and the less likely unattractive individuals are to mate); balancing the size of the female's tournament and the size of the mating candidate's pool is therefore key to an appropriate balance of selection pressures.

The context created by these opportunities should be ideal for Mate Choice to evolve. Polygamy as well as lek-like competition between males, boosted by the fact that individuals can be left out of reproduction, is bound to put pressure on low fitness or low attractiveness genes. Given that the initial population is diverse, individuals selected as females should bias selection towards their own choices. The resulting differential mating frequencies should be enough to trigger a Fisherian process. Despite the runaway process, it doesn't mean that the preferences involved have to be for good taste rather than for good choice. It's true that Fisherian preferences require less assumptions than Wallacean to model, but, as shown by Zahavi, preferred traits may work as viability indicators if the preferred traits in potential mates correlate with offspring survival [322]. If, otherwise, they correlate with reproductive success through good taste or attractiveness of offspring, then the process evolves all the same as shown by Fisher-Darwin theory [59, 97]. Of course, different traits can play different roles. Also, the same trait can be processed for both roles by complex evaluation functions.

Moreover, a simultaneous hermaphrodite population doesn't necessarily mean that sex can't emerge as a specialization. In fact, if runaway sexual selection does result from this setup, specially in a way where traits are pushed in a direction different than that of Natural Selection, it is viable that the population experiences a form of sympatric speciation through genders. In that case, part of the population may specialize in being fit and competing as females, and part of the population may specialize in being attractive and compete as males, both dropping the odds of being selected for the opposite role. The resulting dynamics have been previously discussed. Among them, it has been discussed that gene dynamics between males and females can act like a means of macro mutation. Despite the comparison, the effects of (micro) mutation on traits and preferences are subjected to design choices as well, which can have important impacts on evolution.

The nature of Koza's mutation [165] can be quite destructive. It works by selecting a node in the target tree and substituting its sub-tree with a newly generated one. Such an operator can truly impact Mate Choice, both if acting on traits or preferences. As previously discussed, self-reinforcement of mating preferences relies on mating preferences choosing for themselves, with traits acting as evidence for the presence of certain preferences in mating candidates. Therefore, mutations on traits can cause such evidences to be misleading, disrupting the self-reinforcement process by making preferences unknowingly choosing for other competing preferences. Also, choice consistency, which is critical for self-reinforcement, can be effected by mutation on preferences. By affecting the way individuals rank mating candidates, the consistent choice of preferences for themselves throughout the generations can be interrupted. Still, mutation can be important to counter periods of no evolutionary progress, finding new search directions and escaping local optima, and should be set accordingly. The effects of mutation should be specially important when dealing with complex mate evaluation functions, as inconsistency can be rather easy to come up, moreover if the mutation point is close to the tree root.

Without mutation, variation is dependent on crossover alone. Koza's crossover operator [165] switches sub-trees between individuals, thus producing offspring that together maintain the genetic material encoded by their parents although reorganized. This allows the evolutionary process to exploit the existent genetic pool. On the perspective of mating preferences, this results in interactions between preferences being swapped in positions thus affecting also dimensionality and complexity. Arguably, specific operators dealing with different parts of the evaluation process could have been used (for mutation also), ensuring terminals could be swapped without effecting the interactions, or the opposite, or other logical behaviors. However, while the standard operator makes no such assumptions, and as a result acts on all components concurrently with no particular care, it shouldn't represent a barrier for Mate Choice to emerge.

5.1.6 Restrictions and Generalization

The discussed framework introduces a number of well justified assumptions. However, two of these assumptions regarding representation of mating preferences can be seen more as restrictions and need further clarification on how much they impact the designed approaches. The first regards using a Genetic Programming representation for the second chromosome and the second one concerns the evaluation of phenotypic ornamentation only. The introduction of these restrictions was necessary to contain the scope of the experimental setup to a realistic size. As a trade off, it allowed for the opportunity to focus on a deeper analysis of the behaviors and effects of Mate Choice which should generalize quite well outside of such restrictions.

Within these limitations, CMP-GP shows higher generalization capabilities when compared with PIMP, as the latter requires a Genetic Programming representation to be available for the target problem while CMP-GP depends only on the researcher to find a number of phenotypic features to evaluate as ornament, regardless of the representation used on the first chromosome. However, if the study was to extend to allow any representation for the preferences chromosome, then PIMP may always rely on the same representation for both chromosomes, whatever that may be, which greatly boosts its applicability to a wide range of problems. In that regard, PIMP really only depends on a distance metric on the phenotypic space to compare mating candidates to a reference ideal mating partner. CMP-GP can already be applied to any problem, and can even accommodate other representations for preferences, as long as they allow for dimensionality and complexity to evolve explicitly (this is a keystone of the approach), but with a higher design effort.

That effort may however be reduced by allowing the evaluation of genotypic characteristics as ornamentation. In nature that would be most unusual, however in Evolutionary Algorithms individuals can benefit from direct access to their own genotype as well as to those of mating candidates. Bluntly, CMP-GP may make it simpler for researchers to set a number of genotype-based characteristics to be evaluated as ornamentation. Arguably they could even be transversal to multiple problems sharing similar representations for candidate solutions. PIMP would also benefit greatly from being allowed to work on the genotypic space, as it could make direct genotype-based comparisons using an appropriate distance metric. This would allow PIMP to generalize quite well, making it even easier to apply than CMP-GP. Moreover, in both approaches the combination of phenotypic and genotypic information on the same evaluation function would be reasonable, despite making perception less nature-like.

As shown by this discussion, the introduced assumptions on representation of preferences are quite restrictive and have a deep impact on the generalization of the two proposed approaches, more so on PIMP. Lifting these limitations in future studies may bring important insights. So far, it's known that both PIMP and CMP-GP could more easily generalize to scenarios not covered in this study, which is a quite important characteristic. Moreover, it may be shown that different representations or that relying on the genotypic space may bring more than those gains, boosting performance for instance while reducing design efforts. However, the necessary experimental setup to address this question is extensive and will be postponed to future studies.

5.1.7 Two Scenarios for Proof of Concept

The discussion from the previous subsections covers important characteristics of the proposed framework. However, while the discussion on inheritance and design choices is somewhat transversal, the one on representation and evaluation can't avoid focusing on particularities of each of the proposed approaches in an attempt to give a general sense of its workings. Hopefully, this will allow for an overview of the whole framework, however it doesn't provide enough information on the design of each approach specifically. The following two sections will fully cover each approach and their distinctive characteristics. In order to help with such analysis, it may help to illustrate their application on a couple of optimization problems. Moreover, their application on such problems will contribute to proving the concept, as a preliminary study. The following two subsections cover the two scenarios considered.

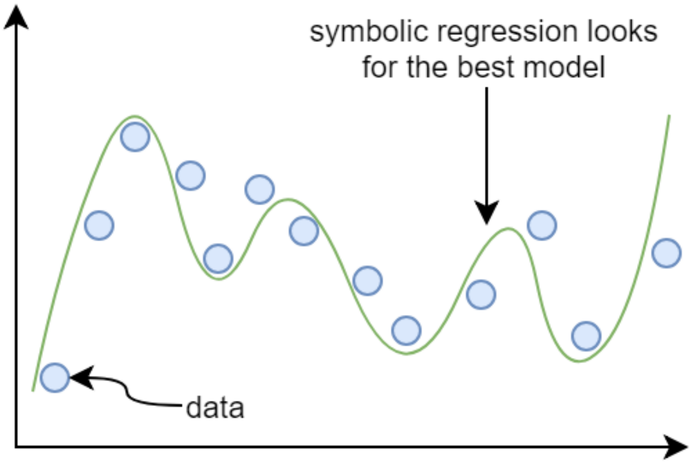

Figure 5.2: An example of symbolic regression

Symbolic Regression

The straightforward goal of a regression task is to fit a mathematical model to a given dataset. In a common scenario, a regression function is established beforehand and it's up for regression to take upon itself the search for the numerical values of its unknown parameters. Hopefully, in the end, a function that approximately describes the dataset is achieved, which can be useful for a variety of tasks. Over the years, multiple regression analysis algorithms have been introduced. Genetic Algorithms, for instance are suitable for such a task. By encoding unknown parameters as an array, a standard evolutionary process can search the associated search space and achieve a suitable setup. In that scenario, fitness can be measured quite simply: for all input-output pairs in the dataset, feed the input to the mathematical model and measure the error to the output in the dataset; after all data points have been covered, aggregate all error values in a final fitness value; try to minimize the error. An example of an error metric commonly used is Mean Squared Error over all data points.

It was Koza [165] who introduced the use of Genetic Programming for regression purposes. Rather than pre-establishing a specific function for regression, it was proposed that the function itself falls under evolutionary pressure. It's easy to see how that may be possible by evolving procedures. Instead of providing an initial function as a starting point, sets of terminals and non-terminals are provided, in this case representing input variables and mathematical operators respectively (constants, etc. can also be included). By combining building blocks from those sets, whole functions can be built, and their fitness measured against a dataset much like done in any other regression algorithm as seen in Figure 5.2. Given that scenario, the effort is left for the evolutionary process. This Genetic Programming model has the benefit of not needing an initial model to evolve, instead searching through the whole search space of potential functions. On the other hand, such a search space can be quite large in comparison to evolving only a set of parameters.

Over the years, Symbolic Regression has been extensively used and is broadly regarded as a benchmark for Genetic Programming methods [193]. It's applications to real world datasets are broad, but they have also been extensively applied in lab like

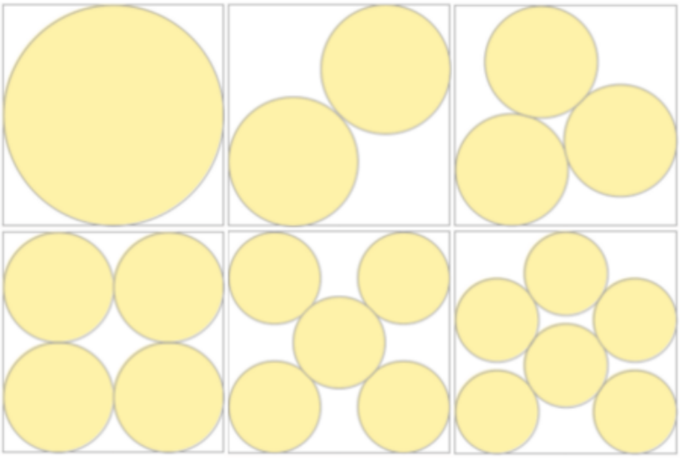

Figure 5.3: Optimal solutions for the Circle Packing in Squares problem.

conditions, using equidistant data points generated within an interval of a given function. Different authors have targeted many different functions, from linear to polynomial, comprising one or multiple dimensions, with multiple degrees of ruggedness, and using varying combinations of terminal and non-terminal sets. A collection of target functions for regression, broadly regarded as relevant for benchmarking has been published by McDermott et al. [193].

Geometrical Optimization

This type of problem aims at finding the best arrangement possible for a group of items so that they maximize or minimize a given function. Usually, they refer to spatial arrangement either in the 2D or 3D spaces, and depending on the characteristics of the items and the interactions between them, many scenarios can be represented. In this study, two problems of geometry optimization are considered: Circle Packing in Squares, which takes place on the 2D space; Optimization of Morse Clusters, which takes place on the 3D space. These problems offer various interesting characteristics: i) they offer a large range of test instances; ii) as the number of items increases, so does the complexity and difficulty of the problem; iii) they bring an opportunity for solution visualization. The last one is of particular interest to help illustrate the workings of the proposed approaches.

Circle Packing in Squares is a surprisingly challenging geometrical optimization problem. It consists in finding the spatial disposition of a set of non-overlapping circles of unitary radius, in a way that minimizes the area needed for a containing square [186]. Figure 5.3 shows a few examples of known optimal solutions. Optimal solutions have been found for up to 24 circles and putative optima are available for much larger sets. For the matter of representation, candidate solutions encode a vector of Cartesian coordinates representing the absolute position of each circle. These coordinates are translated to the phenotypic space so that a fitness value can be attributed by measuring the area of the smallest square that can enclose the resulting circles.

Chemical clusters are also geometrical structures, although on the 3D space, with Cartesian coordinates being all the same a viable representation for candidate solutions.

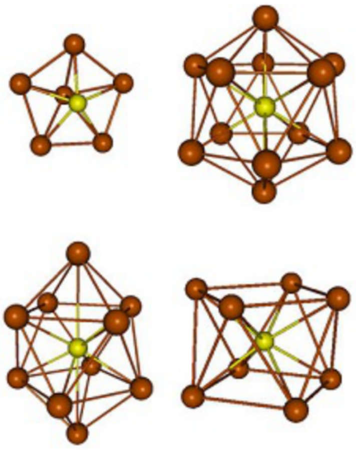

Figure 5.4: Optimal solutions for some instances of Morse clusters

As aggregates of particles ranging from a few to thousands, such structures can be highly complex. Finding structures of maximal stability is of great relevance to many research fields [326]. In order to do so, one would look for the geometry of atomic or molecular clusters so that the potential energy held is minimal (such structures are consequently more stable). An alternative view of the problem is that of finding the global minimum on the potential energy surface, which in this scenario corresponds to a fitness landscape [80]. Potential energy surfaces are multidimensional functions that describe the interactions between the particles that compose the cluster ($3N$ dimensional when a cluster of N atoms is modeled on the three dimensional space). Such functions are regarded as highly complex, showing roughed landscapes, rigged with a large number of local minima and a deep multiple-funnel character [74, 279, 290]. Moreover, the number of attraction basins increases exponentially with cluster size [48].

Finding the lowest potential energy of a cluster and the corresponding geometry is a NP-hard task that provides difficult instances to challenge optimization algorithms [48]. Among the possibilities, Morse clusters [206] are regarded as particularly challenging [74], more so if modeling short range interactions between particles. They often represent very different organization motifs depending on the number of particles, some of which can be seen in Figure 5.4, making it quite difficult to design algorithms that specialize on a geometric motif alone. Putative optima are available for clusters ranging up to 80 atoms, making for a good range of testing instances with a variety of characteristics. For that reason, Cluster Geometry optimization has become relevant as a test problem to benchmark the effectiveness of global optimization algorithms [48, 173, 175].

5.2 PIMP: Mating Preferences as Ideal Mating Partners in the Phenotype Space

As briefly covered previously, PIMP relies on two fundamental and interlinked principles: i) the modeling of taste through the representation of a conceptually ideal mating partner; ii) the measuring of attractiveness to mating candidates by comparing how similar they are to that fantasy representation. Notice the emphasis on the fact that individuals represent their own taste as an abstract idealization, that may or not be met to some degree by others. Even though it may not be mandatory in the genetic space, preferences and solutions share the same phenotypic search space, which may give an idea that it would be most beneficial for their search process to follow similar paths. However, Fisher-Darwin theory proves otherwise. Assuming that the approach complies with the assumptions on Mate Choice, which it does, then the underlying processes are bound to emerge. Nonetheless, PIMP adds specifics and new assumptions, that need covering. The following subsections will do so based on examples.

5.2.1 Representation and Evaluation

Ideal mating partners may be represented in the same phenotypic space either using the same representation used for the first chromosome or an alternative one. The go-to choice is most likely to be to use the same representation, as it takes most of the development effort from researchers. This is arguably one of the most attractive characteristics of the approach. For instance, when tackling symbolic regression tasks, one would rely on the same terminal and non-terminal sets, as well as use the same initialization procedure to build both chromosomes and thus successfully minimize implementation efforts. Figure 5.5 illustrates the discussion with an example. It also shows how the evaluation of mating candidates is a process that is much similar to that of fitness evaluation, focusing on the displacement between the female's phenotypic mapping of mating preferences and the phenotypic mapping of a mating candidate's encoded solution. The attractiveness value is calculated using an aggregation function, similarly to how fitness is measured (Mean Squared Error for instance). The individual that minimizes the function is regarded as the most attractive.

Of course, researcher may find it useful for each chromosome to be built under distinctive rules. Hereafter focusing on Genetic Programming representations, this can be achieved by either expanding, reducing or changing the available terminals and non-terminals. Tweaking the parameters associated with initialization, mutation or crossover (maximum tree size, etc.) may also make sense, depending on the research objectives. For instance, one may aim at comparing setups where preference chromosomes are more or less restricted in size or complexity. While this study doesn't follow that research path, it is relevant to point out that PIMP would maintain its core characteristics, even if heavily tweaked, assuming that the phenotypes are mapped with the same dimensionality or in a away that allows for a distance metric to be employed.

Figure 5.6 shows a potential representation and evaluation scenario for a Circle Packing in Squares problem, which can easily be projected to the three dimensional space and to cluster geometry problems. Two thing are relevant to mention regarding this scenario. Firstly, the problem relies on an array representation, which evolves under traditional Genetic Algorithms operators. While it would be straightforward to encode preferences (by means of an ideal mating partner) using the same representation, Figure 5.6 shows that a viable tree representation (circles are placed consecutively taking as input the position of the last one) that maps to the same phenotype space and that is subject to the same assumptions and considerations as other preferences encoded and evolved using Genetic Programming. Secondly, while in the Symbolic Regression scenario the attractiveness value is calculated as an aggregation of multiple point-to-point measures, the same can't be accomplished in this scenario without moving away from the traditional fitness function. Simply put, an analogous metric would simply

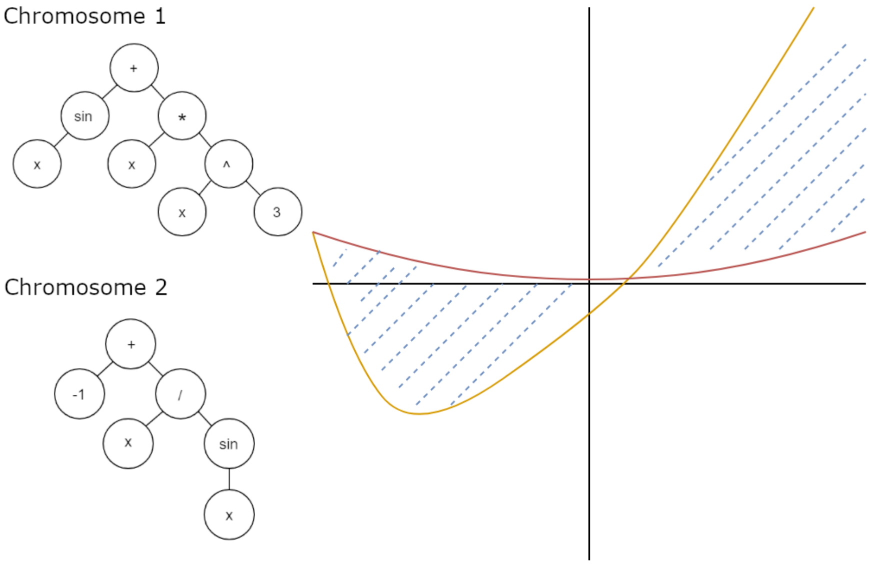

Figure 5.5: Example of representation and evaluation for a Symbolic Regression problem. On the right, the preferences of a particular female are shown in red and the phenotype of a mating candidate is shown in yellow. Distance is shown in blue.

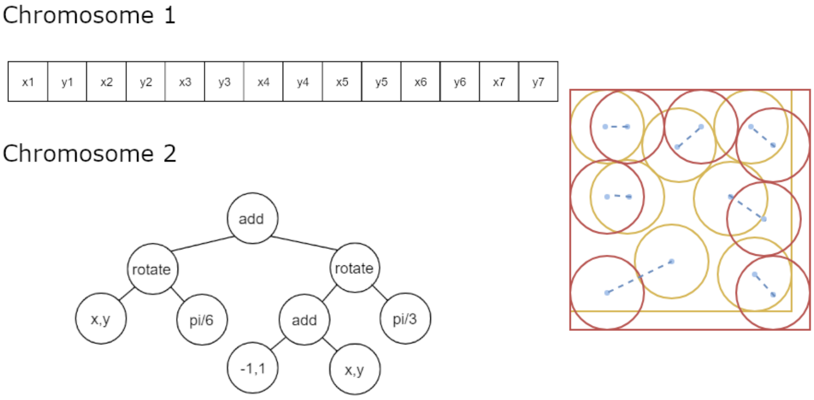

Figure 5.6: Example of representation and evaluation for a Circle Packing in Squares problem. On the right, the preferences of a particular female are shown in red and the phenotype of a mating candidate is shown in yellow. Distance is shown in blue.

compare the area of the containing squares from preferences and candidate solutions, which is not acceptable under current assumptions and rules. As Figure 5.6 shows, a metric can still be found on the phenotypic space, by measuring the euclidean distance between pairs of items and then aggregating their values, using for instance a Mean Squared Error function.

5.2.2 Assumptions and Considerations

Perception

By definition, PIMP encodes mating preferences as a whole solution. Given that females have access to the phenotypes of mating candidates without restrictions, they might as well collect knowledge on whole solutions as well (all data points on Symbolic Regression phenotypes, all circles in Circle Packing problems, and so on). The upside of doing so is that attractiveness can be computed using full knowledge, which may or may not be a good idea, since the evaluation of mating candidates introduces computational overhead. In some scenarios the increase in computational effort can be significant. Still, PIMP offers the possibility of using only part of the phenotype for evaluation (data points at every few steps or only some circles) if it's found that processing all data points is an overkill. Nonetheless, from a perception perspective, females have full access to the full phenotype of mating candidates and therefore, no perception restrictions. Also, perception is immutable throughout evolution.

Context interpretation

Following the discussion above, there may be times when balancing computational effort and the size of the knowledge base become part of the development effort for researchers. That issue will be kept out of the scope of this approach, however, it does bring an important discussion on context. One might think that the size of the knowledge base has a direct impact on the evaluation context. After all, when looking at phenotypes, it's easy to think of data point pairs, or circle pairs (one from the the female's phenotype and one from the candidate's phenotype) as preference-traits pairs, and attractiveness as the aggregation of very fine grain evaluation measures. While partly correct, if one looks at this from a genetic level perspective and particularly on Genetic Programming representations, all points are the expression of the same genes, which makes it odd to look at each point as isolated traits or preferences. Focusing on preference encoding, increasing or decreasing the number of points does not influence the evaluation context (data point pairs are compared with no influence from others). Moreover, the evolution process, while acting on preference trees, has no effect on the context. For all purposes, the evaluation context is immutable and coarse-grained.

Aggregation function

One of the main reasons why perception and contexts are static in PIMP is that the function that ties everything together is externally set. If it were to fall under evolutionary pressure, in the right conditions, the above discussions would be quite different. Consider for instance that a Mean function is used for aggregation. It might be encoded as a Genetic Programming tree, with one operator alone and one terminal for each comparison value (a very large number of terminals in the Symbolic Regression scenario), resulting on a shallow but wide tree. If it were given liberty to remove some of those terminals, or introduce other operators in-between the terminals and the root node, then it might be said that both context and perception are subject to change (interactions between inputs as well). This would result in a three-chromosome system, one for candidate solutions, one for ideal partner representation, and one for the evaluation function of candidates. This system will not be pursuit in this study. Still, it gracefully illustrates how the aggregation function, by being externally defined, is static and immutable, and a constraint on the remaining parts.

Preference interactions
Because of how preferences are expressed and how the aggregation function works, there are no explicit preference interactions in evaluation. However, because of how they are represented, relying on a coarse-grained way on the same tree, it could be said that there's a genetic linkage between preferences. In simpler terms, because a single tree is used to represent preferences by means of an ideal mating partner, operations (such as mutation) that could influence one preference, influences all of them. This doesn't sustain that there are explicit interactions in evaluation of mating candidates, but it does support that there are interactions in how preferences are expressed, which indirectly impacts how they measure attractiveness.

Complexity
The discussion naturally extends to preference complexity. Keeping in mind that there is no explicit form of assessing evaluation complexity on this particular approach, individuals are likely capable of influencing complexity indirectly. Because preferences are encoded using Genetic Programming trees, there are means to assess the complexity of those trees. While the meaning of such trees is not the same as that of an evaluation function combining multiple preferences, they do represent how individuals are visualizing their ideal mating partners. They might go for very complex representations or suit for very simplistic ones. In a Symbolic Regression scenario for instance, they might choose a polynomial or a linear representation. Arguably this is informative on how complexity competes in Mate Choice.

5.2.3 Proof of Concept

Symbolic regression offers a simple yet interesting opportunity to apply PIMP with minimum effort. For those reasons, it has been used for the purpose of proofing the concept. At this point, the focus is not on developing a benchmarking test set or to carefully deliberate on the impact of certain design choices, nor on being particularly attentive on the characteristics of each target instance. There's been of course an effort to produce a reasonable experiment, but mostly focused on making sure that the framework is viable, that it follows the assumptions on Mate Choice that have been established, and that consequently the means for Mate Choice to emerge are present. There's also a particular interest on seeing if preliminary results are promising. Remarks on the internal workings of PIMP are left out for a further extensive and careful analysis on a wider experimental set.

For this experiment, six target functions were used (four keijzer [155], one koza [165], and one nguyen [292]), with setups similar to those found in McDermott's paper on benchmarking Genetic Programming [193]. The three families of functions offer different test scenarios, and an additional keijzer function is used with three different intervals for the data set. Overall, the functions should not be too difficult to tackle and are restrained to one dimension. Later on, other scenarios will be tested. The setup used was quite straightforward: terminal and non-terminal sets are summarized in McDermott's proposal [193] and in Appendix E; the same sets were used to build both chromosomes; the same overall parameters and operators are applied to both chromosomes as well; crossover is applied with a 90% probability and replication with a 10%

Table 5.1: Mean Best Fitness obtained over 50 runs obtained with a standard, mate choice and random approaches on the symbolic regression of 6 functions

Function	Standard	Mate Choice	Random
Keijzer-1	0.0080	**0.0059**	0.0072
Keijzer-2	0.0063	**0.0052**	0.0062
Keijzer-3	0.0071	**0.0056**	0.0067
Keijzer-4	0.0890	**0.0833**	0.0840
Koza-1	**0.0006**	0.0014	0.0006
Nguyen-5	0.0014	**0.0004**	0.0025

Table 5.2: Mean Cumulative Destructive Crossovers obtained by the Standard, Mate Choice and Random approaches on each function over 50 runs.

Function	Standard	Mate Choice	Random
Keijzer-1	6013.14	**7062.88**	6484.58
Keijzer-2	5892.56	**7149.06**	6929.12
Keijzer-3	6173.56	**7198.20**	6808.86
Keijzer-4	5968.18	**7239.40**	6805.04
Koza-1	34889.32	**36399.72**	36797.82
Nguyen-5	27597.62	**34656.84**	30013.76

probability, mutation is not applied; females are selected through a tournament operator with five slots and choose their mating partners from a set of five randomly selected mating candidates; a population of 100 individuals is used for keijzer functions and a population of 500 individuals was used for other functions; only training data was used for optimization.

The experimental set consisted of three scenarios: standard selection with both individuals selected through tournament selection; Mate Choice through PIMP as described above; random selection of the male individual. Each approach was run fifty times and data regarding fitness and the result of crossovers was collected. In the study, an offspring is considered to be the result of destructive crossover if its fitness is worse than the female parent. If the offspring has the same fitness as its mother, it is considered to be the result of neutral crossover. Otherwise, the offspring is the result of positive or constructive crossover. Offspring are compared to female parents alone because they are the ones actively choosing a mate whereas males mate indiscriminately. Table 5.1 shows the obtained fitness results. Tables 5.2 and 5.3 show results on crossovers. Instances where PIMP performed statistically different from the standard one are shown (using a Wilcoxon Mann Whitney test [195] with a significance level of 0.01).

As shown in Table 5.1, PIMP outperformed the standard approach in five out of six instances. The koza-1 function, where it performed worst is however regarded as a particularly easy one [193], probably mapping into a landscape that is rather smooth, allowing for the standard approach to effortlessly converge faster and gain advantage over other, more exploratory strategies. Nonetheless, differences in Mean Best Fitness, although significant, are not high, with all approaches reaching near optimal fitness values. This suggests competitiveness. The random approach achieves slightly better results than the standard approach on the keijzer functions and comparable results on the koza function, which may indicate that the evolution process may benefit from a

Table 5.3: Mean Cumulative Neutral Crossovers obtained by the Standard, Mate Choice and Random approaches on each function over 50 runs.

Function	Standard	Mate Choice	Random
Keijzer-1	3124.60	**1760.94**	2524.54
Keijzer-2	3278.84	**1708.12**	2060.58
Keijzer-3	2852.96	**1741.40**	2187.86
Keijzer-4	2997.26	**1528.56**	2169.32
Koza-1	8666.42	8016.44	7397.52
Nguyen-5	17749.86	**10583.78**	15592.58

lower selective pressure. However, results on the nguyen function show that it is not a given that such a strategy effects performance positively. PIMP results also suggest that a lower selection pressure may be beneficial but that the directional selection provided by Mate Choice is more contributing than random selection of male parents.

Regarding the result of crossovers, the summaries in Tables 5.2 and 5.3 show how the different approaches influence selection and pairing of individuals. Neutral operations are consistently kept to lower cumulative values when applying PIMP, whereas a Standard approach ends up promoting so, by being subject to a faster convergence. Such offspring make no contributions to fitness enhancements nor to exploration or exploitation. Mate Choice seems to promote destructive crossover, which may indicate the pairing of individuals that are genetically different, in a negative assortative fashion. This may indicate competitive advantages in exploration in this particular scenario. Ecological opportunities given to lower fitness individuals may ultimately contribute to advances in the fitness of the best individual found. A comparison between PIMP and Random approaches also suggests that both algorithms promote different behaviors. This indicates that whatever the behavior of PIMP, it is able to evolve something that is different from a random behavior. A longer discussion can be found on a study by Leitão et al. [174].

5.3 CMP-GP: Complex Modeling of Mating Preferences with Genetic Programming

As previously introduced, CMP-GP relies on three principles: i) the perception by females of a set of characteristics flaunted by male candidates; ii) the evaluation of characteristics according to female preference, both individually and on a particular context; iii) the complex modeling of multiple tastes and their interactions into an attractiveness value. The outcome is a scenario that allows for the explicit modeling of preference multicomponency, by representing preference-trait pairs as terminal nodes and the interactions between them as non-terminal nodes. The resulting tree represents a full mate evaluation function whose parts are under the influence of evolutionary forces. Its multidimensional phenotypic space is certainly different from that of evolving candidate solutions, potentially following very different (but interlinked) search paths. As it complies with the assumptions on Mate Choice, it also introduces its own assumptions and particularities, which will be covered in the following subsections.

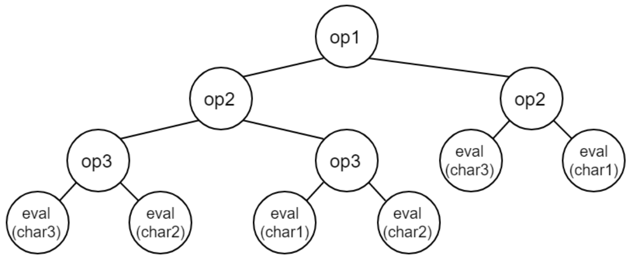

Figure 5.7: An example of an Mating Evaluation Function.

5.3.1 Representation and Evaluation

Mating evaluation functions mean a different search space from that of candidate solutions. Whereas the development effort on PIMP was kept to a minimum through the use of the same tree building and variation rules for the representation of preferences, the same opportunity is not given by CMP-GP. It does arguably offer different opportunities that are worth exploring, such as the explicit representation of preferences, a fine grain perception and assessment of characteristics in mating candidates and their evaluation through a clear chain of interactions between them. As previously discussed in great extent, such a model results in a preference landscape of self-adaptive character, which, through the influence of various factors, has its ruggedness and overall nature under constant evolution.

In order to accomplish such an approach, two main design tasks should, for the purpose of clarity, be carefully explained and illustrated through the use of examples: i) the outline of a a set of terminals representing the perception and evaluation of individual traits; ii) the planning of a set of non-terminal operators representing potential interactions to be chained into a tree. Figure 5.7 shows how an evaluation tree may look like, with leaf nodes representing the individual perception and evaluation of traits, and the branches representing interactions contributing to a global attractiveness value in the root of the tree. Much like any other tree in Genetic Programming, the sets from which they are built determine which behaviours they may produce. Obviously, these trees may make use or not of all available terminals and operators. This freedom of design is significant specially for terminals, as they allow for an adaption of the perception system, potentially leaving out the influence of certain traits in Sexual Selection, or empowering other features through their repeated use.

Regarding the design of the terminal set, a task that might be the most significant and influencing in CMP-GP, a parallelism with multi-criteria optimization can be done. After all, as shown by Figure 5.7, multicomponency in Mate Choice implies the evaluation of multiple criteria (and its combination into an attractiveness value, analogous to fitness value in multi-criteria Evolutionary Algorithms). Whereas in multi-criteria optimization the different objectives or functions are usually established, Mate Choice relies on human knowledge and depends on problem specific characteristics for determining each individual trait for evaluation. As a general rule, problems can be subdivided into multiple tasks, offer multiple instances for testing (like geometrical optimization), are related to other problems, or plainly offer certain characteristics that can be assessed easily. Usually, the connection of such possibilities with fitness would be an important question, but for the purpose of Mate Choice, such assumptions are unnecessary. As long as there's a chance to extract traits from a phenotype and evalu-

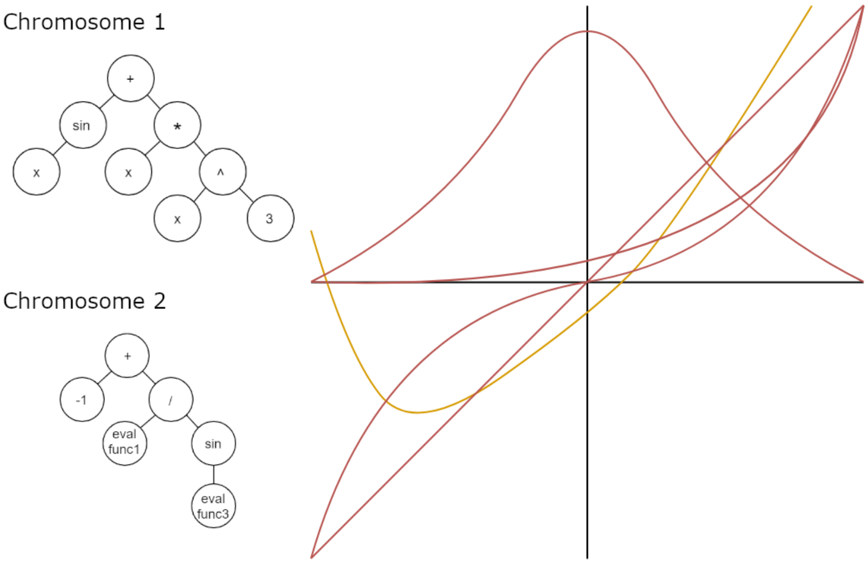

Figure 5.8: Example of representation and evaluation for a Symbolic Regression problem. On the right, each red line corresponds to a single trait preference (terminals in chromosome 2), and the mating candidate's phenotype is shown in yellow.

ate those traits for the purpose of Mate Choice, Fisherian preferences can be applied. Nonetheless, there may be a relation between some of those characteristics and fitness (a cost), either positive or negative, being up to evolutionary forces and competition to establish which are fruitful or not.

A general equation for the evaluation of individual traits can be thought of as $|p_n - f(t_n)|$, where p_n is the preference of a given female (the desired outcome) for trait n, and $f_n(t_n)$ is the performance of trait t_n on task $f(t_n)$. For instance, in the example shown in Figure 5.8, mating candidates are evaluated on a number of minimization tasks, $f(t_1)$ and $f(t_3)$. For each task, the result is measured against a preferred value, p_n, possibly set to a random number during instantiation. As a result, when evaluating a single trait, females compare what they observe in males to their own desire. Notice that the individual evaluation of traits is a minimization scenario, however, that doesn't imply that global attractiveness should be a minimization effort, as preference-trait pairs can be bound to increasing their differences rather than reducing. Assuming attractiveness as a minimization effort requires extra assumptions.

While these preferences are easy to understand due to their relation to the workings of PIMP, they might be computationally expensive, depending on the settings. Simpler, more straightforward traits can be used with no risks. For instance, one might formulate preferences in the following format: sample a fixed number of equidistant x values from the function interval; for each value of x, randomly initialize a preference for the corresponding $y = f(x)$ value, y_p; apply the equation above as $|y_p - f(x)|$ as the evaluation of individual preferences. Aggregate single evaluations by applying the function encoded by the preferences chromosome. Figure 5.9 illustrates such a scenario. While these preferences are simple and follow all assumptions of Mate Choice, they raise an few discussion points. Firstly, it's important to make sure that no further assumptions are being made on the relation between traits and fitness. This may be tempting on

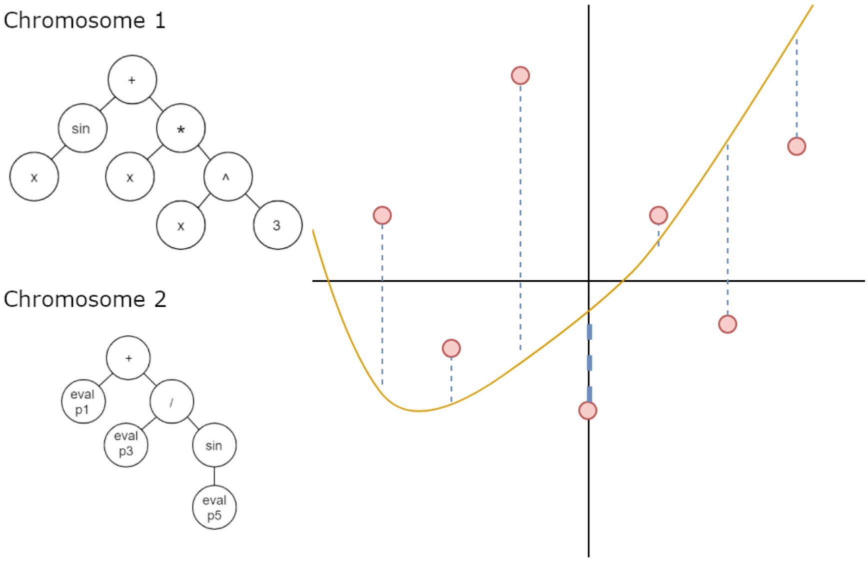

Figure 5.9: Example of representation and evaluation for a Symbolic Regression problem.

problems where the optimal solution is known. For instance, if the values of y were to be used directly as input for the Mating Evaluation Function, a direct relation between preferences and optimal values could bias evolution. The use of a preferred value (y_p) helps distance perceived traits and fitness. In an extreme scenario where all points in the symbolic regression function are analyzed as traits, an ideal mating partner such as the one from PIMP, could be represented by preferences. CMP-GP refrains from doing so, which brings up a second topic of discussion. In Figure 5.9, perceived traits are placed equally distanced in the x axis, which assumes that the perception system of individuals is built from well defined terminals and can change only within that space. Alternatively, the perception of traits, through the values of x, can fall under evolutionary pressure, through appropriate initialization and mutation operators, thus introducing a new layer to evolution, where not only preferences evolve, but also perception.

The definition of a terminal set for the problem of Circle Packing in Squares demonstrates a different way that the extraction of traits for evaluation can be done. The problem is among a family of problems that offers a range of instances of increasing size and complexity. As shown by Figure 5.10, there's a relation between those instances which offers an opportunity for the purpose of Mate Choice. Briefly, the figure shows the optimal solution for the packing of sixteen circles and, in red, how certain sub-instances are also present in their perfect form, or in an approximate formation. There are also those sub-instances that are present in a not so good, or even plainly bad arrangement. Independently of performing well or bad, how an individual behaves in such sub-tasks is bound to hold information on the genetic quality it holds for the target instance. Therefore, assessing individuals by how they perform on a subset of sub-instances (not necessarily all) can provide a good perception system. Some additional remarks are worthy. While sometimes the optima has been proven and other times there is a putative optima, the relationship between instances and sub-instances is not direct like in the previous example of symbolic regression. In this case, instances

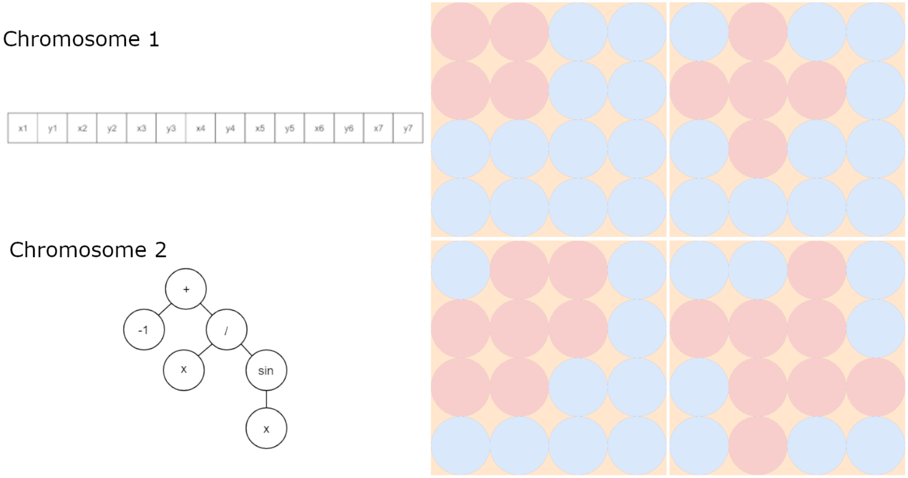

Figure 5.10: Example of representation and evaluation for a problem of Circle Packing in Squares.

may be very different in arrangement and motif when compared to others, and so, performing well in one may or may not be an honest indicator of how they perform in others. Thirdly, for these reasons, assuming $p_n = 0$ for all preferences is suitable. Of course, other values can be used, but because no assumptions are made on how p_n is related to fitness (it may be positively or negatively related in some instances and not at all in others), the choice is good enough to meet the assumption on Mate Choice.

In this scenario, a decision on the number of extracted traits, and which, needs to be made, following suit with the second Symbolic Regression scenario. While many sub-instances are available, evaluating all of them can be demanding. The same analysis applies, a number of sub-instances can be pre-selected (equally spaced for instance) from the full range, or the introduction of initialization and mutation operators that allow for the variation of the perception system can take place. Of course, the full analysis on the problem of Circle Packing in Squares also applies to the problem of optimization of Morse clusters, although on three dimensions rather than two. Finally, to close the discussion on terminals, its important to notice that none of the preferences used on any of the examples makes any assumptions on the representation of candidate solutions.

While the design of a terminal might demand some thought, establishing a non-terminal set is quite simple. As seen in Figures 5.8, 5.9 and 5.10, arithmetic operators are used independently of the meaning of each terminal. In these scenarios, all terminals produce real values, within the same order of magnitude, making simple arithmetic operators a suitable choice. Depending on the data types returned by terminals, adjustments may be needed in other scenarios. For instance, it may make sense to introduce qualitative data types and problem specific operators to deal with them. Also, operators combining more than two inputs can also make sense, in order to mirror interactions that combine many inputs in one step. Such situations will not be experimented with in the current study, as they shouldn't represent absolute needs for Mate Choice. As a non-terminal set is built, it's up to evolution to select which interactions are competitive and which are not, both regarding node frequencies and tree size. The resulting behavior might be very difficult to analyze, because operators can have different impacts on multiple contexts, either boosting the influence of certain preferences in the presence of others, or the other way around. Not only that, but the distribution of traits in male candidates can also influence how interactions impact overall attractiveness.

5.3.2 Assumptions and Considerations

Perception
It is not in the nature of CMP-GP for individuals to have access to the full phenotype of mating candidates. Rather, perception of others is bound by the terminal set built for each problem. It is up to researchers, in a first stage, to determine how many and which perception abilities are made available in the pool. As discussed, terminals may be subject to stochastic initialization and may mutate throughout the evolution process, making it so that the perception of others can vary, potentially finding new traits of interest to Mate Choice and dropping others. This process is a part of a second stage of determining perception abilities, which is bound to evolutionary forces. The frequency of terminals in the population may vary, making it viable for some to be completely dropped, but also imposing an active competition through self-reinforcement. After all, perception bias can kick-off Fisherian runaway processes. In summary, perception is not immutable, being therefore subject to evolutionary forces.

Context interpretation
Following the discussion on perception, context is also bound by the terminal set as well as by the distribution of terminal nodes in the population. For each particular trait, context is dependent on what other terminals are present in the particular preference tree being processed, but also on the non-terminals present and tree depth. Consider a well balanced tree, with a given depth and two-input operators only. As the tree is processed from leafs to root, the evaluation context for each particular preference increases exponentially. When processing the leaf layer, each trait-preference relation is processed independently. When moving to a layer above, the context of each preference will be influence by one other. In the layer above it will be influenced by three other and so on. In the root node, the full evaluation context is present and all independent preferences are processed into an attractiveness value that takes into account the full context. This example generalizes to any tree, either balanced or unbalanced, of any size and independently of operator characteristics. Tree structures can of course change during evolution, making context to be under evolutionary forces.

Mate evaluation function
When discussing the aggregation function on PIMP, a three tree system was described. The system used in CMP-GP is a natural simplification of that system, where the tree used for the representation of the ideal mating partner has been removed, making the inputs dependent on the perception system or terminal set defined. Still, the mate evaluation function is what ties everything together (perception, context and interactions). Unlike PIMP, a function is not externally determined, being up for each individual to encode and apply their own evaluation to mating candidates. As a result, evaluation functions are able to freely evolve, bounded only by the assumptions on terminal and non-terminal sets, and on the operators used. These assumptions are however on a higher level, which better suit the assumptions on Mate Choice that aim at keeping evolution as less constrained as possible. By keeping the evaluation function away from rules and constraints, evolutionary freedom is extended to perception, context and interactions.

Preference interactions

The modeling of mating preferences through evaluation functions allows for the explicit representation of preference interactions. Much like perception is controlled by the terminal set, preference interactions are controlled by the non-terminal set and, as previously discussed, they also influence context by establishing how preferences are related. The chain of interactions can transform the impact of each individual preference in multiple ways. Some preferences can be placed very close to the root of the evaluation function, having a more direct impact on the attractiveness value, while others can go through various operations until its influence is determined. Also, the same way that sub-trees can boost each others impact, they can also null each other. As a result, parts of preference chromosomes, while present genetically, may have no expression, which can account for preference pre-existence or dormancy. Mutation or variation can suddenly cause such preferences to express themselves at some point in the evolutionary process.

Complexity

Following the discussion on preference interactions, complexity is influenced by two main factors. Firstly, non-terminals may be n-adic with $n \geq 1$, where $n = 1$ corresponds to an operation that transforms an input rather than represent an interaction. As n increases, operators take a higher number of inputs that interact with each other in increasingly complex ways. Most arithmetic operators are 2-adic, and therefore all contribute in the same way to complexity. As the second factor will clarify, this doesn't mean in no way that complexity is static or restricted by each available non-terminal. Secondly, while interactions within a single operator may be bound by the number of inputs accepted, they may be chained in a tree with many layers, thus allowing for complexity to increase or decrease accordingly and under the influence of evolutionary pressure. Still, tree size restrictions may keep complexity from growing indefinitely, but still, it may be assumed that complexity has appropriate means to evolve through explicit and chained interactions.

5.3.3 Proof of Concept

The two aforementioned problems of geometry optimization have been used for proofing the concepts of the CMP-GP. Similarly to the use of Symbolic Regression in PIMP, the goal is not to benchmark the approach nor to make a deep analysis of its behavior, nor to study particular design choices. Rather, these applications aim at showing that the approach fits our general framework, that the general assumptions are being followed and that an appropriate scenario for Mate Choice is built. It also aims at demonstrating that the traits chosen for Mate Choice evaluation are suitable. Finally, there's an interest in the performance of the algorithm on these two problems, which constitute large sets of testing instances of increasing challenge. Specially for the optimization of Morse clusters, the collection of testing instances is particularly difficult to tackle, and so can be indicative of the competitiveness of CMP-GP in hard optimization tasks, and in comparison to other state of the art methods.

As extensively described, the problem of Packing Circles in Squares consists on finding the configuration of a set of circles of fixed radius so that they minimize that area of a containing square [186]. Individuals encode candidate solutions on their first chromosome using a vector of Cartesian coordinates representing the position of each circle, which is then mapped so that the area of the enclosing square can be calculated. Regular Genetic Algorithms operators are applied on this chromosome ensuring genetic crossover and mutation. For the purpose of encoding mate evaluation functions, a second chromosome is added with a Genetic Programming representation, which is to be used by each individual to assess mating candidates based on its own mating preferences. Specifics on the terminal and non-terminal pools can be found in the original study [186] but relies on the following notes: when tackling an instance with n circles, all $[2, n-1]$ sub-instances are available in the terminal set; a set of arithmetic operators are available as non-terminals.

To measure the performance of an individual packing n circles in all instances of lower dimensionality, one would need to consider a total of $C_2^n + C_3^n + ...C_{n-2}^n + C_{n-1}^n$ arrangements. In order to drastically reduce the computational effort needed for the evaluation of mating candidates, a simplification was used where only the first k circles represented in the chromosome are considered, instead of C_n^k possible combinations of k circles. Other than this process, the setup used was rather straightforward: traditional operators were used for both chromosomes; the first chromosome is subject to crossover with a 90% probability and mutation with a 2% probability; the second chromosome is subject to crossover with a 90% probability and no mutation; selection of females is done through a tournament of 5 individuals; each female chooses its mating partner from a set of 5 randomly selected mating candidates.

An alternative approach was designed based on the encoding of mating preferences as a vector of weights, one for each sub-instance being evaluated. The attractiveness of a candidate male is determined by its performance on each sub-instance and the weights encoded in the female, combined through the following weighted sum: $\sum_{k=2}^{n} w_k^f P_k^c$, where w_k^i is the weight encoded by female f for sub-instance k and P_k^c is the performance of candidate c in sub-instance k. Notice that P_k^c values are the same as used on terminal nodes in the mate evaluation functions (on the Genetic Programing approach). Therefore, this vector representation evolves only the weights of a predefined aggregation function, which arguably represents a smaller search landscape. It would be expected that the evolutionary process could make it so that useful weights evolve, distinguishing between sub-instances that have a positive, negative or null effect on the profiting selection of mating candidates.

Four setups were tested: traditional selection with both individuals being selected through tournament selection; Mate Choice through the encoding of weights; Mate Choice through the use of mate evaluation functions; random selection of the male parent. Experiments were run on instances ranging from 2 to 24 circles, for which the optima is known. Each setup was run thirty times, and final best fitness values were saved. Table 5.4 shows the Mean Best Fitness values achieved by each setup on each instance. Experiments where statistical differences (using a Wilcoxon Mann Whitney test [195] with a significance level of 0.05) from a standard approach were found have been highlighted. Regarding Mate Choice, the Genetic Algorithms approach achieved better results in four instances, one with statistical significance, while the CMP-GP achieved better results on eighteen instances, eight of which with statistical significance.

Overall, the obtained results can be summed in the following remarks: random selection of males performed better than a standard approach, suggesting that the algorithm may benefit from a decrease in selection pressure for a higher exploration effort; the weights based setup performed below expectations, as it should have been able to make a better use of information extracted from mating candidates; results suggest that the tree based encoding of mate evaluation functions contributed positively to a better performance by the algorithm. Independently of the inner workings of CMP-GP, from

Table 5.4: Mean Best Fitness over 30 runs obtained with a standard, random, mate choice with GA representation and mate choice with GP representation on the packing of N circles in squares

				Mate Choice	
N	Optimal	Standard	Random	GA	GP
2	3.4142	3.4142	3.4142	3.4142	3.4142
3	3.9319	3.9320	3.9320	3.9319	3.9319
4	4.0000	4.0266	4.0001	4.0255	4.0001
5	4.8284	5.0056	4.9911	**4.9250**	**4.9475**
6	5.3282	5.3669	5.3674	5.3685	5.3804
7	5.7321	5.8227	5.8081	5.8296	5.8098
8	5.8637	6.0212	5.9615	5.9913	5.9898
9	6.0000	6.5184	6.4907	6.5401	6.5154
10	6.7474	6.8936	6.8854	6.9110	**6.8536**
11	7.0225	7.1619	7.1764	7.2232	7.1564
12	7.1450	7.3966	7.3565	7.4809	7.3438
13	7.4630	7.8088	7.8167	7.8355	**7.7147**
14	7.7305	8.0705	8.0950	8.1509	**8.0048**
15	7.8637	8.3324	8.4173	8.4345	**8.2581**
16	8.0000	8.7014	8.8632	8.8153	**8.6012**
17	8.5327	8.8765	9.2345	9.0836	8.8665
18	8.6564	9.0996	9.4966	9.2724	9.0984
19	8.9075	9.4442	9.9422	9.6036	**9.3511**
20	8.9781	9.7212	10.2839	9.7641	**9.6030**
21	9.3580	9.9788	10.7402	10.1307	9.9425
22	9.4638	10.2610	11.0512	10.3705	10.2693
23	9.7274	10.5201	11.5476	10.6498	10.5892
24	9.8637	10.7725	11.8382	10.8163	10.8034

the perspective of performance, it could be said that the proposed approach was able to make good use of the information extracted from mating candidates. This doesn't imply the emergence of good sense, as the algorithm is built for self reinforcement through good taste, but it may point out that good taste can positively contribute to good sense. Finally, the results back up that Mate Choice emerges in a way that is fundamentally different from selecting males randomly. A longer analysis of results can be found in a study by Machado and Leitão [186].

Morse cluster optimization consists in finding the geometry of a cluster so that its potential energy is minimized. In a way, it's an extension of the packing problem to three dimensions, where instead of minimizing an area, the goal is to find an arrangement that minimizes the cluster's potential energy. Over the range of potential cluster sizes, CMP-GP has been applied to clusters sizing from 41 to 80 atoms. These 40 instances provide a robust test set, with a diversity of geometric motifs and characteristics that challenge how Mate Choice can be used to tackle each one specifically without requiring careful customization to each instance. While most of the discussion on implementing mate evaluation functions through Genetic Programming would be just an extension of the setup used for the problem of Circle Packing in Squares, there are a few things worth clarifying: the first chromosome encodes Cartesian coordinates for the location of each particle in the three dimensional space and evolves through Genetic Algorithms operators; the second chromosome encodes a mate evaluate function; the terminal set includes arithmetic operators and the non-terminal set follows the idea that each individual can also be evaluated on sub-instances of the target problem. Regarding the terminals, not all sub-instances are available, as it could mean having a terminal set with up to 80 possible nodes. Instead, 5 equally spaced sub-instances are used. Details can be found in the full study [173].

CMP-GP was introduced in a state of the art model for tackling the optimization of Morse clusters, focusing on the importance of maintaining diversity [223]. The steady-state model relies on a substitution mechanism that controls which offspring are allowed in the population, therefore assuming a very powerful role. Substitutions are allowed in two situations: either the new offspring is structurally similar (according to a distance measure) to one individual in the population, in which case the fittest of the two is maintained; or the new offspring is structurally dissimilar from all individuals, in which case it may replace the worst individual if it is fitter; otherwise, the new offspring is discarded. This replacement mechanism may have a strong enough grip on the population to effect evolution, after all, producing sexy offspring and reinforcing mating preferences is secondary if new offspring are unable to be introduced in the population. In a way, it surely is more important for mating preferences to adapt to the replacement operator as a strategy to maximize the number of offspring they can introduce in the population and thus attempt at self-reinforcement.

Table 5.5 shows the success rate at finding the putative optima on 30 runs for each instance of the problem. This metric as been regularly used for performance assessment on cluster geometry optimization problems. A pairwise proportions test was used to find significant differences [283], using a significance level of 0.01. Out of 40 instances, CMP-GP was able to achieve a higher success rate on 20 instances, 4 of them with significant differences. Ties were found on 7 instances as well. Overall, CMP-GP was able to find all putative optima. From a performance perspective, and even though Mate Choice is bound by the replacement operator, the strategy seems able to contribute positively to the optimization effort. A deeper analysis on the interplay between Mate Choice and the replacement operator is worth expanding.

As discussed, the replacement strategy relies on two main rules. In a way, it either

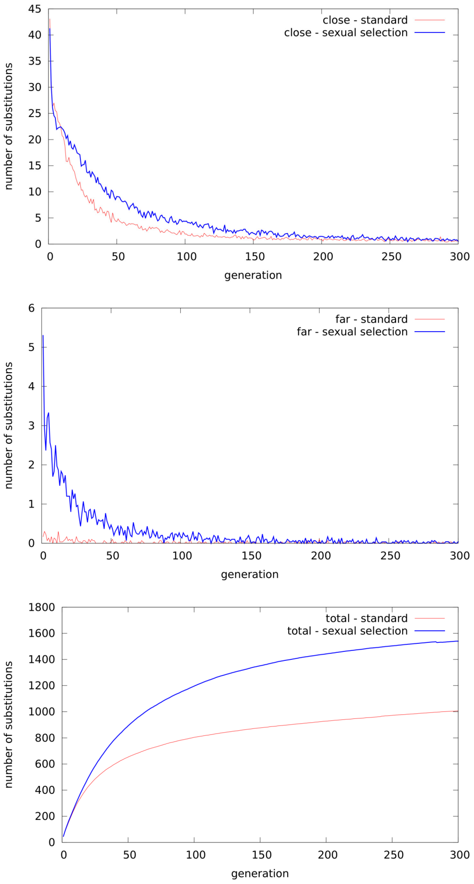

Figure 5.11: Top: Average substitution rate from 30 runs with clusters of size 61, where close corresponds to individuals replacing a similar one in the population. Middle: Average substitution rate from 30 runs with clusters of size 61, where far corresponds to individuals replacing worst one in the population. Bottom: Cumulative average number of substitutions obtained in 30 runs with clusters of size 61. A generation counter is incremented at each 100 individuals bred.

Table 5.5: Success rate over 30 runs obtained by a standard and mate choice approaches on the cluster geometry optimization of morse clusters of size N

N	41	42	43	44	45	46	47	48	49	50
Mate Choice	**24**	**21**	18	**18**	12	14	6	16	16	2
Standard	15	12	14	7	5	9	2	14	18	5

N	51	52	53	54	55	56	57	58	59	60
Mate Choice	2	9	4	7	7	11	9	5	3	**7**
Standard	7	6	5	12	6	11	8	4	2	0

N	61	62	63	64	65	66	67	68	69	70
Mate Choice	1	6	8	8	9	10	5	3	6	6
Standard	1	12	6	11	8	8	5	4	6	8

N	71	72	73	74	75	76	77	78	79	80
Mate Choice	6	3	6	5	5	3	3	4	2	5
Standard	6	7	6	1	2	4	7	3	6	5

allows exploratory offspring that are at least as good as the worst individual in the population or exploitative offspring that improve on the fitness of their closest individual. The top and middle graphs in Figure 5.11 shows that CMP-GP increases the number of offspring accepted by both rules. It's important to notice that the replacement strategy is quite restrictive, making it so that very few individuals are accepted for every 100 offspring bred (in both approaches). Still, CMP-GP is able to increase the number of exploratory individuals in the beginning of the population, which may be important for the population to be more distributed in the search space and therefore able to exploit more areas concurrently. The increase in exploiting offspring accepted throughout the runs seems to corroborate this view. Even though Mate Choice can produce a lot more destructive crossovers, this scenario shows how such a behavior can be important for exploration and even boost the success of exploitation.

The bottom graph in Figure 5.11 shows the overall impact on accepted offspring, which increases cumulatively roughly 50%. While such a behavior doesn't necessarily translate into better performance, it shows an adaptation to the exploratory and exploitative rules of replacement. A key factor for this process, which as been previously discussed, may be the momentum that mating preferences and self-reinforcement give to newly discovered search areas. Not only does CMP-GP increases the chance of exploring new areas but also gives them a longer chance to be exploited. This behavior is different from exploration through mutation, where a new individual may stumble upon a new search area, but due to its low fitness, is given no further opportunity to contribute. In the end, the population keeps a less elitist character, benefiting from a directional drift. As a result, a relation between exploration and exploitation is possible, accounting for less moments of stasis. A more complete analysis on the behavior of Mate Choice on the optimization of Morse Clusters is available [173].

Chapter 6

Applications and Experimentation

The modeling of Mate Choice has been shown to be possible using a general framework. Independently of design choices, or even on the introduction of complex mating preferences, the proposed framework clarifies which are indeed the requirements and assumptions behind Mate Choice, and which are not absolutely needed. Moreover, it outlines the processes of representation, evaluation, inheritance and design choices, which together determine the workings of evolution. On top of that framework, two approaches relying on Genetic Programming to represent and evolve mating preferences have been introduced (PIMP and CMP-GP), both abiding by the rules of Mate Choice, but also showing diverging inspirations and designs.

Despite the proof of concept of each approach on at least one problem, briefly discussed in the previous chapter, and the theoretical discussion on behavior included on Chapter 3, a broader, more complete study would be most beneficial to the study of Mate Choice and its applications on Evolutionary Algorithms. For that purpose, the present chapter discusses a large experimental set that has multiple goals. Firstly, there's the issue of performance, and how Mate Choice compares to standard selection in achieved results. Secondly, and while the two approaches were not built as direct competitors but rather as two choices that may be more or less suitable on different scenarios, it should be fruitful to compare the performance of both approaches. Thirdly, experimentation should bring to light behavioral aspects that may: i) corroborate hypothesis or research questions; ii) contradict theoretical analysis or assumptions; iii) provide further knowledge on the workings of Mate Choice; iv) contribute with information to a better understanding of how Mate Choice may be an asset to Evolutionary Algorithms.

6.1 Experimental Setup

Symbolic Regression has been chosen as the target problem for experimentation with Mate Choice. This family of problems has been sufficiently introduced in subsection 5.1.7, and the arguments in favor of its use for benchmarking have also been discussed, requiring no further comments. Regarding the application of each approach on Symbolic Regression, the scenario has been previously considered as part of the lengthy introduction on their motivation, particularities, and design, included in sections 5.2

Table 6.1: Operators and Parameters used for experimentation with the standard approach.

Standard Approach

General Parameters	population size	100	
	generations	500	
	elitism	1	
Selection of First Individual	operator	tournament	
	size	5	
Selection of Second Individual	operator	tournament	
	size	5	
Individual Builder	operator	ramped half-and-half	
	full	tree depth	random(2,6)
	grow	max tree depth	random(2,6)
		grow probability	0.5
Breeding	crossover prob.	0.9	
	copy prob.	0.1	
	mutation prob.	0.0	
Crossover	node selection	terminals prob.	0.1
		non-terminals prob.	0.9
		root prob.	0.0
	max depth	17	
Mutation	node selection	terminals prob.	0.1
		non-terminals prob.	0.9
		root prob.	0.0
	grow	max tree depth	5

and 5.3. As shown, PIMP has also relied on the scenario for proof of concept, producing a restricted study that shall now be expanded. On the other hand, CMP-GP has not been applied to Symbolic Regression up to this point, but two potential methods were discussed and illustrated in Figures 5.8 and 5.9. Experimentation will follow the approach represented by Figure 5.9, whose motivation and outline can be found in Section 5.3. It should be noted that the standard design considers a number of terminals with fixed spacing between them and random preferences for each, sampled at instantiation.

The following subsections will complement on the approach's descriptions for a complete exposition of the experimental process. A base standard approach, as well as the two Mate Choice variants are discussed. Firstly, general operators and parameters are introduced, followed by specifics on the builders and particularities for each approach. Following, the custom scenarios considered in experimentation are discussed and the setup and methodology used in each individual experiment is described. Finally, implementation details are given. Most information has been organized in tables for easier access, and because many design options follow traditional choices, enough argumentation has been already included.

Table 6.2: Operators and Parameters used for experimentation with Mate Choice (both PIMP and CMP-GP).

Mate Choice		
General Parameters	population size	*same as standard*
	generations	
	elitism	
Selection of Female Individual	operator	tournament
	size	5
Selection of Male Candidates	operator	random
	pool size	5
First Chromosome		
Builder	*same as standard*	
Breeding		
Crossover		
Mutation		
Second Chromosome		
Builder	*same as standard*	
Breeding		
Crossover		
Mutation		

6.1.1 General Operators and Parameters

Tables 6.1 and 6.2 summarize the operators and parameters for the Standard and Mate Choice approaches respectively. From the chromosome builders to the selection and breeding operators, as well as general parameters, the whole process is covered. These setups will be the basis for performance and behavioral analysis, and for comparisons between approaches. There are two choices that require a brief explanation. Firstly, the mutation probability on the base scenario is 0%. While mutation may play an important role in search, its absence makes sense for analysis purposes because: i) mutation is not a requisite for Mate Choice; ii) behavioral analysis is cleaner without the introduction of noise through mutation; iii) mutation may share some of the effects of Mate Choice (for instance higher exploration), which shouldn't be falsely attributed to the wrong causes. Scenarios combining Mate Choice and mutation will be discussed later.

Secondly, both Mate Choice approaches rely on the same operators and parameters on both chromosomes which are also equivalent to those used in the Standard approach. While on PIMP the search space is similar on both chromosomes, the same can't be said about CMP-GP. Also, as previously discussed, mating preferences may benefit from different search processes, independently of the search space that they correspond to. A full parametric study would contribute to the discussion of such design choices, specially on whether the performance and behavior of either approach can be improved by more carefully chosen operators and parameters. Then again, such choices may be highly dependent on the context and on the target problem. As this study will focus on the Symbolic Regression problem family only, it also refrains from including a complete parametric study, leaving the subject for future efforts. Alternatively, it will rely on the traditional choices depicted in each table.

Table 6.3: Non-terminal and terminal sets for the PIMP and CMP-GP approaches.

PIMP

Non-terminals	*same as first chromosome*
Terminals	*same as first chromosome*

CMP-GP

Non-terminals	+,-,*,/,%	
Terminals	$l \vert l \in S[a_n,b_n,s] \subset \Re^n \rightarrow \vert p_l - f(t_l) \vert$	$S[a_n,b_n,s] \subset \Re^n$ is s samples equally spaced in $\Re^n$. In each of the n dimensions, samples are between a_n and b_n. For each sample l, there's a terminal $\vert p_l - f(t_l) \vert$ comparing a preference-trait pair. Preferences p_l initialization is individual. Traits t_l perception is phenotypical $f(t_l)$.

6.1.2 Specifics for Each Approach

While there was an attempt to maintain the design choices as transverse as possible, the terminal and non-terminal sets are exceptions that need to be addressed independently. The issue has been extensively discussed in sections 5.2 and 5.3, with each set being summarized in Table 6.3. As expected, the sets in PIMP are simply dependent on the terminals and non-terminals used for building the first chromosome, which is determined by the target problem. Regarding CMP-GP, the two sets can be described as follows: the terminal set correspond to points equally spaced in each dimension of the search space (within the intervals shown in function descriptions); for each point, the corresponding terminal encodes a preferred value that is sampled randomly every time the terminal is used in initialization or mutation processes; during evaluation of mating candidates, the value mapped for that point in the phenotype of the candidate is measured against the encoded preference; the distance is fed as input to the non-terminal functions; the function set encompasses simple mathematical functions that are suitable to deal with the real value data type resulting from terminals; these operators represent interactions between individual preference-trait evaluations.

Although not specially important for the the introduction of Mate Choice, there's a second particularity that is worth a brief discussion. The equally spaced points used for establishing terminals in the CMP-GP are not guaranteed to belong to the set of points used for fitness evaluation. While some may overlap or be closely similar, others (or all) may be different. Also, this observation may vary between experiments. As a result, the relation between trait assessment for Mate Choice and for survival is more than just considering whether they pull in the same direction or not. For some traits, the impact of survival may be direct (if the corresponding point is also used for fitness assessment) or rather indirect, even if impacted by the placement of other points or by sharing the same genotype. This allows for a certain freedom favoring Mate Choice, while at the same time keeping ornaments or traits favored by Mate Choice deeply linked to other traits through the phenotype. It also prevents the need from introducing further assumptions on the relation between Sexual and Natural Selection. PIMP may not always be covered by this discussion, as the same parameters and builders are used for both chromosomes, however, in part of the test set, initialization is done through a random distribution of points within an interval (see Appendix E), thus allowing for

Table 6.4: Custom scenarios introducing mutation in addition to Mate Choice.

Trait Mutation

First Chromosome		
Breeding	crossover prob.	0.89
	copy prob.	0.1
	mutation prob.	0.01

Second Chromosome		
Breeding	*same as standard*	

Preference Mutation

First Chromosome		
Breeding	*same as standard*	

Second Chromosome		
Breeding	crossover prob.	0.89
	copy prob.	0.1
	mutation prob.	0.01

Trait + Preference Mutation

First Chromosome		
Breeding	crossover prob.	0.89
	copy prob.	0.1
	mutation prob.	0.01

Second Chromosome		
Breeding	crossover prob.	0.89
	copy prob.	0.1
	mutation prob.	0.01

the points used for fitness and attractiveness assessment to be unequal.

6.1.3 Custom Scenarios

The base scenario, which will be most scrutinized to explore the role of Mate Choice, doesn't include mutation as one of its operators. As previously discussed, mutation is not an necessity for Mate Choice, taking no particular role in the development of self-reinforcement and the resulting runaway processes which is characteristic of Fisherian Mate Choice. However, there are several arguments in favor of combining mutation and Mate Choice, even though the reasons may be difficult to discuss with absolute certainty due to preference complexity and interactions. Nonetheless, both Fisherian and Wallacean models of Mate Choice discussed in Section 3.1 suggest that self-reinforcement shall guide the population into a state of equilibrium, where preferences and traits, either for survival or attractiveness purposes, maintain a frequency distribution that is balanced and unlikely to be disturbed without the intervention of an external force.

Such an external force can be determining for a search process, as an extended state of equilibrium may contribute to a stoppage in the search efforts. In a non-dynamic scenario such as that of Symbolic Regression, such a force is most easily introduced by means of mutation. Therefore, three setups, each with its own characteristics, have been idealized as alternatives to the base scenario: i) introducing mutation in mating preferences; ii) introducing mutation in traits; iii) introducing mutation in both concurrently. Table 6.4 summarizes the parameters involved in each approach, which require a succinct but important discussion on their differences and potential impact. Firstly, trait mutation has a two fold impact. On the one hand, it introduces variability into candidate solutions which can produce breakthroughs in terms of fitness that spread through the population. On the other hand, it can disrupt Mate Choice equilibrium, by introducing non-existing traits in the population that can either gain advantage in face of relevant preferences, or trigger pre-existent non-expressed preferences. Alternatively, the introduction of preference mutation can both change the perception system of females, or the role that each individual trait plays in the overall evaluation of mating candidates (this impact should be seen with the particularities of each approach in mind, as discussed in Sections 5.2 and 5.3). In either case, mutation can change the way individuals are ordered when being evaluated for mating, and thus trigger directional runaway processes in new directions, providing further means for exploration. Finally, the third scenario combines both previous ones in an attempt to mix both behaviors.

6.1.4 Testing Setup

Symbolic Regression has been established to be the benchmarking problem for the current study. Ideally, as has been discussed by McDermott et al. [193], a wider test set would be used, including instances from many families of problems, in an attempt for orthogonality and a chance to uncover weaknesses that may show in certain domains. While two other problems were used for proof of concept, in an extent that follows suit to most of the criteria discussed by McDermott et al. for proper benchmarking problems (some criteria can be conflicting) [193], the task of tackling the full range of proposed problems is overwhelming. Although that may be prone to changes, most studies focus on a particular subset of that set of problems, and so does this one. Still, the set of Symbolic Regression instances, which has been compiled by McDermott et al. [193] and originating from a set of studies [155, 160, 165, 218, 292, 299], follows most of the criteria that make for a good benchmarking set.

The set is composed of 52 target functions showing variance in difficulty (51 in the revised paper and one more made available with the implementation package by the same authors), sampling, as well as training and testing approaches. Tunable difficulty is an important characteristic of this set, with instances ranging from unidimensional, well understood functions (ex: koza-1 is a quartic function regarded as relatively easy [193]) to multidimensional, complex functions (ex: pagie-1 is considered particularly challenging [193, 218]). The number of variables ranges from one to five - 18 with one variable, 15 with two variables, 2 with three variables and 16 with five variables. While the distribution is not uniform, it still allows for search spaces with different characteristics and sizes. Sampling sizes also contribute to that, varying from a few (ex: 20 in some instances) to many (10.000 in the most extreme case). Moreover, some instances were meant for optimization while others were intended for regression and therefore rely on separate training and testing sets [193]. Finally, functions also vary on their build sets and on how their sample points are generated [193]. It should be noted that experimentation focused on optimization and relied only on training sets.

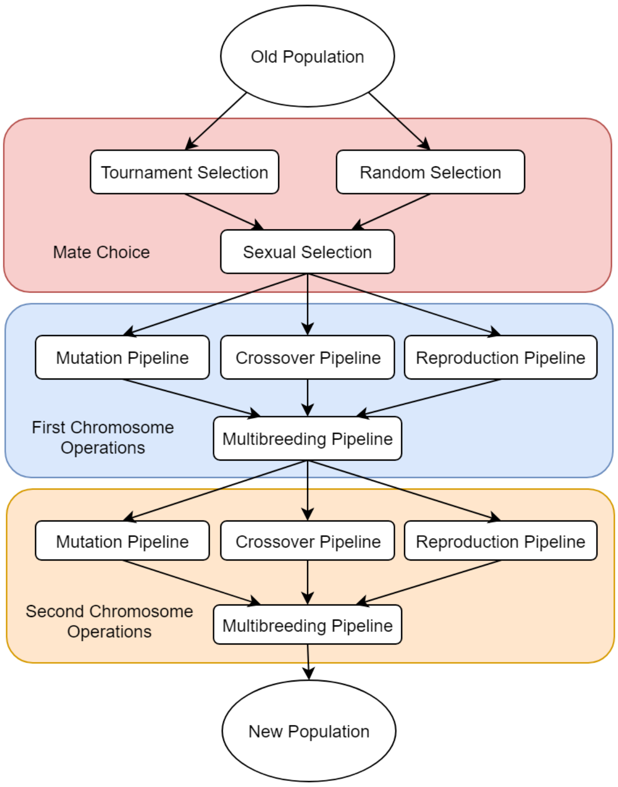

Figure 6.1: The Breeding Pipeline implemented to accommodate both Mate Choice and breeding assumptions.

For all 52 functions, particularities on the terminal and non-terminal sets for the first chromosome can be found in the McDermott et al. study [193] as well as in Appendix E, while the second chromosome is built abiding by the rules discussed in the previous subsections. The study also summarizes information on training (see Appendix E) and testing sets and other details. For any instance, each of the following approaches were run 50 times, and statistical and behavioral data was registered for future analysis: standard approach; standard approach with mutation (same probability as mutation on Mate Choice); Mate Choice without mutation; Mate Choice with mutation on the first chromosome; Mate Choice with mutation on the second chromosome; Mate Choice with mutation on both chromosomes. Both Mate Choice approaches were tested on all of the above variations.

6.1.5 Implementation Details

For the current study, Mate Choice has been implemented as a functionality for the widely used java-based ECJ toolkit [183]. The framework is well known among researchers and enthusiasts as one of the top competing, freely available software and has an active community, thus being continuously extended and put to the test on many scenarios. Over time, the toolkit has grown into a full-fledged evolutionary computation system, and is currently undergoing deep changes for consolidation under its version 25 [184]. In what regards Mate Choice, the approaches work all the same either in the backward-compatible version 24, or in the new version. ECJ offers a customizable framework where new paradigms can be introduced without requiring an overwhelming effort from developers while at the same time accounting for reliability and consistency. In regards to the Symbolic Regression task at hand, ECJ offers application examples describing how to implement and parameterize Genetic Programming approaches successfully on many scenarios. Moreover, Mcdermott et al. [193] built an implementation which is now distributed with ECJ covering all 52 function sets, with their particular building sets, training and testing sets, and so on.

The workings of ECJ on a high level have been covered by Luke on a recent paper regarding the future of ECJ [184] and can be understood on a low level in its user manual. In the end, the effort to build the two chromosome Mate Choice was mostly put on the Breeding Pipeline that connects population N to population $N+1$ through a chain of operations covering selection and breeding. Figure 6.1 shows the end result of the developed functionalities. Two main challenges were found: adapting selection to abide by the rules of Mate Choice; adapting the Breeding operators to act independently on traits and preferences. For the first task, as shown in Figure 6.1, the tournament and random operators were re-purposed to produce individuals from the population, either for the female role or to populate a pool of mating candidates. A new operator was coded to accommodate the produced individuals, and to perform the candidate evaluation and female choice steps, thus returning two individuals, the female and the chosen male.

For the second task, while ECJ supports the encoding of multiple chromosomes on the same individual, and thus can encode the two trees for traits and preferences, it doesn't abide by the assumptions that chromosomes should change genetic code according to their role (traits with traits and preferences with preferences). The two-part breeding operation was devised to separate operations on each chromosome individually and therefore to allow a simple parameterization of each step independently. In the end of the pipeline, two offspring are produced, potentially accommodating changes in each chromosome in comparison to their parents, which can be introduced into the new population. The process is repeated until the new population is full. As a side note, problems that imply two representation schemes, such as the geometric optimization scenarios used for proof of concept in Section 5.3, require much bigger changes to ECJ, as the framework expects all chromosomes to be of the same representation type. Nonetheless, ECJ is designed to be easily hacked, and while depending on changes on multiple classes, the customization is possible and fruitful.

6.2 Assessment, Metrics and Analysis tools

The evolution of evaluation functions for the purpose of Mate Choice introduces a paradigm that is not straightforward to study. While a standard application of Evolutionary Algorithms has a population adapt to a static environment, the self-adaptive character of Mate Choice introduces an ever-adjusting process of evolution, where the genetic pool is not only adapting to a certain search space, but also to the encompassing population itself. Despite the parallelism with dynamic problems, the resulting dynamic search space has the particularity of being influenced by the search process itself, in an entanglement that not only adds unpredictability but also makes it difficult to assess the emerging behaviors. This feedback process of influence between preferences and traits, and between preferences and preferences in an indirect way, has an impact on how the evolutionary process may be successfully studied.

On top of that, the encoding of mating preferences as trees and the introduction of complex interactions, independently of the approach being tested, introduces its own challenges to analysis that should be carefully considered. Moreover, the evaluation of mating candidates through phenotypic characteristics as well as the mapping of survival and ornamental traits from the same genetic sequence (or the extraction of ornamental traits from a phenotype for survival) is bound to make the assessment of the impact of mating preferences on the expression of particular traits a non-trivial task. The following subsections discuss means for analysis of Mate Choice and how to address particular research questions. The discussion will include performance analysis, which shouldn't deviate much from traditional means, but also means for behavioural analysis, which may be quite specific for Mate Choice.

6.2.1 Performance Analysis

The analysis made focuses on end results, which while being coarse grained for behavioral analysis, are straight to the point in evaluating evolutionary algorithms as goal oriented models. When dealing with models with different assumptions and potentially different behaviors, fitness is one of the few metrics that are transverse to all models and is therefore appropriate for comparison purposes. There are a few straightforward yet important questions that should be tackled:

How do the approaches compare in performance over the whole test set?
For each approach and custom scenario, on each test instance, the results from all 50 runs will be summarized using the Mean Best Fitness (MBF) and the associated Sample Standard Deviation (StDev), shown in Equations 6.1 and 6.2 respectively, where bf_n stands for the best fitness of run n. Moreover, the five number summary regarding the median and interquartile range is built as well, detailing the minimum, first quartile, median, third quartile, and maximum values. The mean of the average population fitness of all 50 runs is sometimes also used as an indication of performance, however, because individuals can be evaluated as infinitely bad, the metric can be skewed and was opted out. Additionally, several functions, mostly coming from the koza and nguyen families, may be suitable for comparisons using the number of hits (runs where the optimum was found with an error below $1E-04$). However, on most cases, no hits are achieved, making it unfeasible to extend this metric to all functions.

$$MBF = \frac{\sum_{n=1}^{50} bf_n}{50} \tag{6.1}$$

$$StDev = \sqrt{\frac{\sum_{n=1}^{50}(bf_n - mbf)^2}{50-1}} \tag{6.2}$$

These resulting summaries on mean and median values shall be presented in tables comparing each approach on their non-mutation base scenario, as well as comparing each base scenario with custom scenarios.

Are performance differences between approaches statistically significant?
On each Symbolic Regression instance, approaches and scenarios will be compared using the median and a two-sided Wilcoxon Mann Whitney test [195] will be used to assert if samples are significantly different. Instances where differences are found will

be flagged and results will be summarized in tables for a course-grained perspective. Additionally, regarding the number of hits found, a Taillard's pairwise proportions test [283] will be used to find significant differences between approach-scenario pairs. An extensive discussion on why analysis is made based on a non-parametric test rather than using a parametric test will be included, properly justifying the use of Wilcoxon Mann Whitney test and the median for comparisons (see Section 6.3.1). The discussion will be focused on potential assumption violations on parametric tests, specifically regarding normality, homogeneity of variance, the presence of outliers and the nature of the samples. For the purpose, interquartile information will be used in addition to Shapiro-Wilk's test for normality [260], Bartlett's test for variance homogeneity [23] (as a post-hoc to normality tests) and an interquartile range process for the identification of outliers [305].

How do design choices compare in terms of performance gains?
Focusing on the custom scenarios introduced and looking transversely at the results on all approaches should allow for a discussion on the impact of mutation as a whole, and in each chromosome in particular. Moreover, differences between the relation of each approach and mutation may highlight differences and similarities between them that may at this point be analyzed, relying on performance alone. This analysis will focus particularly on the impact of all three mutation setups on each Mate Choice approach and will then compare the best performing setup to the Standard approach, with and without mutation.

6.2.2 Behaviours and Associated Metrics

When studying Mate Choice and the underlying behaviors, performance metrics fall short on providing sufficient information to fully study potential impacts. Relying on finer-grain levels of information becomes imperative, either encompassing full populations, focusing on the selection steps or on each individual's genotype and phenotypic expression. Such granularity can be demanding computationally, therefore relying on measures that capture the right level of information becomes critical. Studying models based on different assumptions also adds to the challenge. While metrics that cover genotypic or phenotypic information extracted from the first chromosome (such as fitness or diversity measures) may carry comparable information, metrics that focus on preferences have no counterpart in standard approaches. More importantly, their interpretation is subjected to the underlying assumptions of each model and should be used carefully even when comparing between Mate Choice approaches. For the purpose of clarity, and more importantly to bring attention to such challenges, each research question and the means for analysis is discussed in the remaining of this section.

Is Mate Choice truly taking place or are the results the product of some other unexpected behaviour?
While the system has been designed, to the best knowledge, to successfully model Mate Choice processes through the individual encoding of preferences or mate evaluation functions and their self-adaptation, the emergence of Mate Choice needs to be empirically validated. Otherwise, the study would lack an important safeguard from the possibility that the framework may be incapable of introducing Mate Choice, and that in fact the end results are the outcome of lower selection pressure or other byproduct behaviors. Luckily, Mate Choice is dependent only on the self-reinforcement of mating preferences, which shouldn't be difficult to demonstrate. It is expected that over the

generations, females increasingly select males through characteristics that are indicative of the presence of their own mating preferences in the male genotype, therefore increasing their own reproductive advantage by following the attractive sons theory. As a result, the distance between female mating preferences and those encoded in selected males should decrease. Two metrics can be considered across both approaches as indicative of this behavior:

Genotypic distance - Koza [165] suggested comparing individuals in a binary way (either equal or different) using the whole genotype. As a distance measure, binary comparison is very coarse grained and little informative, but it does ensure that genotypes are undoubtedly structurally similar, allowing for no false positives. In this case, they can be used to compare preferences in females with those of their selected males, thus checking for self-reinforcement. Other more advanced metrics such as tree edit distance [225] can be more informative and offer more valuable insight but may also be prone to errors, for instance due to non-expressed sub-trees. On the one hand, the use of the binary genetic distance can leave some self-reinforcement occurrences unidentified, but on the other hand, those that are found are certainly true, which for the current purpose is advantageous. Therefore, binary comparisons will be used to measure the rate of matching preferences in selected mating pairs, as a measure of genotypic self-reinforcement

Phenotypic distance - The genotypic distance is quite strict and, similarly to other metrics, on scenarios where many-to-one relationships between genotypes and phenotyes can happen, it can be lacking [36]. Phenotypic measures can be helpful but some are dependent on representation. For instance, the Mean Squared Error could be a good metric for PIMP but would not work to measure the distance between preferences in CMP-GP. Alternatively, the following metric was used on both approaches at each selection step: i) the female ranks the male candidates according to its preferences; ii) the selected male ranks the same male candidates (including itself) according to its preferences; iii) Spearman's rank correlation coefficient [276] is used to compare ranks (in the case of tied data such as when all candidates are evaluated as equal, random ranks are attributed, which is consistent with the employed selection method and should result in negative coefficients). The coefficient is used to compare preferences from totally diverging (-1 coefficient) to absolutely agreeing (1 coefficient).

$$MD = \frac{\sum_{n=1}^{steps} d(p_f, p_m)}{steps} \tag{6.3}$$

On each run of Mate Choice approaches, both distances are calculated for each selection step and averaged over the total of selection steps in a generation, as shown by Equation 6.3. They are then averaged over the whole 50 runs for each generation, and both the average and each single run is plotted for assessment. For self-reinforcement to be shown, and therefore for preference distances to decrease, both plotted metrics should increase to the proximity of 1.

Do mating preferences have a Fisherian or Wallacean character?
As long as Mate Choice has been confirmed, results may be the product of females developing good sense mating preferences as argued by Wallace, or the implication of good taste as backed up by Fisher-Darwin theory. Arguably, both may be present, even within the same mate evaluation function. While fully unveiling which preferences fall under each category is a complex task, some feedback can be studied regarding

the overall character of preference functions (for good sense or for good taste). As previously discussed, the process behind the emergence of ornaments for good taste or as indicator mechanisms are mostly the same, relying on a Fisherian feedback loop. Therefore, what most distinguishes ornaments on their purpose are how they impact viability, in which case Wallacean models imply the coupling of preferences with high viability.

Both ideas can be studied by looking at which males are being selected and how they relate to fitness. In short, the correlation between preferred mating candidates and fitness can be informative. The following metric was used at each selection step: i) mating candidates are ranked by the female according to attractiveness; ii) mating candidates are ranked according to fitness; iii) Spearman's rank correlation coefficient [276] is used to compare ranks. A coefficient close to 1 would indicate the Wallacean character of a female's preferences while a coefficient close to or lower than 0 would indicate Fisherian preferences. The metric attributes a larger spectrum to Fisherian preferences, arguably making it rigged in their favor, however, this unbalance is in agreement with Wallacean preferences relying on more assumptions to emerge. The mean coefficient over the selection steps as shown by Equation 6.3, averaged over he whole 50 runs, will be plotted as will the results for each run in an broader attempt to find multiple strategies emerging.

Does gender emerge with Mate Choice?
While the system's assumptions don't imply the explicit definition of genders, it also doesn't impose any rules that prevent the specialization of individuals on being male or female. Specially if males are selected for beauty's sake, it may happen that individuals in order to get a chance of selection, have to either specialize on being fit or on being attractive (individuals in-between may be less competitive and be given fewer reproduction chances). While it is not a given that individuals selected as males are unfit, or in that case, that individuals can't compete both as males and as females, it would be important to understand exactly how well separate both roles are (or not) in the evolution process and in the composition of populations.

In order to study the behavior, at each selection phase, one may log how often individuals are selected as females, or as males (candidates for both positions are selected randomly, so all should have a fair chance), and consequently study the size and interception of both groups. In one scenario, the interception may be high, suggesting that gender separation has an insignificant role. An alternative scenario would show two well separated groups, with individuals specializing on either role. Visualizing the average size of the groups over 50 runs will be made possible through generational plots and allow for conclusions to be taken on the subject.

Is perception of variation being promoted with Mate Choice?
Lerena [178] described perception of variation as the ability to perceive differences in traits, even if on one locus. While directly assessing how each individual preference tracks differences in particular traits would be extensive work, it's expected that such differences are reflected in fitness and/or attractiveness. Regarding Mate Choice, if mating preferences aren't sensible to changes between mating candidates, they may end up selecting randomly whereas they should be choosing for particular traits. Entropy diversity [245] can help out in assessing if Mate Choice is capable of perceiving variation between mating candidates. Succinctly, entropy identifies the unique values in a sample and how the sample is distributed among such values. In this particular case and when applied to fitness, high entropy among a group of mating candidates indicates

a high variation of fitness, with many unique values and a more evenly distribution of candidates. In contrast, a low fitness entropy would mean small to no variation of fitness, with many individuals sharing the same evaluations. Likewise, when applied to attractiveness values on the same group of mating candidates, entropy can show how well each female's mate evaluation perceives variation between candidates. Therefore, after n partitions have been identified, Equation 6.4 shows the procedure for calculating entropy, either for fitness or for attractiveness, where c_k is the portion of candidates that correspond to partition k.

$$S = -\sum_{k=1}^{n} c_k \cdot ln c_k \quad c_k = \frac{|k|}{|c|} \tag{6.4}$$

Because a tournament-like Mate Choice operator is being used, each unique fitness or attractiveness value is being identified as independent, rather than using intervals, as they will not compete as equals for selection. At each selection step, after fitness entropy and attractiveness entropy have been calculated for the set of mating candidates, their difference, $S_a - S_f$ can be used to assess if Mate Choice increases (positive difference), maintains (difference equal to 0) or decreases (negative difference) the perception of variation for selection of a mating partner, when compared to selection through fitness (which is akin to a standard tournament). The metric is then averaged over the selection steps of that generation and plots are included representing, over the course of the evolution process, how the metric evolves for each run as well as on average for the 50 runs.

Is evaluation contrast being promoted with Mate Choice?

While entropy gives a good measure of how well mating preferences are able to distinguish between mating candidates, it fails to demonstrate the extent of that distinction. Contrast, as the unsigned difference between the evaluation value of two individuals should be able to elucidate on that [178]. When assessing a group of mating candidates, a female's overall contrast ability can be found by averaging the pairwise contrast between all elements. Also, as the goal is to compare the contrast between attractiveness and fitness, their relation may as well be done on a pair to pair basis.

Equation 6.5 shows how contrast can be measured between two values. It should be noted that because pairwise contrast is within the interval $[0, +\infty]$, tanh was used as a squashing function to keep values within $[0, 1]$. Equation 6.6 shows how the overall contrast can be measured for a single selection step, where n represents the number of mating candidates and i and j a particular pair of candidates whose attractiveness, a and fitness, f, difference is calculated. As a result, if the contrast between the evaluation of mating candidates increases through the use of Mate Choice, when compared to using fitness, the difference between their respective contrast values should be positive, while a decreasing contrast leads to a negative value. If the contrast is maintained between the two scenarios, the difference value will be 0.

$$c(x_i, x_k) = \tanh(|x_i - x_k|) \tag{6.5}$$

$$OC = \frac{\sum_{i=1}^{n-1} \sum_{k=i+1}^{n} (c(a_i, a_k) - c(f_i, f_k))}{\binom{n}{2}} \tag{6.6}$$

Due to the nature of a tournament-like Mate Choice operator, a higher or lower contrast will play no relevant immediate role, as only the most attractive individual will be selected, independently of how much it distances from competitors. However, higher contrast can show robustness in the evaluation process, as the ranking of individuals is less prone to switching due to small changes in traits (highly depending on preference dimensionality). As discussed, choice consistency can play an important role in self-reinforcement and the maintenance of runaway processes. Contrast can be particularly important if the male population is densely located in a small region of the phenotypic space, with only small variations between them, making perception more important. After contrast has been calculated for all selection steps in a generation, its mean is calculated and plots are included representing, over the course of the evolution process, how the metric evolves for each run as well as on average for the 50 runs.

What are the dynamics of preference dimensions and complexity?

Perception of variation and contrast are under the direct influence of preference dimensions and complexity. It could be said that, while also depending on the context of evaluation, they are the phenotypic expression of the dynamics induced by both features. As discussed in Chapter 3, mostly in Section 3.3.1, such dynamics are likely to be delicate: higher dimensionality should promote higher perception of variation, while low dimensionality promotes the opposite but is also a better fit for maintaining contrast; higher complexity is linked to higher contrast but low complexity presents a lower risk of choice inconsistency; high complexity combined with high dimensionality are the most prone to choice inconsistency while there's a clear evolutionary advantage from simpler mate evaluation functions; such dynamics are very dependent on the extent of trait variation present in the population, and how they allow for differences to be easily found.

Given the results presented regarding both perception of variation and contrast, it is relevant to study their link to dimensionality and complexity as a means to provide empirical evidence of how such behaviors extend to both the Genetic Programming representations of PIMP and CMP-GP. Assumptions are particularly important here, as genotypic information is interpreted. Dimensionality and complexity in PIMP regard to the composition of the ideal mating partner being represented by the preferences chromosome, whereas interactions between signals are explicitly modeled in CMP-GP, making it so that direct comparisons can't be made between approaches on this information. Because both dimensionality and complexity evolve freely in the system, it may be difficult to pin down their impact individually, specially considering the barriers brought by particularities of tree representation. One way to look into the internals of preferences is by using pseudo-isomorphs [35, 36] to describe trees as tuples with the following format:

$$< \#(terminals), \#(non-terminals), depth >$$

It should be considered though that constant terminals introduce no increase in dimensionality and that non-terminals that have only one input, while transforming and impacting preferences, don't represent interactions between singular preferences. Furthermore, it should be kept in mind that while pseudo-isomorphs are simple to compute and more informative than considering the uniqueness of trees, they are still prone to some errors (most metrics are). For instance, non-terminals combining two constants shouldn't be considered interactions and shouldn't be considered for complexity analysis, but weeding out such situations can be rather complex. With these considerations in mind, for the purpose of analysis, trees will be summarized a such:

$$< \#(terminals_v), \#(non-terminals_{2c}) >$$

Depth is implicit and adds no further information, being sufficient to use the number of variables and non-terminals with two children to have a proper indication of dimensionality and complexity respectively. Firstly, at each selection step the female preference's dimensionality and complexity is measured, as is the perception of variation and contrast. As a global overview, the mean dimensionality and complexity, and mean entropy and contrast, of the population is calculated for each generation of each run. An average of all runs is plotted including the four metrics for a sense of how they relate as preference related features, subject to evolution. Finally, three-axis graphs comparing, for each female, its dimensionality (x-axis), its complexity (y-axis) and either its perception of variation or contrast capabilities (color) will be shown. To populate such graphs, all females in the first 150 generations of all 50 runs will be used. Arguably, relations between genotypic characteristics and their phenotypic impact should be found. The graphs are limited to the first 150 generations to attempt at a higher dimensionality and complexity diversity as well as higher trait variability, which further on may be compromised by means of self-reinforcement.

Is diversity being promoted with Mate Choice?

Two measures of diversity will be considered: fitness entropy as a measure of phenotypic diversity and tree edit distance as a measure of genotypic diversity. Entropy has been described in Equation 6.4 and will be used to measure the distribution of the population by unique fitness values. A more uniform distribution using many fitness values (high entropy) will be representative of a higher phenotypic diversity. While this may seem like a little informative measure, evaluation of solution quality and selection (partially in Mate Choice) acts on this information alone, making it appropriate to study its distribution. Regarding tree edit distance, the metric works by making two trees overlap at the root node and measuring how many operations are needed to transform one tree into the other [36, 83, 115]. Tree edit distance is one of the most informative diversity measures out there, allowing for a more reliable differentiation of individuals than pseudo-isomorphism and unique tree differentiation.

Both phenotypic and genotypic diversity will be measured over the whole population but will also be measured within the female and male populations. The first scenario will give a sense of the population composition but if genders happen to emerge, and because of the possibility that self-reinforcing preferences guide the male population away from the female neighborhood, then such an overall metric may become skewed. After all, if females converge to an area of the search space and males converge to a different area, overall analysis may show population diversity, while truthfully, the population has converged genetically. Inner gender metrics will allow for a more detailed analysis of the subject and may be more appropriate as honest indicators of diversity.

Two characteristics should be noted regarding the metrics used: i) fitness entropy may be directly linked with selection of females but not with male selection. Nonetheless, it should be indicative of how much males differentiate among themselves as the goal is not to assess directly how they respond to selection. ii) tree edit distance is a computationally expensive metric to calculate. Following other studies that use the metric [36, 115], the edit distance of each individual will be measured against the fittest individual in the population, at each generation. A population's average diversity is measured by summing all individual measures and dividing by the number of operations. This extends to inner-gender diversity, where individuals are measured against the most reproductive individual of their gender (as a tie-breaker, the fittest is used).

Plots will show an average population diversity at every 25 generations as well as inner-gender average diversity measures. Comparisons will be made between approaches and scenarios. Also, it should be fruitful to measure and show the average diversity between matching parents. This may not only help explain how the metrics evolve over generations but will also provide insight on the relation between mating preferences and diversity, for instance by allowing the analysis of the degree of assortative mating associated with preferences. Preference diversity shall also be considered, by analyzing the set of active preferences at each generation.

Does Mate Choice promote the emergence of complex innovations?
The rate of neophilia allowed by Mate Choice, potentially promoted by a taste for new ornaments, directly impacts the rate of innovations allowed to be introduced in the population. Consequently, it also influences the degree of cumulative innovations that are allowed to account for complex innovations. While measuring the rate of neophilia is extremely difficult, it has been discussed that Mate Choice can cooperate with recombination and mutation in proposing diverging candidate solutions by allowing them a higher frequency. Hopefully, studying such behaviours will allow for a comprehension of the emergence of complex innovations.

The previous analysis on diversity is relevant: diversity may be indicative of the introduction or maintenance of innovation, specially when considering inner-gender measures; more importantly, a tendency for pairing dissimilar individuals should be indicative of a taste for exploration, which can more easily result on innovation when compared to mating between very similar individuals, even at the risk of destructive crossover and the possibility of producing low-fitness, low-attractiveness offspring. However, either metric alone can't ensure that innovations are sustained for more than one generation or that they have a chance of reproducing and contributing to complex innovations and to the search effort as a whole. A metric that relates the survival of individuals to their dissimilarity should be discussed.

$$GR = \left(\frac{\#(descendants_{c+n})}{\#(individuals_c)}\right)^{\frac{1}{n}} - 1 \tag{6.7}$$

As an indication of survival rate, the compound growth rate [13] (adapted following inspiration from the survival rate proposed by Gustafson et al. [115]) was used. In demographics, the metric shows how a population size varies over a number of years, taking into account that from year to year, a varying size is being studied, thus returning an adapted growth rate. In this scenario, when applied to generations, the compound growth rate is indicative of how an individual or group of individuals impacts a future generation through the presence of its descendants. Equation 6.7 describes the process, where $individuals_c$ is a subset of individuals in generation c, and $descendants_{c+n}$ represents their descendants after n generations. A compound growth rate of 0 would show that after n generations, the presence of descendants of the subset of individuals under analysis is the same as in generation c, showing that they are successfully reproducing but not increasing their significance in the population. On the other hand, a positive compound growth rate would show the ability of a subset of individuals to increase the presence of their genes, through their descendants, while a negative growth rate would show that their presence is diminishing.

The metric is valid for assessing either a single individual or a set of individuals sharing a particular characteristic, and can be applied on a particular run or covering a sample of individuals from multiple runs (as if they were in the same population). It also allows measuring the impact of a subset of individuals on the next generation, as well as after *n* generations. In this study, their impact will be studied after 2 generations, as an indication of how their children are viable or sexy enough to produce grandchildren, thus showing their potential to contribute to the search effort. In order to tie survival as measured by the compound growth rate with the level of innovation associated with each individual, the following process will be followed at each generation: i) during selection, each female or male's dissimilarity to its parents same-gender most-reproductive individual is measured through tree edit distance; ii) its dissimilarity is normalized by the previous generation's average genotypic diversity (so that 0 means that the individual's dissimilarity is the same as the previous population's average, while a larger value means increased dissimilarity and a smaller value means decreased dissimilarity); iii) after going through all selected individuals, group them by gender and by dissimilarity value in one of 50 groups of similar size in the resulting dissimilarity range; iv) assess the survival rate of each group and plot the results for each gender separately.

For proper clarification, a few notes on the process should be discussed: i) by calculating an individual's dissimilarity and comparing it using the previous population, it is attempted to measure the level of innovation brought by such an individual; ii) individuals may be present simultaneously in each gender, in which case it's direct descendants should be considered when acting separately as a male or as a female; iii) only selected individuals are considered, leaving out those that don't contribute to future generations; iv) individuals are grouped so that results can be presented in a less noisy way; v) the survival rate over two generations should help study how dissimilar individuals are able to contribute to each gender by providing innovation in a sustainable way, instead of adding diversity to the population with no impact through reproductive success. Finally, all runs and generations can be studied together for a larger sample, which should be detailed for analysis. In this case, the samples are collected at every 25 generations.

Does Mate Choice contribute to escaping local optima?

While males are potentially more exposed to changes and innovations, mostly due to being subject to Mate Choice, females are likely to remain closer to adaptive peaks through the lack of direct forces pulling them away. However, while being mostly subject to Natural Selection, they can still be pulled away from local peaks by genetic reproduction with males. It may be that males don't reach new adaptive peaks, but if they find new traits with survival value, then new highly fit individuals may be produced, with a high probability of being selected as females, and thus pull the population into new search areas and successfully escaping local optima.

Identifying instances where such behaviors are empirically observed can be a complex task, however, focusing on females can help look for the effect. For instance, when a new female is found, one of two aspects can be observed: i) the dissimilarity between the new individual and the previous most reproductive female is within the distribution shown by all females in the previous generation, suggesting that the new peak is the result of exploitation of the same search location; ii) the dissimilarity seems to be outside the expected values, which may indicate a disruptive adaptation, away from the previous search location, and thus being indicative of escaping local optima.

In summary, new females that are regarded as outliers when compared to the previous female's generation may be seen as disruptive. In order to identify such outliers, median and interquartile range information extracted from dissimilarity data is used. The study focuses on identifying instances that distance 1.5 times the interquartile range (conventional value) from the third quartile, in the appropriate direction. Other methods exist for this purpose, based for instance on standard deviation, however the chosen method relies on no specific distribution assumptions, which should be a better fit for this task at any phase of the evolutionary process (such as the initial chaos). Over 50 runs such occurrences are to be counted at every 25 generations (and comparing with the previous studied generation) and plotted. A more conservative approach is also considered, where only new females whose fitness is better than the previous best-so-far are considered. Moreover, the average dissimilarity of dissimilar individuals and their parents are to be measured in an attempt to check which gender makes direct contributions to such offspring most often. Plots averaging the metric over all occurrences in the 50 runs are to be included for analysis as well.

6.3 Performance Analysis: a Comparison of Base Scenarios

Deciding on the most appropriate way to analyze and compare samples can be far from straightforward. On the one hand, one should aim for the approach with most statistical power, but on the other hand it's extremely important to confidently meet all assumptions behind a particular test so that imprecise conclusions are kept at bay. Following this idea, parametric tests should be first considered, more specifically the Student's t-test [2] for independent samples, since it will provide higher statistical power when compared to non-parametric tests, if (and only if) all its assumptions are met. If such is not possible, then the roles invert and the conclusions reached through a non-parametric test will be backed up by stronger statistical inference. In order to study which test is most appropriate for the collected data, samples of the best individuals will be analyzed, but five number summaries will also play a role.

6.3.1 Using Parametric Tests vs. Non-parametric Tests

When considering the use of Student's t-test the following assumptions should be carefully confirmed, which will be done in order: i) are the samples collected in an appropriate, independent way and following a fitting scale; ii) do the samples follow a normal distribution; iii) if so, do samples show variance homogeneity; iv) are there identifiable outliers and are they potentially influential on the outcome of the tests; v) do the previous points, in addition to median and interquartile information, back up the use of parametric tests. At this point it's important to keep in mind that 10 scenarios are run on 52 functions, resulting on a large number of samples to be studied. The analysis will focus on base approaches (with no mutation) for simplification and each particular function will be considered independently. Arguably, each function may be analyzed independently using either parametric or non-parametric tests but, as will be shown, a consensus may be less controversial for a wide analysis.

Table 6.5: Instances where a Shapiro Wilk test for normality resulted on a p-value above 0.05, therefore not allowing for the rejection that the population is normally distributed.

	Standard	PIMP	CMP-GP
korns-5	*	*	*
korns-6	*	*	*
korns-8	*		*
korns-9	*		*
korns-11			*
korns-12		*	*
korns-15	*	*	*
keijzer-8	*	*	*
keijzer-13	*		*
keijzer-14	*	*	*
keijzer-15	*	*	*
vladislavleva-1	*	*	*
vladislavleva-4		*	
vladislavleva-5		*	
vladislavleva-6	*	*	*
vladislavleva-7		*	

The first point of analysis is quite simple considering the experimental setup. Every instance in every sample is collected from an independent run, whose components are strictly its own. Stochastic behavior is based on a disposable seed that isn't shared or reused. For these reasons, there's no hint of implicit factors in the data, and therefore no correlations or dependencies between them. Instances in a given sample have no particular order and show no unexpected relational patterns. Regarding the potential normality of the samples, a Shapiro Wilk test [260] has been run on each available sample with an alpha level of 0.05. The null hypothesis is that the population represented by the sample is normally distributed (therefore, in instances where the p-value is above 0.05 the hypothesis can't be rejected), and although the test doesn't offer explanations as to why a sample is non-normal, it also doesn't require assumptions on the hypothesized normal distribution (such as the mean and variance), making it suitable for a direct, simple analysis. Table 6.5 summarizes the results of the test, showing that normality wasn't rejected on only a small subset of the samples (*log* transformations brought no advantages in finding normality when compared to a no-transformation approach). As a post-hoc test on the samples that seem to follow a normal distribution and are comparable, Bartlett's test with a alpha level of 0.05 was used to assess variance homogeneity. Its main assumption is that compared samples follow a normal distribution, which has been covered previously by Shapiro Wilk's test. Table 6.6 shows the results obtained by the test, highlighting instances where the null hypothesis that the samples come from populations with equal variance can't be rejected.

The results shown in Tables 6.5 and 6.6 suggest that while being a minority, there are some instances where the assumptions of Student's t-test are met. This suggestion would point towards the use of parametric tests on a subset of the samples and non-parametric tests on the remaining. However, it's important to further scrutinize the composition of the samples, despite their nature and means for collection being well established. By looking at the five number summaries in Tables A.7 and A.8

Table 6.6: Results obtained on Bartlett's post-hoc test for variance homogeneity, showing instances where the null hypothesis that the samples come from populations with equal variance can't be rejected.

	Standard vs PIMP	Standard vs CMP-GP	PIMP vs CMP-GP
korns-5	*	*	*
korns-6	*	*	*
korns-7			
korns-8			*
korns-9			*
korns-12			*
korns-15	*	*	*
keijzer-13			*
keijzer-14	*	*	*
keijzer-15	*	*	*
vladislavleva-1	*	*	*
vladislavleva-6	*	*	*

(included in Appendix A), particularly focusing on the relation between quartile placements, hints at the presence of outliers. Further analysis relying on the interquartile range process for the identification of outliers is summarized in Table 6.7. The study focuses on identifying instances that distance 1.5 times the interquartile range (conventional value) from the first or the third quartile, in the appropriate direction. While a more conservative distance could have been used, sensitivity to outliers is helpful in remaining conservative in regards to meeting test assumptions. As shown by Table 6.7, outliers are found quite often and sometimes in relevant numbers, including in several instances where normality and variance homogeneity was found, pushing for a discussion on their influence.

Much like Student's t-test, both Shapiro Wilk's and Bartlett's tests are sensible to the presence of outliers, potentially raising false positives and thus reducing their statistical power. One way to overcome such problems would be to trim or winsorize outliers, thus removing their possibly deceptive effect. However, doing so would require plausible justification that such outliers are infiltrators in the populations represented by the samples, such as by being the result of errors in the processes of running or collecting data. In the studied scenario, such would be very unlikely and thus, the outliers must be accepted as part of the distribution. Arguably, if the size of the sample was increased to very large numbers, such instances would no longer be marked as outliers. As that is not an option, their skewness effect on the mean and variance of the samples needs to be considered and raises questions on the validity of using Student's t-test based on the reported results on normality and variance homogeneity. Alternatively, rank-based non-parametric tests may be considered as an approach more resistant to the presence of outliers (due to the use of ranks). Also, such tests make no assumptions on the distribution of the samples, which doesn't mean that they aren't suitable for samples following normal distributions.

On the current scenario, and based on this discussion, it may be argued that relying on non-parametric tests can provide greater statistical power than relying on parametric tests whose assumptions may be complied with faultily. Moreover, instances where

Table 6.7: Number of outliers found through the interquartile range process on each sample.

	Standard	PIMP	CMP-GP
koza-1	8	6	5
koza-2	9	4	2
koza-3	8	7	12
nguyen-1	10	11	11
nguyen-2	6	5	8
nguyen-3	8	9	7
nguyen-4	5	7	9
nguyen-5	5	5	8
nguyen-6	6	10	11
nguyen-7	7	10	11
nguyen-8	9	4	10
nguyen-9	4	3	4
nguyen-10	4	0	1
pagie-2	2	0	0
korns-1	11	7	12
korns-2	9	8	8
korns-3	9	6	12
korns-4	11	2	9
korns-5	2	0	2
korns-8	0	3	0
korns-9	1	4	1
korns-10	10	11	11
korns-11	2	4	0
korns-12	2	1	1
korns-13	10	9	10
korns-14	7	6	12
keijzer-1	0	0	1
keijzer-2	2	1	0
keijzer-3	0	0	1
keijzer-5	8	10	7
keijzer-6	12	12	0
keijzer-7	0	12	0
keijzer-10	2	2	3
keijzer-11	9	4	3
keijzer-12	7	4	5
keijzer-13	0	0	1
vladislavleva-1	0	1	0
vladislavleva-3	0	2	1
vladislavleva-4	6	2	2
vladislavleva-8	1	2	2

there's a potential for the use of parametric tests are a minority, and thus applying the same test, following overall assumptions rather than tailoring tests for subsets can be beneficial for a wide assertion of the results. Wilcoxon Mann Whitney's test with a alpha level of 0.05 has therefore been chosen as the approach to compare between samples. Moreover, as an extra step to mitigate the effect of outliers, samples will be compared based on the median best fitness rather than the MBF as it should be a more resilient metric for their central tendency.

6.3.2 Performance Results and Statistical Analysis

Appendix A details the performance results obtained through the testing of the Standard approach as well as both PIMP and CMP-GP on the full test set of 52 functions. Firstly, Tables A.1 through A.6 show information on the best individual found as well as on the MBF obtained in each sample. Secondly, information on the central tendency of each sample as well as their variance, based on median and interquartile range, is fully depicted in Tables A.7 to A.12, and briefly summarized in Tables A.13 to A.18. Approach to approach comparisons showing statistical significant differences are shown in full in Table 6.8. Furthermore, available information on hits is shown on Table 6.9 and proportion test results are shown in Table 6.10. A global summary and approach to approach comparison is shown in Table 6.11.

As previously discussed, median and interquartile range information may be better suited as metrics for perceiving a sample's central tendency and spread. Still, traditional information on fitness can be found in Appendix A, including information on the best individual found on each 50 run sample, as well as the MBF and standard deviation associated. Making a three-way comparison based on this data allows for the following observations: i) when it comes to obtaining the best individual in all tests, the Standard approach does so $\approx 37\%$ of the times, while PIMP is able to do so on $\approx 17\%$ of the instances, with CMP-GP reaching $\approx 21\%$ and leaving $\approx 25\%$ to ties; ii) however, the Standard approach only obtains the overall lower MBF on $\approx 17\%$ of the problems, while PIMP and CMP-GP reach $\approx 37\%$ and $\approx 46\%$ respectively; iii) in regards to variance, the Standard approach shows a lower standard deviation on $\approx 35\%$ of the instances, compared to $\approx 37\%$ and $\approx 29\%$ measured in either PIMP or CMP-GP.

A bird-eye look at these results brings two conflicting ideas, one being that based the best individual produced, the Standard approach has a clear advantage, while a comparison based on the MBF suggests an advantageous performance by Mate Choice. A pairwise comparison between approaches can bring forth additional information: i) regarding the best individuals found, the Standard approach wins $\approx 44\%$ of the times against PIMP and loses on $\approx 37\%$ instances, also winning $\approx 42\%$ of the times against CMP-GP while losing on $\approx 40\%$ instances. Between the two Mate Choice approaches, each one reaches a better solution on $\approx 38\%$ of the problems; ii) on MBF, each of PIMP and CMP-GP reach better values on $\approx 69\%$ and $\approx 77\%$, and worst on $\approx 31\%$ and $\approx 23\%$ of the instances respectively, when compared to the Standard approach. Results between them are split at $\approx 42\%$ and $\approx 58\%$; iii) when considering variance, Standard has a lower deviation on $\approx 42\%$ and $\approx 48\%$ of the problems when compared to PIMP and CMP-GP respectively, and higher on $\approx 58\%$ and $\approx 52\%$ respectively. Finally, PIMP has a lower standard deviation than CMP-GP on $\approx 52\%$ of the instances and higher on $\approx 48\%$. Pairwise comparisons can be easily visualized in Table 6.11.

While a three-way comparison suggests that the Standard approach largely outperforms the Mate Choice approaches in regards to finding the best solutions to the range of problems, the pair-wise comparison shows that differences may be smaller than they seem. The Standard approach still outperforms both others, however, results suggest that in instances where PIMP outperforms Standard, so does CMP-GP, and vice versa, thus accounting for their increase in win rates. This shows that Mate Choice as a strategy may be fruitful in some instances while being less favorable on others, however doing so on very frail evidence. This analysis is made based on the results of one run from each approach, that happens to be more successful than average, and is therefore subject to fortune. When looking at MBF values, the discussion changes considerably, with both Mate Choice approaches showing approximate competitiveness between them but both showing much higher performance than the Standard approach, in both analysis (overall and pair-wise). In fact, they both seem to share similar gains in comparison to the Standard approach. Arguably, with a larger sample size, or in a one-run situation, either Mate Choice approach would be a safer choice to achieve best solutions to most of the problem instances. Similarities between results achieved by Mate Choice approaches also suggest that performance may rely more on the strategy than on each particular representation of mating preferences, although they likely also play a relevant role. A slight advantage in favour of CMP-GP is suggested by the summarized results. Finally, in regards to differences in variance, all approaches seem to be similarly consistent in their samples.

It's important at this point to assess if an analysis on median and interquartile information is in agreement with the previous analysis. Although Tables A.7 to A.12 includes full information, Tables A.13 through A.18 summarize the relevant central and variance metrics for analysis. Best solution information is not included as it has been previously discussed. A similar three-way analysis as the one above allows for the following observations: i) in regards to the median value, the Standard approach achieves the lowest value on $\approx 8\%$ of the instances while PIMP and CMP-GP do so on $\approx 27\%$ and $\approx 60\%$ respectively; ii) the IQR is shown to be smaller on $\approx 23\%$ instances for the Standard approach, on $\approx 33\%$ instances for PIMP, and on $\approx 44\%$ instances for the CMP-GP. A pairwise analysis shows the following: i) regarding the median value, the Standard approach outperforms PIMP on $\approx 25\%$ of the instances, in comparison to its $\approx 75\%$ rate, while the difference is higher regarding CMP-GP, with a $\approx 10\%$ win rate for the Standard approach against a $\approx 88\%$ rate for the CMP-GP. When comparing both Mate Choice approaches, PIMP has a lower median on $\approx 29\%$ of the instances and CMP-GP has a lower value on $\approx 65\%$ of the instances; ii) the IQR is smaller for the Standard approach on $\approx 33\%$ of the instances when compared to PIMP, against $\approx 67\%$, and on $\approx 37\%$ when compared to CMP-GP, against $\approx 63\%$. Between the two Mate Choice approaches, PIMP has a lower IQR on $\approx 46\%$ of the instances while CMP-GP has a lower IQR on $\approx 54\%$ of the problems. As before, a global view and approach to approach comparisons can be found in Table 6.11.

In short, the median based comparisons do not disprove most of the summarized results regarding the mean based analysis, but have the particularity of enhancing differences in performance comparisons between all three approaches. Notably, a higher performance of Mate Choice when compared with the Standard approach is highlighted, specially regarding CMP-GP, which in this analysis performs consistently better when compared against either of the alternatives. In light of having a higher resistance to the effects of outliers, such differences further back up the choice of Mate Choice as a sturdier strategy for tackling Symbolic Regression, despite the Standard samples showing a better rate of best overall solutions. Moreover, the analysis suggests that representation in Mate Choice does play a relevant role in behavior, which may affect performance. In this case, both three-way and pairwise comparisons back up the importance of the assumptions behind CMP-GP, as a vehicle for gains.

Table 6.8: Instances where the p-value obtained by the Wilcoxon Mann Whitney test was below the 0.05 alpha value.

	Standard vs PIMP	Standard vs CMP-GP	PIMP vs CMP-GP
koza-1	PIMP	CMP-GP	CMP-GP
koza-2		CMP-GP	
koza-3	PIMP	CMP-GP	
nguyen-2	PIMP	CMP-GP	
nguyen-3	PIMP	CMP-GP	
nguyen-4	PIMP	CMP-GP	
nguyen-6	PIMP		PIMP
nguyen-9		CMP-GP	
pagie-1	PIMP	CMP-GP	
pagie-2	PIMP	CMP-GP	
korns-1	PIMP	CMP-GP	
korns-2	PIMP		
korns-4	PIMP	CMP-GP	
korns-6	Standard		
korns-13	PIMP	CMP-GP	
keijzer-3		CMP-GP	
keijzer-4	PIMP	CMP-GP	
vladislavleva-2	PIMP	CMP-GP	CMP-GP
vladislavleva-7		CMP-GP	

While the ongoing discussion is insightful in terms of overall performance differences between Mate Choice and Standard approaches, as well as between the two Mate Choice strategies, it falls short in asserting which performance differences are statistically significant, rather than the possible result of fortuity. Following the discussion in Section 6.3.1, the Wilcoxon Mann Whitney test has been used to compare pairs of relevant samples, with the instances where significant differences are found being signaled for analysis in Table 6.8. As shown, it can be said that based on the gathered samples and with a confidence level of 95%, the approaches perform differently on $\approx 37\%$ of the test set, while on $\approx 63\%$ no performance differences can be backed up with sufficient certainty. Regarding the overall instances where differences are found, a pairwise analysis is shown, as differences are not always found between all three approaches.

Regarding the subset of functions where statistically significant differences were found, the following can be observed: i) the Standard approach performs significantly better than PIMP on only one instance and is unable to outperform CMP-GP; PIMP and CMP-GP perform significantly better than Standard on $\approx 74\%$ and $\approx 84\%$ of the instances respectively; the subset of instances where PIMP performs better is different than the one for CMP-GP, although intersecting on $\approx 63\%$ of the 19 instances; on $\approx 32\%$ of the instances, only one of the Mate Choice approaches was able to show significant gains; when comparing between the Mate Choice approaches, PIMP was significantly better on 2 instances whereas the opposite is true on 1 instance.

An alternative comparison can be made on the number of hits reached by each approach. Although on most of the test set the optima is considerably difficult to reach, there is a subset where it may be expected for the optima (or close) to be found, al-

Table 6.9: Number of runs where the error between the best individual and the optima was below $1E-4$.

	Standard	PIMP	CMP-GP
koza-1	18	27	39
koza-2	23	36	37
koza-3	35	41	42
nguyen-1	34	31	37
nguyen-2	18	27	33
nguyen-3	26	31	28
nguyen-4	14	20	25
nguyen-5	23	27	27
nguyen-6	15	38	25
nguyen-7	22	19	25
nguyen-8	19	20	12
nguyen-9	8	15	13
nguyen-10	12	12	16
korns-1	0	1	0
korns-4	1	0	0
keijzer-1	1	0	1
keijzer-5	2	3	1
keijzer-6	1	0	1

Table 6.10: Instances where the p-value obtainded by Taillard's proportion's tests was below the 0.05 alpha value.

	Standard vs PIMP	Standard vs CMP-GP	PIMP vs CMP-GP
koza-1	PIMP	CMP-GP	CMP-GP
koza-2	PIMP	CMP-GP	
koza-3		CMP-GP	
nguyen-2	PIMP	CMP-GP	
nguyen-4		CMP-GP	
nguyen-6	PIMP	CMP-GP	PIMP
nguyen-8			PIMP
nguyen-9	PIMP		

lowing for a comparison between approaches regarding their ability to hit the optima on such a subset. In this case, runs where the error to the optima is below $1E-04$ are considered a hit, which were found at least once on $\approx 35\%$ of the test functions. The number of hits found in such functions for the three approaches are shown in Table 6.9, which can be summarized as such: i) the Standard approach was able to outperform PIMP and CMP-GP on $\approx 28\%$ and $\approx 17\%$ of the instances respectively, while being overrun on $\approx 67\%$ of the functions in pairwise comparisons to each Mate Choice approach; when comparing between those strategies, PIMP performs better on $\approx 33\%$ of the instances while CMP-GP does so on $\approx 56\%$.

The hit based analysis seems to show an advantage of Mate Choice over the Standard approach on most instances as well as a slight advantage of CMP-GP over PIMP. Nonetheless, pair-wise differences on each function must be assessed for statistical significance. Taillard's proportions test [283] is a suitable and rather conservative choice that requires very little assumptions on the setups. Table 6.10 shows a summary of such tests for an alpha value of 0.05, which shows the following: i) the hit proportion is significantly higher for PIMP on $\approx 28\%$ and for CMP-GP on $\approx 33\%$ of the functions when compared to the Standard approach; the latter is unable to outperform either Mate Choice approach; PIMP has a significantly higher hit proportion on two instances when compared to CMP-GP with the opposite happening on one instance. Overall, the proportions test confirms a better performance of Mate Choice when compared to the Standard approach, although to a lesser extent, while also showing that both Mate Choice approaches perform on par, rather than confirming a greater ability to reach the optima by CMP-GP.

6.3.3 Summary

The previous section includes a descriptive analysis of the performance of each approach and how they compare with each other according to different metrics, backed up by well upheld statistical tests. Table 6.11 shows a summary of the results, with each row showing a different approach and how they compare with those on each column. Each cell shows how often the pairwise comparison is better. MBF and variance (IQR) values are shown along with the results of the Wilcoxon Mann Whitney test. Hit rates and Taillard results are also included. Overall, this table allows for a clear view of how each approach compares to all others (although losing a sense of how performance relates to each particular function in the process).

The results summarized in Table 6.11 indisputably show an advantage by Mate Choice approaches, successfully achieving better win rates when compared to the Standard approach on all analyzed metrics. The comparison is specially relevant when focusing on the Wilcoxon Mann Whitney and Taillard results. Such translates to gains by the Standard approach on only one occasion while showing gains for both Mate Choice approaches on a significant number of test functions. Arguably, it could be said that Mate Choice is a safer choice, almost never performing subpar when compared to the standard approach while bringing gains often. This analysis accounts for performance only, without considering differences in computational effort. Genetic Programming makes the issue far from straightforward to address. Nonetheless, as will be shown, differences are behavioral, more than computational.

When comparing between PIMP and CMP-GP, results show a close tie. Their overall performance is quite similar, either when comparing between themselves or against the Standard approach. Such results suggest that gains may be more of a direct result of the Mate Choice strategy, despite of representation. Possibly, their population level dy-

Table 6.11: Summary of the results observed in the full extent of the performance analysis.

Median

	Standard	PIMP	CMP-GP
Standard		13	5
PIMP	39		15
CMP-GP	46	34	

IQR

	Standard	PIMP	CMP-GP
Standard		17	19
PIMP	35		24
CMP-GP	33	28	

Mann-Whitney

	Standard	PIMP	CMP-GP
Standard		1	
PIMP	14		1
CMP-GP	16	2	

Hit Rate

	Standard	PIMP	CMP-GP
Standard		5	3
PIMP	12		6
CMP-GP	12	10	

Taillard

	Standard	PIMP	CMP-GP
Standard			
PIMP	5		2
CMP-GP	6	1	

namics are similar and affect the search process similarly, however further behavioral analysis is needed to backup this claim. Nonetheless, there are a few instances where either approach outperforms the other, and there are also a few instances where they compare differently to Standard, suggesting that, at least on some instances, performance similarities are thinner than they seem by looking at overall results. Following that line of thought, an advantage may be argued in favor of CMP-GP.

6.4 PIMP: Behavioural Analysis

Following the research questions discussed in Section 6.2.2, the upcoming analysis will focus on empirically demonstrating (if not all, at least some) the underlying behaviors of Mate Choice, as well as the relationships of evolving dimensionality and complexity, and its impacts on the evolutionary process. Interpretation of results is subject to the approach's assumptions (see Chapter 5), specially regarding representation of preferences and their meaning. The examination will be split into three subsections which cover different aspects, although topics may overlap: i) selection analysis; ii) perception analysis; iii) effects analysis. For the purpose, including the analysis of all 52 functions through graphics would be impossible, therefore 4 functions are considered: nguyen-4 (1 variable), korns-2 (5 variables), keijzer-3 (1 variable), and vladislavleva-7 (2 variables).

6.4.1 Selection Analysis

Data collected regarding Female Choice at each selection step is important for the purpose of confirming that the proposed model, along with the assumptions that PIMP follows, is capable of introducing Mate Choice. Additionally, that same data allows for studying the character of choice and how populations are likely to behave on the grand scale. The analyzed metrics have been properly introduced in 6.2.2 and the results have been summarized in Figures 6.2 to 6.5.

The self reinforcing aspect of Mate Choice has been extensively discussed as its own engine, the origin of runaway processes and the mechanism behind the interlinkage between preferences and traits (themselves as the indicators of preferences) which gives both their competitive edge. Demonstrating the effect should therefore provide critical and unequivocal evidence of the emergence of Mate Choice through the proposed assumptions and model. The metrics plotted in Figures 6.2 and 6.3, as discussed, aim at illustrating the same behaviour either genotypically or phenotypically, respectively through the ratio of females that select male partners with the same exact encoded preferences, or through the evaluation correlation between females and their chosen males. In either case, the data should show how a linkage between preferences and traits emerges and contributes to the promotion of their own genes selfishly.

As an overview of all functions shown, the figures demonstrate that both metrics, on average, increase from an initial close to zero value towards values close to one. This tendency is the expression of positive reinforcement of mating preferences, which empirically shows the emergence of sustained Mate Choice. While this over-the-top analysis covers its main goals without requiring further words, interesting illations can be taken from a closer analysis.

Despite the average value having a stable behavior, the metrics show some dispersion when the data from all 50 runs are considered. In both figures, such dispersion seems more obvious below the average line, however, that's the result of runs with

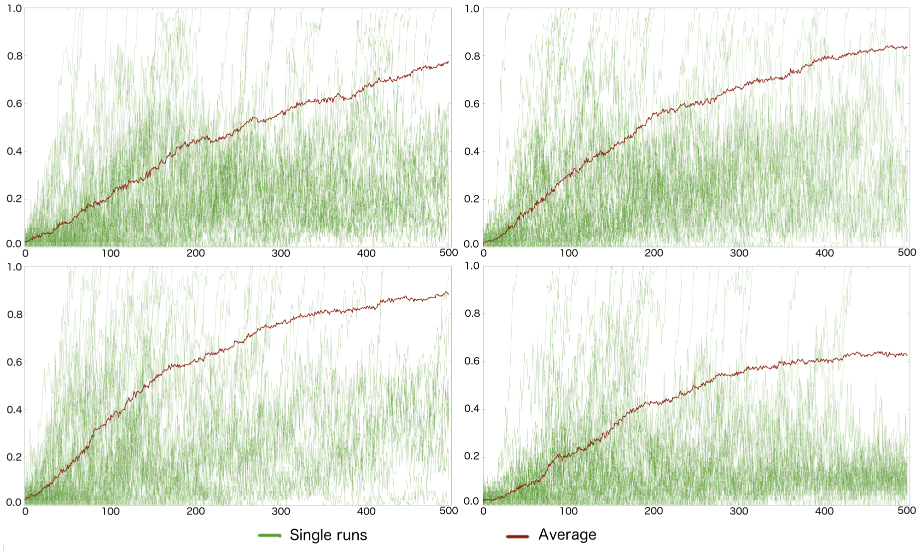

Figure 6.2: Evolution of the ratio of mating pairs that share the exact same preferences genotype. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

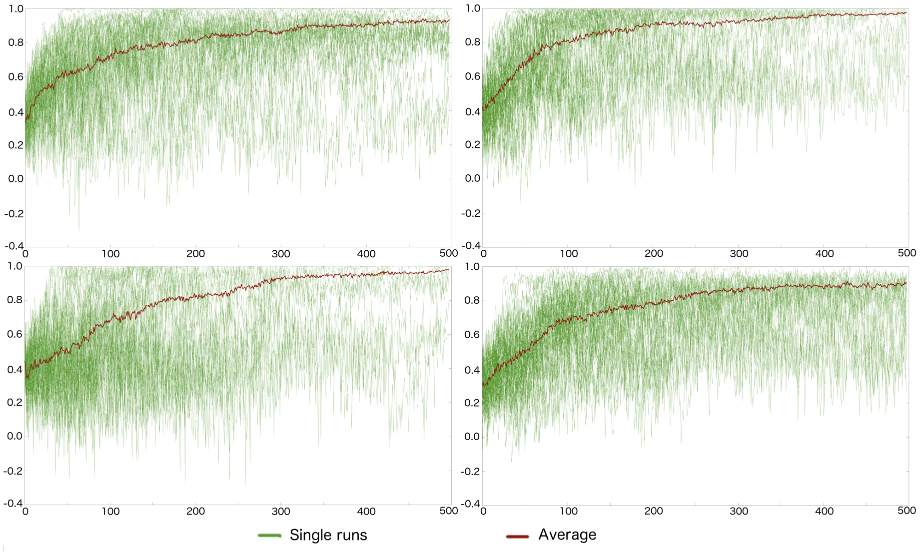

Figure 6.3: Evolution of the Spearman's correlation between phenotypic attractiveness rankings obtained by mating pairs. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

higher-than-average ratios and correlations often reaching the maximum value and remaining there, thus having less visual impact, while obviously pulling the average with them. In such instances, because there is no mutation, preferences getting competitive edge spread through the whole population and maintain an undisturbed equilibrium. However, dispersion also shows that such an equilibrium is not always reached, with variation in ratios and correlations being seen clearly between generations. There are a few reasons that may account for such dispersion: i) initial conditions may be more or less favorable, potentially making it difficult in some runs for reinforcement to kick in; ii) randomness in each selection step may also interfere with the ability of mating preferences to increase their presence by affecting the candidate pools; iii) competing preferences can also delay or prevent momentum for each other. Nonetheless, on the big picture and given the opportunity, Mate Choice seems to provide competitive edge and emerge.

Although both metrics show the same tendency, Spearman's average correlation shows a greater increase speed (specially in the beginning) than the average genotypic ratio. Moreover, the spread of singular runs seems less diverging when analyzing Spearman's correlation than the ratio (consistent when mapped on the same scale). This is the result of limitations discussed regarding the genotypic metric counting only equal chromosomes, whereas Spearman's correlation is a better representation of choice consistency. The differences between the metrics highlight that choice consistency between two individuals can be achieved even when they encode preference chromosomes with various degrees of differences. As a result, multiple preferences can contribute to the same reinforcement process. Regarding the genotypic ratio and despite its shortcomings which cause the metric to be shown as lower than what it should be, its graphs are better at showing runs where reinforcement peaks to a ratio and correlation of 1 (the first implies the second). They show that the process can kick in at any stage of the evolution process, depending on existing conditions, and that when it does, runaway processes can emerge with determination and increasing momentum.

Figure 6.4 says more on the character of evolving mating preferences, specifically regarding Spearman's correlation between attractiveness and fitness rankings within mating candidate pools. As discussed previously, the evolution tendency of the metric can contribute to assessing a Fisherian or Wallacean character. For all four functions, the tendency is for a negative correlation to emerge, both seen in the average value but also in most runs, even though initial conditions seem to be within the positive range. Such a result is incompatible with a good sense view and rather favors a good taste model, leading to a rejection of the Wallacean view by not meeting the full extent of its assumptions. As discussed, runs where the correlation is maintained in the vicinity of 0 also suggest a Fisherian character which also holds for positive correlations even if there's no direct cost for fitness. Nonetheless, the correlation seems to evolve in a common direction, until a kind of equilibrium is found, allowing ornaments and preferences to evolve more or less depending on the return they give in reproductive gains.

Curiously, the keijzer-3 function shows a much higher diversity of behavior than other functions, which may be related to function specific characteristics of the search space or of building blocks. While on average there's a tendency toward negative correlation, although in the vicinity of zero, the behavior doesn't generalize as well to all runs. In most runs, the correlation evolves undoubtedly unrelated to good fitness, however, there are some runs whose attractiveness-fitness correlation remains positive, even reaching and maintaining itself close to one. This behavior demonstrates situations where preferences have not evolved in directions that diverge with fitness, but

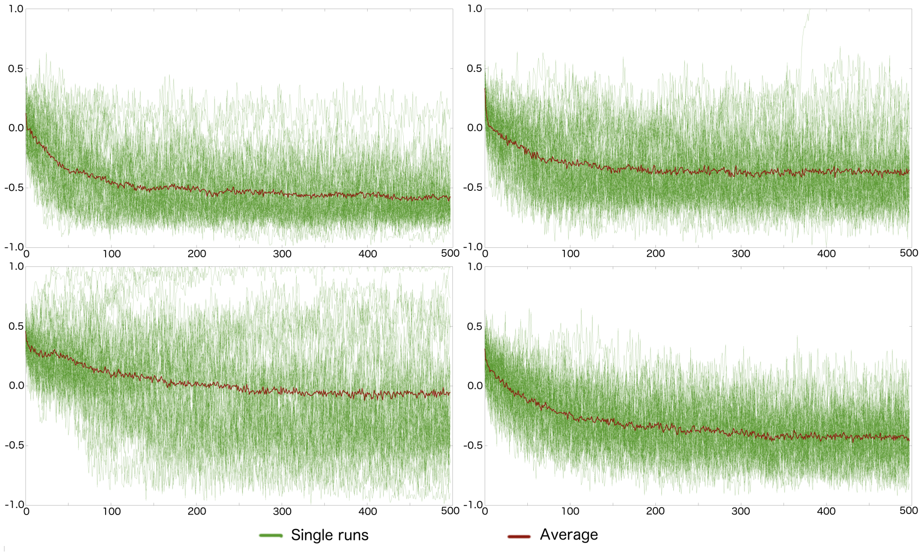

Figure 6.4: Evolution of Spearman's correlation between phenotypic attractiveness rankings obtained by each acting female and the fitness rankings of it's mating candidates. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

have rather evolved in the same direction, making Natural Selection and Sexual Selection strengthen each other. Interestingly, the korns-2 graph also shows an instance where a positive correlation of 1 between attractiveness and fitness emerges late in the run, suggesting a runaway process in directions cooperative with fitness.

Further analysis on the topic is difficult but a few considerations are worth mentioning: i) the developed model, as described in Chapter 5 makes no explicit assumptions on what type of preferences may evolve, which is empirically demonstrated by the ability of mating preferences to evolve in either direction; ii) agreeing attractiveness and fitness rankings may either be the result of initial conditions being favorable for mating preferences to evolve in a particular direction (for instance due to high population density making it easier for preferences to benefit from pulling in it's direction), or it may be the result of Mate Choice pulling females into new landscape peaks, therefore making fitness turn in a direction that agrees with a pre-existing Sexual Selection pull; iii) such effects seem to be dependent on function specific characteristics such as the search landscape. In any case, independently of the direction in which preferences evolve, the underlying process is Fisherian, as there is no direct linkage between ornamentation and fitness.

An alternative yet complementary scrutiny can be done by looking at the distribution of individuals by gender groups. Figure 6.5 allows such a study by presenting the average size of three groups: i) individuals who are exclusively selected as females; ii) those which are exclusively selected as males; iii) and individuals who are simultaneously selected as females and males. As described, candidates for each role are selected randomly so all individuals have a fair chance of enrolling in each group. The shown behavior is transverse for all studied functions and shows that throughout the evolutionary process there's an increasing separation of genders in the population, which can be explained through the following analysis: female selection is bound by

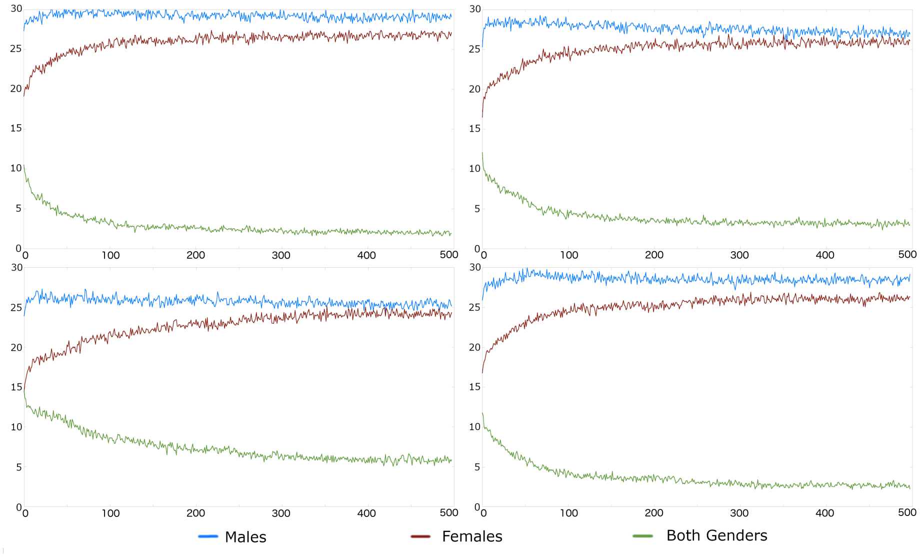

Figure 6.5: Evolution of average population composition by gender. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

the static evaluation function, which asserts pressure; a subset of the population is able to be selected (females and hermaphrodites); on the other hand, male selection is bound by preferences, which due to the initialization procedure are likely to have a close to random behavior in the first generations; at that stage, selection pressure is low, and the opportunity reaches a wide range of individuals (males and hermaphrodites); were mating preferences unable to build pressure and that behavior would likely remain static throughout the evolutionary process, with a few fit individuals being able to act as females, but also keeping a chance of being selected for the male roles, causing the intersection group to remain high and probably on a closer level to the other groups; alternatively, as can be seen in Figure 6.5, as Sexual Selection pressure build up, less individuals selected for female roles are suitable to act as males (which is in-line with the previous analysis of choice character), thus explaining the transference of individuals from the intersection group to the females only group. Due to its nature, selection pressure for males remains smaller than for females, however, there seems to be a slight pressure increase which translates in the graph as a decrease in the males only group, resulting from less individuals being able to keep-up with a self-reinforcing choice.

In summary, this analysis validates that the model and its assumptions are suitable for emerging Mate Choice through the self-reinforcement of mating preferences alone. Furthermore, results show that the assumptions, through their simplicity, allow for Fisherian preferences to evolve in any direction, including in the same direction as the fitness functions. Overall, there is a strong tendency for preferred phenotypes to evolve in a direction that is neutral or likely contrary to fitness, which is in-line with the Fisherian character of the model. Finally, the balance in candidate pool sizes for each role seems suitable for selection pressure to emerge in regards to Mate Choice, enforcing an increasing specialization of the population in competing in one of the two roles, instead of trying to achieve reproductive success through both selection operators simultaneously. Instances where preferences evolve in the same direction as fitness im-

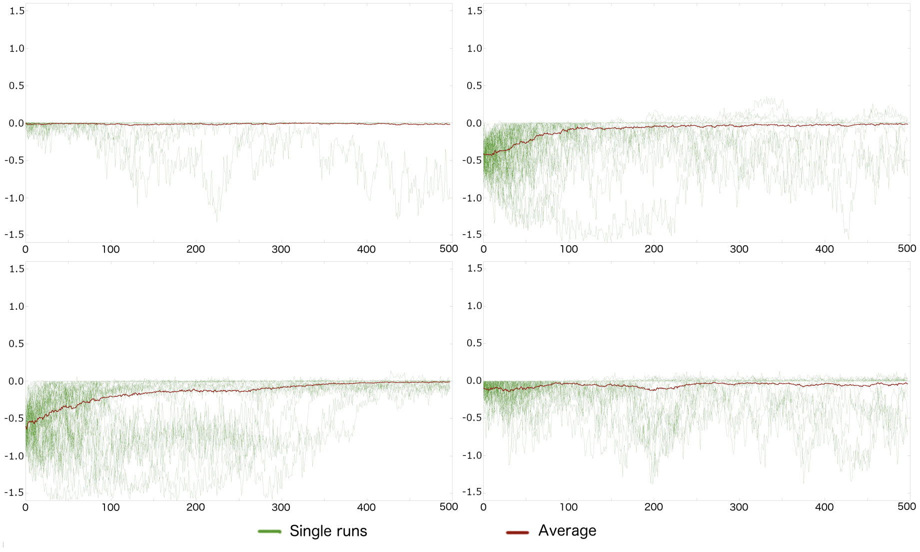

Figure 6.6: Evolution of Evaluation Entropy differences between using Mate Choice or Fitness base selection. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

pose less pressure for specialization, which as seen in Figure 6.5 regarding the keijzer-3 function, results in a higher average number of hermaphrodite individuals.

6.4.2 Perception Analysis

Complexity and Dimensionality analysis and interpretation are strongly tied to the assumptions of the approaches. In regards to PIMP, encoded information represents an ideal mating partner rather than an evaluation function and as a result, the metrics under scrutiny in this subsection are relevant to study the composition of such representations, rather than holding information on perception of mating candidates. In detail, there's an adaptive complexity and dimensionality in the expression of ideal mating partners, rather than on the perception and evaluation of mating candidates, which in this scenario remains static. Nonetheless, entropy and contrast remain valuable phenotypic measures and the discussion on the four metrics should provide interesting feedback. To support the analysis, Figure 6.8 allows for a view of how each metric evolves on average for the four studied functions, while Figures 6.6 and 6.7 show pairwise comparisons of entropy and contrast in each selection step obtained through attractiveness and fitness, averaged over the whole sample.

The ability to distinguish between mating candidates and thus producing positive entropy is a requirement for Mate Choice, as an entropy of zero would restrict choice to a random behavior. In this particular case, unless mating candidates are similar, it is expected that the mate evaluation function can distinguish between them with no setbacks. After all, evaluation is done in the same fashion as within the fitness function and relying on the same amount of data points. However, when looking at Figure 6.6, the differences between fitness and attractiveness entropy can vary, specially in the beginning of the runs. This is the result of two factors: i) preference initialization is unbounded, unlike the static fitness function, and therefore can tend to infinity, causing

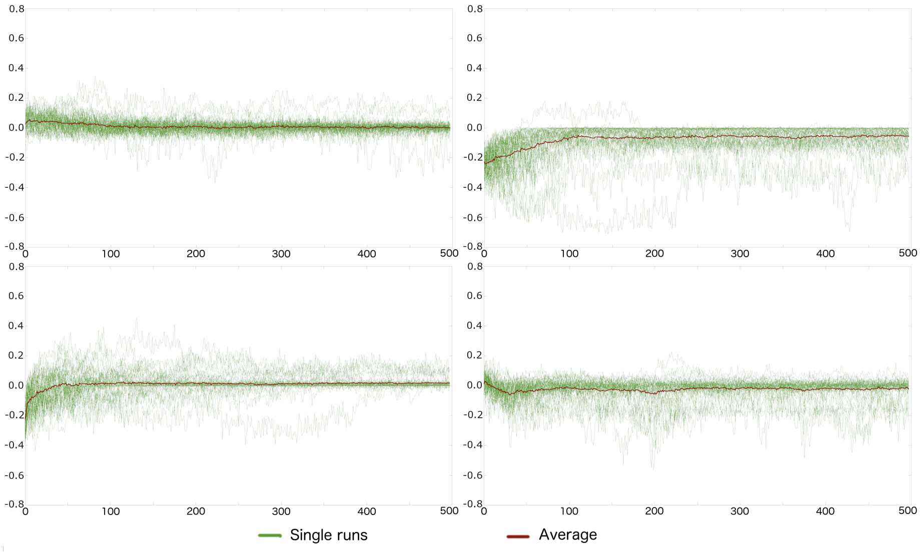

Figure 6.7: Evolution of Evaluation Contrast differences between using Mate Choice or Fitness base selection. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

attractiveness entropy to be lower than fitness entropy on those scenarios; ii) candidates may encode solutions that are seen as tending to infinity when evaluated for fitness and not for attractiveness (or the other way around), specially considering that a quadratic error aggregation is being used.

Regarding the first factor, such individuals are less capable of distinguishing between mating candidates and will lead to choice operations where attractiveness entropy is lower than fitness entropy, ultimately contributing to negative pairwise comparisons, shown on average in the graphs of Figure 6.6, whereas the second factor may contribute to variations in both positive or negative values. The combination of both factors, as shown, is more detrimental to attractiveness evaluation in comparison to fitness differentiation, in regards to entropy, which from an intuitive perspective comes to no surprise. Still, as the graphs in both Figures 6.8 and 6.6 suggest, pairwise differences between both metrics tend to diminish along the evolutionary process, because low entropy preferences struggle more than others to self-reinforce. Alternatively but just as fair, preferences gradually tending to infinity may lead to a pull on candidates in that same direction, eliminating design benefits from fitness evaluation. It shows that despite the limitations of PIMP, attractiveness entropy can compete with the static, hand designed fitness evaluation function.

As to contrast, the results require careful interpretation. Without loss of generalization to CMP-GP, the metric can be seen as a way to measure how much candidates distance from each other according to fitness or to attractiveness. However, whereas in CMP-GP that is a direct implication of the mate evaluation function and represented interactions, in PIMP that depends merely on the position of the candidates in the search space. In other words, assuming that fitness and attractiveness are finite points in the search space used as pivots for measuring linear distances between candidates, contrast differences should be zero. With that being said, the aforementioned issues with initialization have an impact on contrast just as they do on entropy, although on a larger scale due to the metric being sensible to distances rather than ranking based.

It's important to keep in mind at this stage that contrast is a lesser metric, one that while being more sensible to distances, is not necessarily more sensible to the distinction between candidates (a candidates pool with 4 similar individuals and one that tends to infinity can have significant contrast), therefore being somewhat skewed as a representation of the central tendency of a sample. Even with the squashing function limiting the disproportionate impact of such situations, a comparison between the behaviors shown in Figures 6.6 and 6.7 illustrate how contrast can overly show the impact of initialization shortcomings. There may be an effect caused by the nature of the squashing function which may change if others are used.

A closer look at each graph shows a few things worth noting: i) the tendency of average evaluation contrast differences follows suit with that of entropy for each function; ii) in function nguyen-4, while entropy variations are generally small or non-existent, contrast shows variations centered slightly above zero and with a small diffusion; iii) the above zero contrast seems to have no particular impact on entropy; iv) in the vladislavleva-7 function, the behavior is similar although average contrast differences are centered slightly below zero, as are entropy differences, although both metrics show an adjustment toward zero along the runs; v) the lower contrast by PIMP seems to be related to its entropy differences; v) in functions korns-2 and keijzer-3 contrast differences seem to follow suit with entropy differences, both recovering from initial poor values; vi) interestingly, while the first one shows a stabilization on negative values, the second one evolves towards positive ones, although that seems to hold no particularly relevant impact on entropy.

When looking at Figure 6.8, some of the described behaviors can be further explained: i) while in function nguyen-4 contrast differences are centered slightly above zero, the average contrast of attractiveness slowly reduces, which implies that fitness contrast does the same; ii) on the vladislavleva-7 function, the same is not true, with average contrast being higher than on the previous function, although less competitive with fitness contrast; iii) on the korns-2 function, average attractiveness contrast continuously improves along the runs even if its competitiveness with fitness contrast is negative; iv) on the opposite, average contrast difference gains for the keijzer-3 function seem to be resultant of a drop on the fitness contrast, which is better balanced in attractiveness despite the drop in average contrast. Overall, attractiveness contrast either seems to improve but not as competitively as fitness contrast, or to drop slower that fitness contrast does, showing sturdiness and being more competitive on those scenarios.

Additionally, Figure 6.8 shows the relation between evolving average complexity and dimensionality, and average entropy and contrast. A few things are worth mentioning as initial observations: initial conditions are different for each function, hence the high discrepancies in the graphs; average dimensionality and complexity are locked to each other, due to node constraints, which is quite visible; there's a clear tendency for both to reduce on average over the evolutionary process, although there are peaks of increasing complexity and dimensionality that can last for relevant periods (up to 50 generations sometimes); despite the consistent drop in both metrics, there seems to be no immediate connection to the behavior of entropy and contrast, due to the assumptions of PIMP.

Nonetheless, addressing why there's a tendency for simpler preference functions to be favored over the evolutionary process should be interesting. In a Standard approach, tree bloating usually emerges as a defense mechanism against destructive crossover, which may also be true for the first chromosome in the current Mate Choice opera-

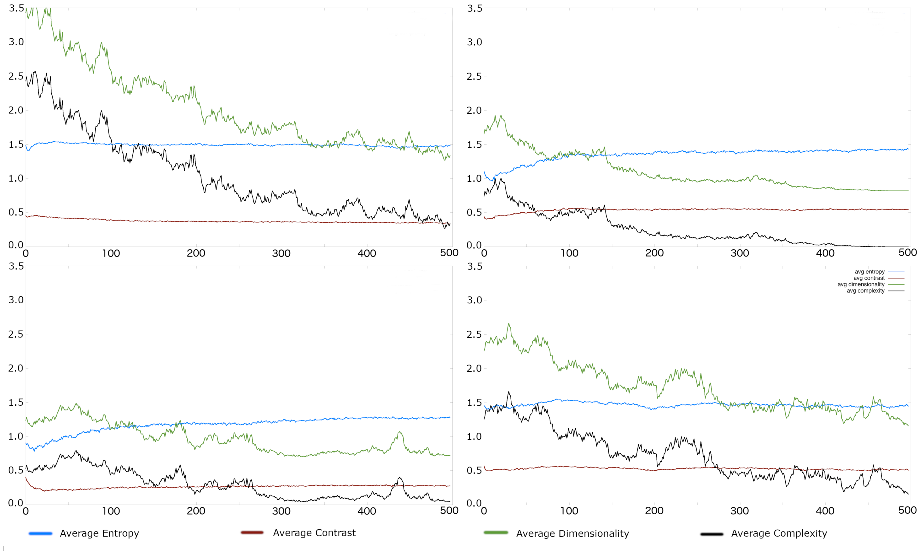

Figure 6.8: Evolution of average Entropy and Contrast as well as average Dimensionality and Complexity. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

tor. However, as has been discussed in Section 3.3.1, recombination can be more destructive for large preference genetic trees than for smaller ones, mostly because they aim only for choice consistency. Simple genotypes and corresponding phenotypes are likely to be less sensible to changes in that regard, giving them competitive advantage over more complex ones, even if the latter provide additional responsiveness to small changes. Mate Choice is rather unbounded, allowing preferences to evolve more freely and fueled by self-reinforcement. As a consequence, and as suggested by the results, the competitive advantage of simpler functions has a stronger impact, partly explaining the tendency shown by the dimensionality and complexity metrics. As a side note, it is likely that such an effect will impact the size of phenotypes being selected for as well. Still, it should be assessed if entropy and complexity have a saying in the tendency of the metrics.

Figure 6.8 is useful for a general view of the average tendency of each metric, but with multiple dimensionality values and complexity values (in this case, regarding the ideal partner representation) competing among themselves, it's impossible to relate each particular preferences structure with entropy and contrast through that data alone. It is likely that the average tendency of each metric results from quite different contributions coming from different competing characteristics. Figures 6.9 and 6.10 shed some light on preferences and the resulting entropy or contrast respectively. Each graph clusters information from all active females in the first 150 generations over the whole 50 runs. Consequently, each dot is not the result of a single Mate Choice step but rather the average of many steps with similar preference characteristics (in regards to terminals and non-terminals in the ideal partner representation, not necessarily having the exact same genotype). With that being said, dots in the lower left corner have the contribution of many more Mate Choice steps, simply because (as can be seen through the average values) there are more individuals sporting smaller dimensionality and complexity.

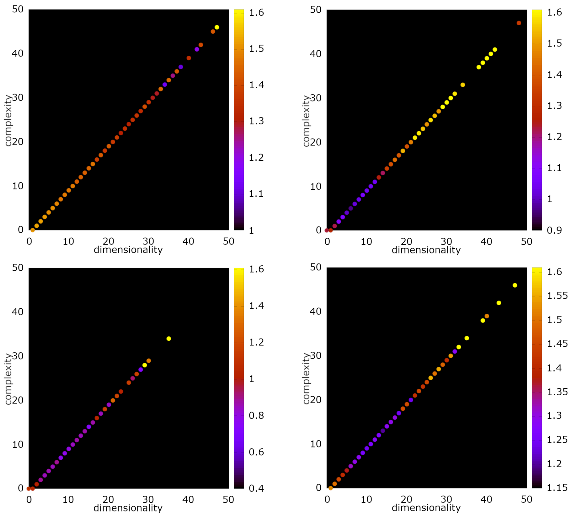

Figure 6.9: Relation between Entropy, Dimensionality and Complexity in the first 150 generations of all runs. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

In each graph, color shows the average entropy or contrast value for a particular pair of dimensionality and complexity values (which, as discussed, are in lock). The color range has been adjusted for each particular function, in order to better fit the data, rather than maintaining a fixed range. This way, a better use of the color pallet is achieved and differences are more visible, but particular care is needed when comparing between graphs. As an overall observation, higher entropy seems to be associated with higher dimensionality and complexity in preference chromosomes. This is particularly easy to see in the graphs relating to the korns-2 and vladislavleva-7 functions. The keijzer-3 function seems to make it difficult to breed and reproduce high complexity and dimensionality, which is probably a consequence of the terminal and non-terminal sets. Still, behavior similar to that produced in the above mentioned functions can be observed. In the nguyen-4 function, a different behavior seems to be promoted, where most extreme values of entropy, both high and low, are more likely with a higher complexity and dimensionality, whereas a more stable behavior is seen in the bottom left corner of the graph. Similar observations are shown regarding complexity in Figure 6.10, although on a different scale.

In this particular context, and considering the assumptions of the current approach, a straightforward analysis of the results seems to support that relying on more complex representations of ideal mating partners promotes a higher evaluation entropy and contrast. However, such individuals are likely rare, which calls for an analysis based on the bottom left corner of the graphs, where most of the considered sample is located. Focusing on such instances, on all graphs in Figure 6.9, there's visibly a higher entropy on simpler individuals when compared to their immediate neighbors. Such behavior is in agreement with what can be seen in Figure 6.8, where entropy increases while simpler individuals are promoted. Although maximum levels of entropy are not achieved by such individuals, the relative advantage is likely to contribute to their promotion, reinforcing the advantages brought by reproductive crossover. The effect is less visible in

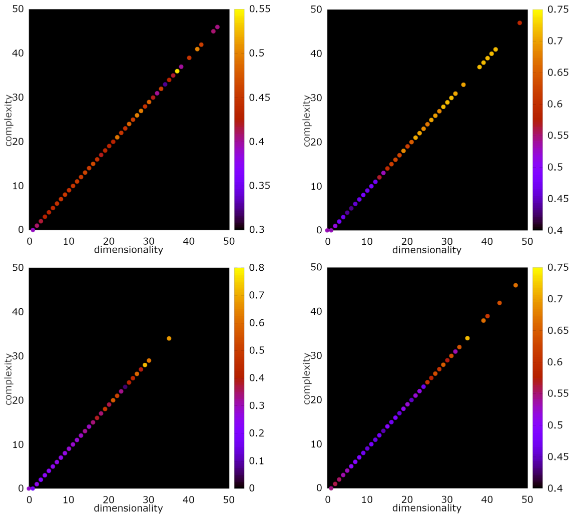

Figure 6.10: Relation between Contrast, Dimensionality and Complexity in the first 150 generations of all runs. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

regards to contrast, in Figure 6.10, which nonetheless is also aligned with the behavior seen in Figure 6.8, and to its lesser role in a tournament like operator.

In summary, close to maximum entropy and contrast seems more likely to be achieved by individuals carrying high dimensionality and complexity within their preferences representation, but, as such individuals are a small minority in the studied sample, they fail to take hold through self-reinforcement. Nonetheless, among individuals of lower complexity and dimensionality, evolutionary advantage should go to those that achieve higher entropy. According to the studied sample, such is relatively achieved with success by simpler preferences, which in addition to potential advantages brought by being less exposed to destructive crossover, promotes the decrease of average complexity and dimensionality while improving the average entropy. The same is less evident for contrast, which remains less relevant for competition due to the nature of the Mate Choice operator. As a side note, the ongoing discussion suggests that, were the genotypic metrics kept higher (possibly by reducing the inherent advantage of smaller sized trees), then it would be easier for entropy and contrast to be kept at higher values as well.

6.4.3 Effects Analysis

Having looked at the specifics of Mate Choice as a selection operator and it's ability to perceive and evaluate mating candidates, it's important to understand its impacts on the population as a whole and how the evolution of self-adaptive preferences influences the search process. A glimpse has been previously included in Figure 6.5, regarding the distribution of individuals in genders but the current section will expand on that discussion, mainly by including genotypic and phenotypic measures of diversity and tackling the approach's ability to promote and maintain innovation. Figures 6.11 to 6.24 will provide data for the discussion, both on population and inner-gender levels

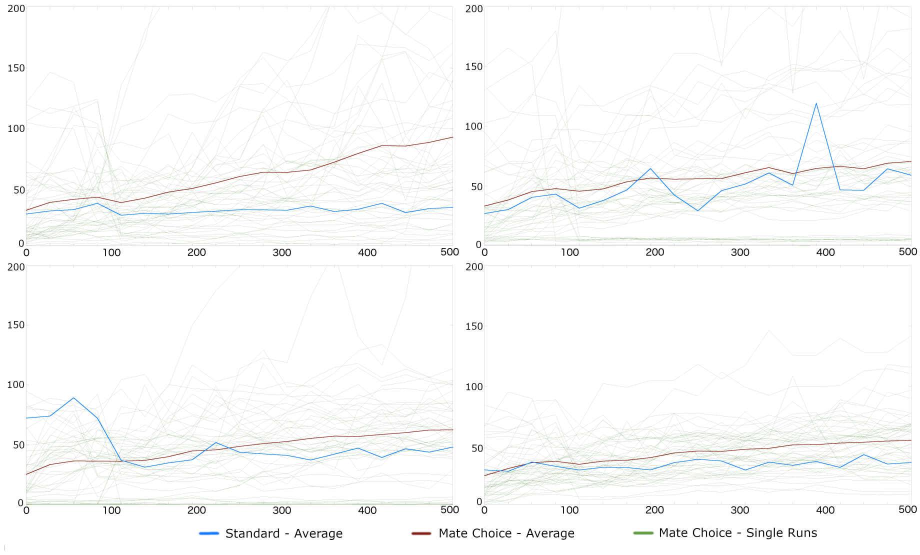

Figure 6.11: Population edit tree diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

and with different topics in mind.

Diversity maintenance is regarded as a key factor in search optimization, fueling upcoming steps with genetic variation, without which search efforts become stale or rather focused on a local genotypical neighborhood that may not hold a chance for improvements. Figure 6.11 gives an overview on population diversity, including each run and an average tendency for PIMP, and the all-run average value for the Standard approach as a base line for comparison. First impressions on these graphs alone are rather optimistic, with PIMP visibly contributing to an increased genetic variation when compared to the Standard approach (at least according to edit tree distances), a difference that increases along the evolutionary process. Such outcome is the contribution of many runs successfully promoting population diversity, but still, on functions korns-2 and keijzer-3 results show a subset of experiments where edit tree diversity drops fast and remains close to zero throughout the evolutionary process. Also, diversity in the vladislavleva-7 function seems more contained in comparison to other functions. Perhaps equally relevant is the perceived ability of the Standard approach to maintain or slightly improve on it's average variation, despite maintaining a more modest tendency.

These observations require careful analysis and should take into account a number of relevant factors that strongly influence their interpretation: i) edit tree distances consider tree structures, but not how they translate to phenotypes (in an extreme scenario, large chunks of a tree may have no phenotypic value, adding non-relevant genetic diversity); ii) the use of a pivot to measure edit distance diversity can be subject to skewness if, for instance, the fittest individual is an outlier of its population; iii) the observed metric takes into account the whole population, including those individuals that end up not reproducing and thus not contributing to the search effort; iv) the splitting of the population into genders in PIMP can boost the measure towards values that don't accurately reflect the genetic diversity found in the population, for instance if the male population gradually distances itself from the female one. Each of these factors can be

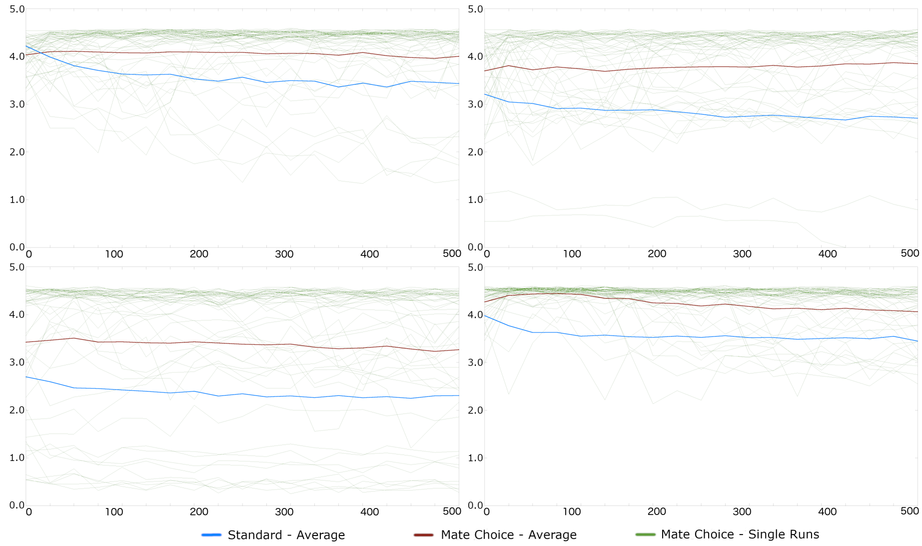

Figure 6.12: Population entropy diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

studied to some extent and one at a time to rule out potential influencing factors, and truly address the impact of Mate Choice on diversity.

Addressing the first two discussion points can be tricky. In a perfect scenario, one would analyze each individual independently and weed out irrelevant parts of the genotypic trees, however, there's no straightforward way to do so in bulk. Additionally, making pairwise comparisons between all individuals in a population can be very computationally demanding. Nonetheless, the absence of mutation should highly reduce the risk of skewness caused by potential emerging outliers. Alternatively to employing more demanding methods, one may look at how genotypic and phenotypic diversity relate to each other in search for clues. Ideally, genetic diversity should translate into phenotypic diversity, specially if the evaluation function is sensible to changes (Sections 6.4.2 and 6.5.2 have shown that the evaluation function is quite sturdy in that regard). With that in mind, one may look at fitness entropy for confirmation of diversity, expecting to find matching behaviors.

Figure 6.12 shows that this is not the case, and specially so for the Standard approach. In that setup, while tree edit distance suggests an approximately stable genetic diversity, it translates into a lowering average fitness entropy. On the other hand, entropy is maintained higher for PIMP, closing to maximum values on a large subset of individual runs as well as on average. Moreover, PIMP shows a more stable behavior across generations, even though there seems to be a tendency toward lower values (most visible in the vladislavleva-7 function despite the initial gains, whereas korns-2 shows the opposite behavior). Additionally, while some runs show low entropy values, instances of close to zero edit tree diversity seem to have less impact than otherwise suggested. While this offers no definite proof of higher genetic diversity in Mate Choice, it does corroborate the differences shown in Figure 6.11, even suggesting that the Standard approach is unable to truly maintain a stable diversity that can translate into meaningful phenotypic variations. Importantly, confirmation through fitness

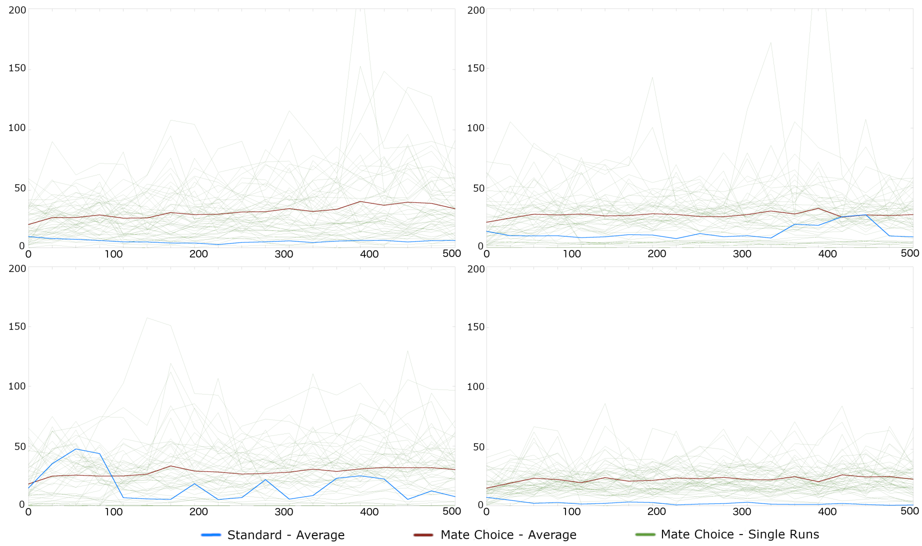

Figure 6.13: Females edit tree diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

entropy keeps some of the risky characteristics of edit tree diversity at bay, such as: i) impact of non-relevant sub-trees; ii) relying on a pivot for distance measures; iii) distancing between genders boosting population diversity (because it relies on unique fitness values, the metric offers a view that isn't distorted by such separation).

Focusing on the third and forth points of discussion, Figures 6.13 through 6.16 offer some insights. Figures 6.13 and 6.15 regard edit tree diversity among female and male populations, while Figures 6.14 and 6.16 show the corresponding fitness entropy metric. For each graph, the sampled individuals are those who have been selected for the roles of female and male respectively, thus leaving out individuals that end up having no impact on future generations, while looking at each gender selection dynamics separately. For comparison purposes, samples from the Standard approach are also studied, either being selected by one of the two tournament selection operators. Arguably, this would be akin to comparing to an approach where the females are selected through fitness, and give preference to the most fit male among candidates. Nonetheless, because rules are similar between the two tournament operators, the selected individuals should equally represent the same asexual population. The plotted Standard approach behaviors, in either the female or male related graphs are similar, suggesting so.

Overall, the figures further distinguish between PIMP and the Standard approach. While in PIMP the population wide edit tree diversity seems to extend its impact onto selected individuals for either role, the same can't be said for the Standard approach. In fact, edit tree diversity among selected individuals in the Standard approach is shown to drop fast and not carrying the higher population wide diversity well. This is a direct implication of the stranglehold put on by selection, boosted by both operators favoring the same subset of individuals, which is reinforced over time (specially without mutation). When comparing this behavior to what is shown in Figure 6.11, results highly suggest that the population wide diversity discussed previously is boosted by individuals that have no competitive potential and thus no particular value, perhaps resulting

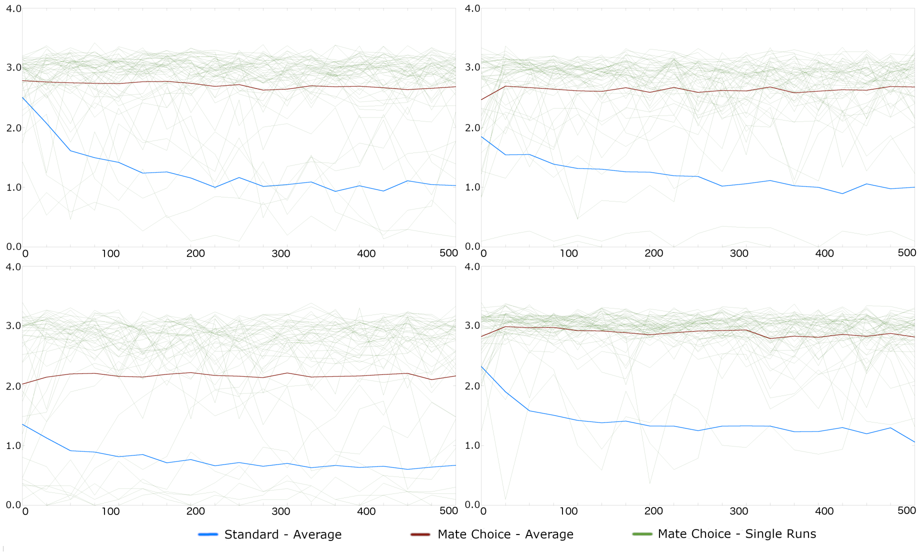

Figure 6.14: Females entropy diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

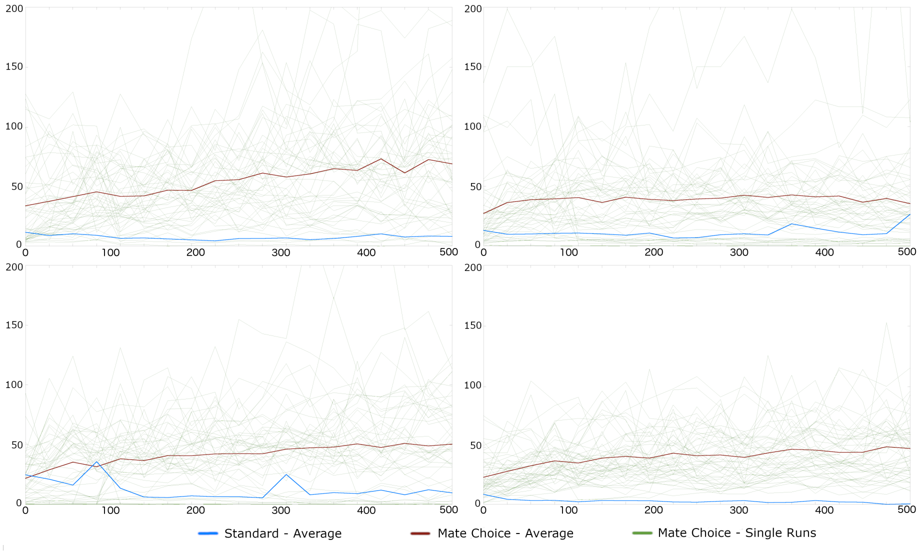

Figure 6.15: Males edit tree diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

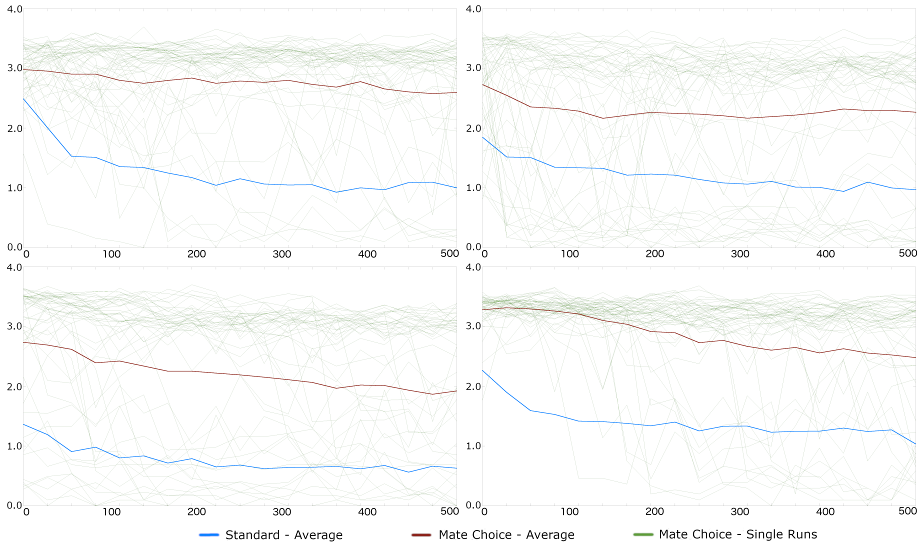

Figure 6.16: Males entropy diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

from destructive crossover operations. This study won't argue further regarding selection pressure on tournament operators, as the testing setups have been designed to keep conditions as similar as possible between approaches.

In comparison, the resulting behavior of PIMP is quite different. It would be unfair not to acknowledge that in some runs, convergence among selected females does happen, particularly in the korns-2 and keijzer-3 functions. However, on many runs and on average, edit-tree diversity among females is kept on considerably higher values than on the Standard approach, while also showing a steadier tendency, even growing on average over generations. This difference to the Standard approach is confirmed by Figure 6.14 which likewise shows an enduring maintenance of fitness entropy, in contrast to the noticeable decay in the Standard approach. This achievement may not look like much but maintaining a healthier distribution of fitness values within the female population is a signal that more distinct individuals are getting a chance at competition and thus at reproducing, consequently passing on not only their survival related genes but also their mating preferences.

This behaviour is surely influenced by lower pressure resulting from having only one, rather than two, operators selecting for fitness, but it can hardly be pinpointed solely on that. Even with lower pressure, a slower but noticeable diversity decay would still be unavoidable. Therefore, the resulting behavior must be a consequence of the dynamics introduced by Mate Choice. The mechanics that allow for this behavior will be further explored ahead, however, it's noticeable in Figure 6.13 that the female role is not always attributed to similar individuals, and that peaks in average edit tree diversity can be seen ranging in magnitude, suggesting the introduction of disruptive individuals in female populations. These may either be hermaphrodite individuals or, as suggested by Figue 6.5, perhaps individuals that have drifted in the search space while being competitive fitness wise.

Looking at diversity within the male populations, there are similarities but also dif-

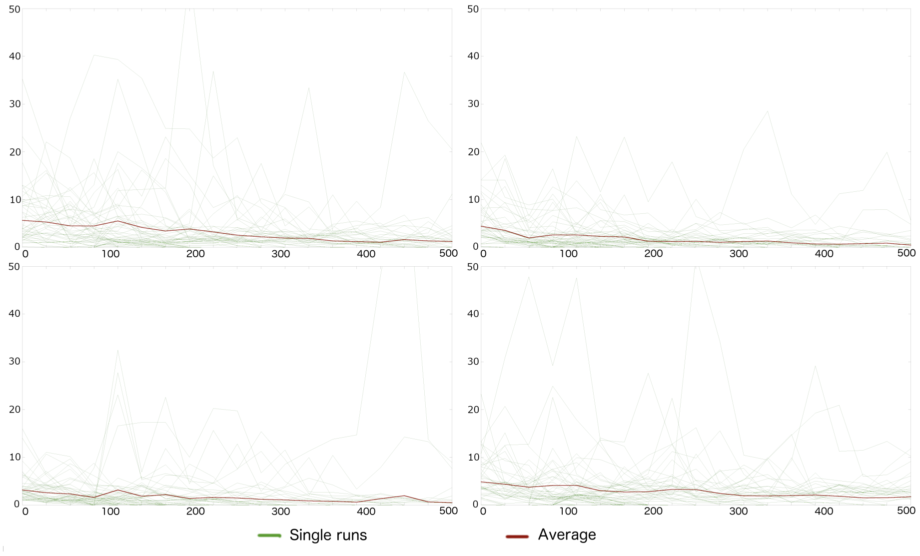

Figure 6.17: Female preferences edit tree diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

ferences worthy of note. Regarding edit tree diversity, the metric generally follows suit to the behavior shown in the females populations, however, diversity is kept higher and the tendency to increase on average towards the end of the runs is noticeably stronger. Exceptions can be found in the korns-2 and keijzer-3 functions, where a subset of runs, probably those same found in the population and female analysis, shows close to zero diversity. Regardless, average fitness entropy is initially higher on average and by the end is somewhat at the same levels as shown for females populations, showing a tendency to decrease that is not observed within female populations. On the one hand, this shows convergence of selected individuals into a smaller subset of distinct phenotypes (which is in agreement with Figure 6.5), but on the other hand suggests larger edit tree distances between those individuals. While female selection is bounded by the fitness based tournament operator, selection of males is self-regulated and therefore somewhat unbounded. This aspect should be at the bottom of the differences in diversity between genders but requires further analysis and careful interpretation.

Higher initial edit tree diversity and fitness entropy in males than in females can be largely explained by the random character of Mate Choice in initial generations. However, for edit tree diversity to increase in a sustainable manner, at least one of two behaviors is expected to be observed: i) preferences evolve in diverging ways, leading males into different paths whose growing distance fuels the apparent increase in diversity; ii) preferences push for extreme features, therefore giving way for individuals that are divergent to be selected as males, and consequently increasing the gender's inner diversity. Arguably, both behaviors may account for the slow drop of fitness entropy by cheer force of self-reinforcement, as Mate Choice gradually substitutes randomness with a selective force. Figures 6.17 and 6.18 tackle both scenarios respectively. On the first one, a decrease in edit tree diversity among preferences in active females is shown, firmly rejecting the first hypothetical behavior described. Despite occasional runs showing peaks of diversity, average preferences seem to consistently self-reinforce

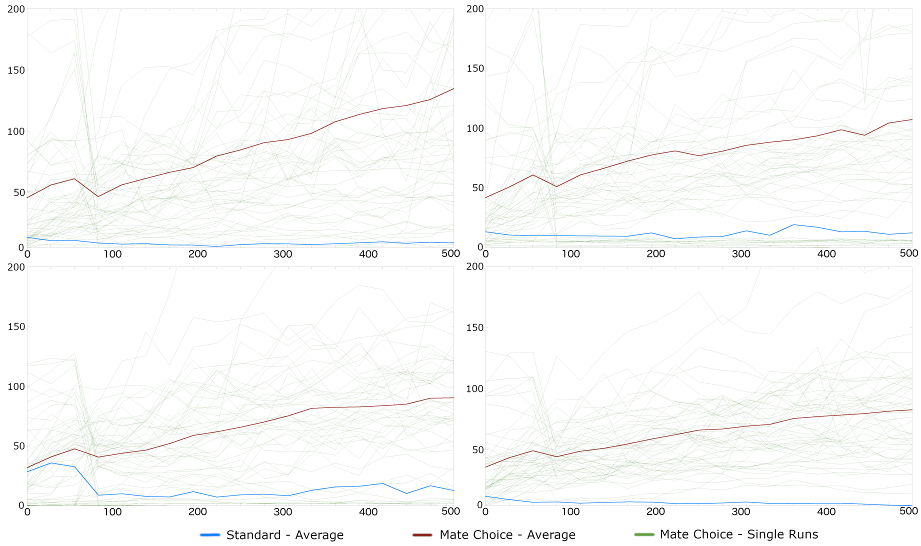

Figure 6.18: Edit tree distance between pairs at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

towards agreement and similar genetic structures. On the other hand, the second figure seems to show exactly what would be expected for the second hypothetical behavior to be confirmed. Over time, females on average pair with more and more diverging males, pushing them to extremes in a negative assortative mating fashion, thus fueling an increased edit tree diversity in the male population.

There are, nonetheless, instances of positive assortative mating, which are likely associated with those plotted in Figures 6.11, 6.13 and 6.15 showing small diversity. It's very likely that those are the same instances in Figure 6.4 showing a positive correlation. In those runs, Sexual Selection and Natural Selection evolve to benefit the same individuals, reinforcing each other and pushing female and male sub-populations into the same region of the search space. As a result, Figure 6.5 shows a higher number of hermaphrodites on the korns-2 and keijzer-3 functions, due to individuals in those particular runs being competitive both through fitness and attractiveness. Nonetheless, most runs show a runaway of male individuals toward high dimorphism, with a driving momentum that is characteristic of such phenomena. This process is poorly bounded by Natural Selection since traits add no particular fitness costs (in a gendered population with no overlaps, the cost of being poorly fit can be absolutely atoned by being proportionally attractive), allowing for preferences and traits to reinforce far-off solutions without ever reaching an equilibra. As a side note, data on female and male behaviors further illustrates the differences between them. Whereas the female population is more conservative and exploitative of fit solutions, the male population shows a more exploratory character, as suggested by Figures 6.15 and 6.18. This can be seen in the average diversity metrics but also when individual runs are considered, with the male population reaching a wider range of possible outcomes. These exploitation-exploration roles are the root of inter-gender dynamics. Despite the risk of destructive crossovers, the approach seems capable of injecting the female population (which promotes fitness) with diversified solutions that can represent new ecological opportuni-

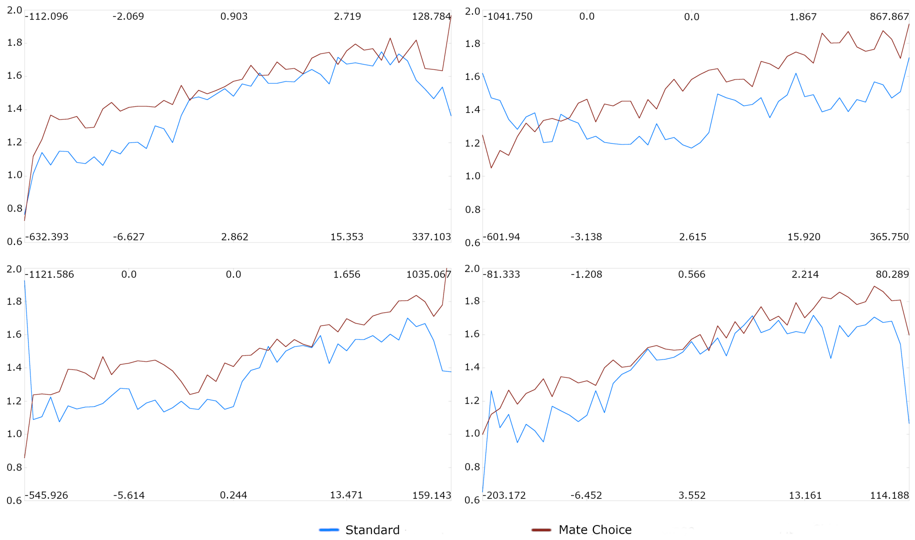

Figure 6.19: Survival rate for females from all 50 runs, bucketed and ordered by innovation rate. Quartile information for PIMP included in the bottom x-axis. Quartile information for the Standard approach shown on the top x-axis. Four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

ties, contributing to progressing steps in the optimization efforts.

Still, a question is raised on whether such diversity has merely an immediate role, with no lasting consequences other than destructive crossovers punctuated by the occasional fortunate outcome, or if it is indeed capable of contributing to future generations by having its descendants (and therefore its genes) be present. In other words, is innovation a result of chance similar to what would happen with a mutation operator, or is it a continuous effort with neophiliac character. Figures 6.19 to 6.24 contribute to this discussion with different data. Along with plots regarding PIMP, the same metrics for the Standard approach are included for comparison. However, population conditions are not quite the same for both scenarios, and interpretation should be done carefully having each scenario in mind. A step by step description and analysis follows.

Figures 6.19 and 6.20 are particularly challenging to analyze, as they include a large amount of information. As described in Section 6.2.2, the graphs map innovation to survivability, through the x and y axis respectively. For each function, individuals are collected at each 25 generations in all 50 runs and joined together in the same sample, representative of each approach. They are then organized on the x-axis according to their prospective innovation, measured according to how each individual is placed in its parents generation's inner-gender edit-tree distribution (Section 6.2.2 offers a full description). While distances are always positive, a sign allows for a sense of direction so that: i) individuals close to zero are in the neighborhood of last generation's average distance, having therefore as much a chance of providing innovative solutions as the average individual in that population; ii) individuals placed at values smaller than zero are closer than average to the most reproductive individual, potentially contributing to the exploitation of that search neighborhood iii) individuals placed at values larger than zero are further than average to the most reproductive individual, potentially introducing exploratory solutions.

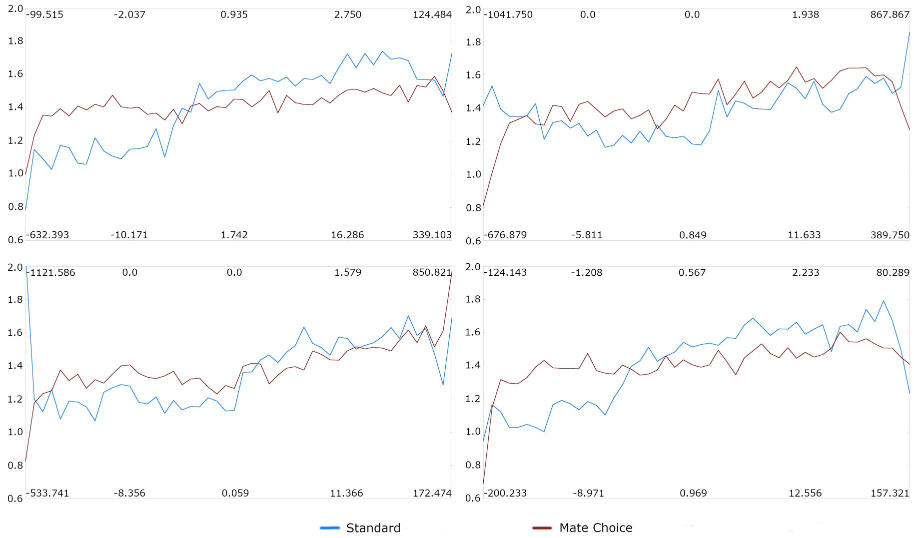

Figure 6.20: Survival rate for males from all 50 runs, bucketed and ordered by innovation rate. Quartile information for PIMP included in the bottom x-axis. Quartile information for the Standard approach shown on the top x-axis. Four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

The resulting sample of distances-to-average is large, and for clarity purposes has been ordered and bucketed into 50 groups, 48 of which have equal size (over 500 individuals each) with the surplus individuals being split into the two remaining groups (24 individuals or less each). Individuals in these two groups are those at each end of the ordered sample, likely including any existing extreme outlier, thus controlling their impact. A five number summary can help assess the composition and distribution of such a sample. Different samples may have different distributions, therefore, each graph's x-axis includes the five number summary for PIMP on the bottom and for the Standard approach on top, allowing for the data to be interpreted on their appropriate intervals. As described in Section 6.2.2, the y-axis corresponds to the survival rate over two generations for each group of individuals. A few characteristics are relevant when analyzing it's outcome, specially regarding the tendency for positive rates: i) because in each figure only the selected females (Figure 6.19) and the selected males (Figure 6.20) are studied, individuals with no survival chances are left out; ii) production of two offspring gives a chance of exponential growth over two generations; iii) rates are measured for each bucket, potentially balancing individuals with either none or an outstanding number of grandchildren; iv) the size of the buckets varies between approaches and genders, on the one hand influenced by gender distributions as shown in Figure 6.5, and on the other hand influenced by particularities of sampled generations; v) finally, the metric is defined in the $]-1,\infty[$ interval. As a result, conclusions regarding growth rates are safe within each approach or gender, but potentially complex between them.

In summary, Figures 6.19 and 6.20 allow for two major points of discussion: i) the five number summaries regarding innovation in each approach; ii) the survival rates of each bucket, as a sense of survivability by level of innovation. Focusing on the first point, the figures show very different sample characteristics between PIMP and

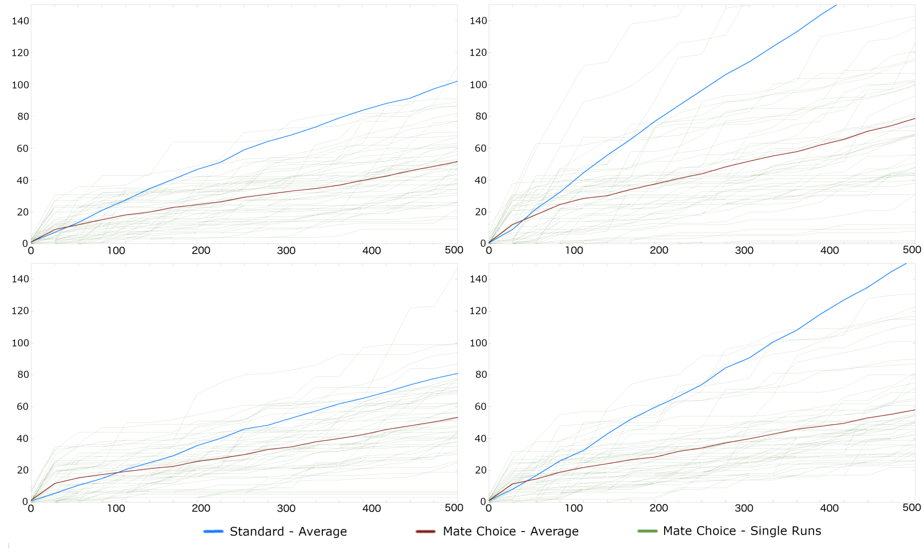

Figure 6.21: Cumulative number of female individuals considered as outlier from previous population's female individuals distribution, measured at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

the Standard approach, both regarding females and males. Whereas the IQR in the Standard approach ranges from ≈ 1.66 to ≈ 4.79, in PIMP it ranges from ≈ 17.44 to ≈ 26.46 , confirming very different variations. The Standard approach is rather conservative in regards to producing innovating offspring with no help from mutation, as expected and partially discussed in regards to population diversity. As a result, the following is observed: i) the median value in all functions is either zero or slightly above, suggesting that nearly 50% of the produced individuals are closer to the most reproductive parent of the same gender, in a exploitative or neutral fashion (possibly more than half if the median is zero); additionally, the third quartile is very close to the median, showing that of 75% of individuals below, those achieving exploration introduce small innovations at best; ii) in the korns-2 and the keijzer-3 functions, the first quartile is the same as the median, with at least 25% of individuals showing no deviation from their parent's population average distance; iii) in those same functions, the minimum and maximum are exceptionally distant from the median, likely representing rare artifacts in the samples, with most individuals deviating lightly from the median value. These observations are true for both selection operators in the Standard approach, illustrating the expected similarity.

In comparison to these observations, the following can be said regarding PIMP: i) the median value in all functions is positive and larger than in the Standard approach asserting that at least 50% of selected individuals follow an exploratory character, and likely more than in the Standard approach in a function-wise comparison; ii) the wider IQRs further suggest that the most reproductive individuals can themselves be distant from other individuals in their genders, reinforcing their own and the population's general exploratory character; iii) the third quartile is more distant from the median than the first quartile, signaling that exploratory individuals are more adventurous in the search space, in comparison to exploitative ones which remain closer to the previous

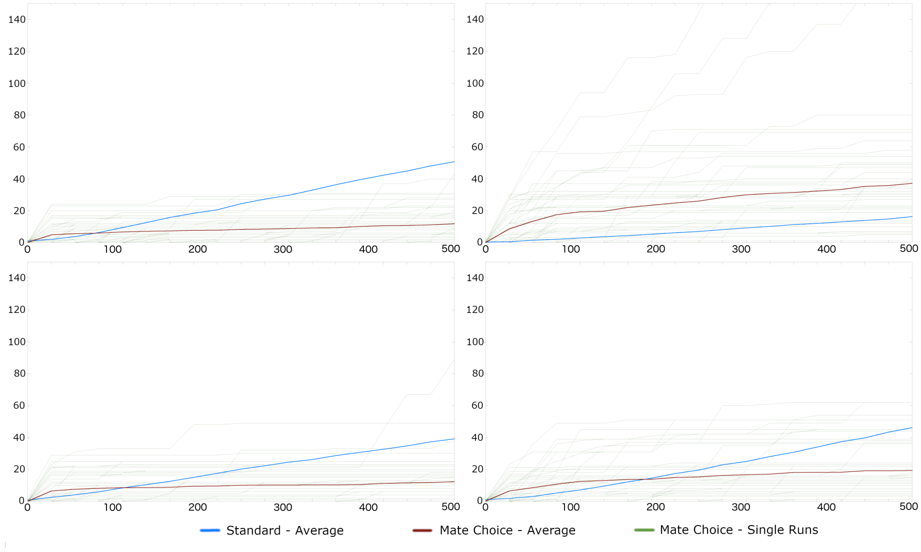

Figure 6.22: Cumulative number of female individuals considered as outlier from previous population's female individuals distribution while also surpassing its best fitness value, measured at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

population's central tendency (this is also true in the Standard approach but on a much smaller scale). These characteristics are true for both females and males in PIMP, with only slight differences between genders, probably the most relevant being the females holding a steadier IQR across functions while in males the values vary as a result of self-ruling preferences producing different behaviors.

Further differences arise when survivability is assessed. In those regards, the following observations are worth noting: i) while the average growth rates remain rather contained, they show a general propensity for favoring innovative solutions; ii) this observation holds true for both approaches but on very different conditions; ii) the same is also true for both genders in PIMP but with different outcomes. At this point, one should remember that only individuals that successfully reproduce are under analysis, certainly other innovations are unsuccessful on being selected for reproduction. Going back to the Standard approach, there is indeed a higher growth rate associated with those individuals that introduce innovation, although it has been discussed that the extent of such innovations is rather small. Nonetheless, the ecological opportunity represented by such individuals seems to take hold and reinforce their genetic presence by reproducing children that are themselves competitive. As expected, the behavior is similar for both selection operators. When focusing on PIMP, some of these observations remain true while others require further discussion. Both genders show a healthier growth rate for innovative individuals, but on a much larger interval than the Standard approach, suggesting that Mate Choice allows for more extreme innovations to successfully impact future generations rather than being discarded. The ability seems particularly relevant for the female population, despite being composed of individuals that have been selected for their competitive fitness. While there are certainly disruptive individuals that don't stand a chance at being selected for female roles, the data indicates that those that are both disruptive and competitive have a relatively higher

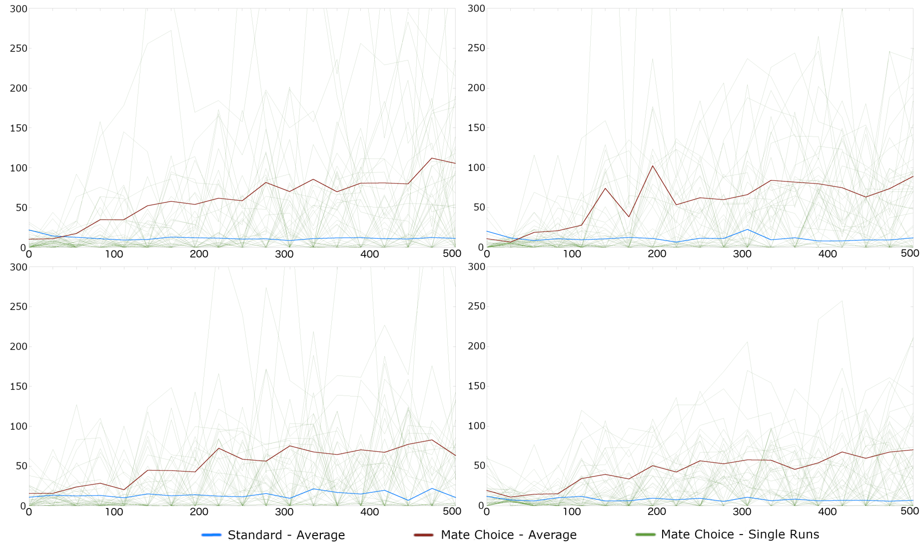

Figure 6.23: Edit distance from female parent for female individuals considered as outlier from previous population's female individuals distribution. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

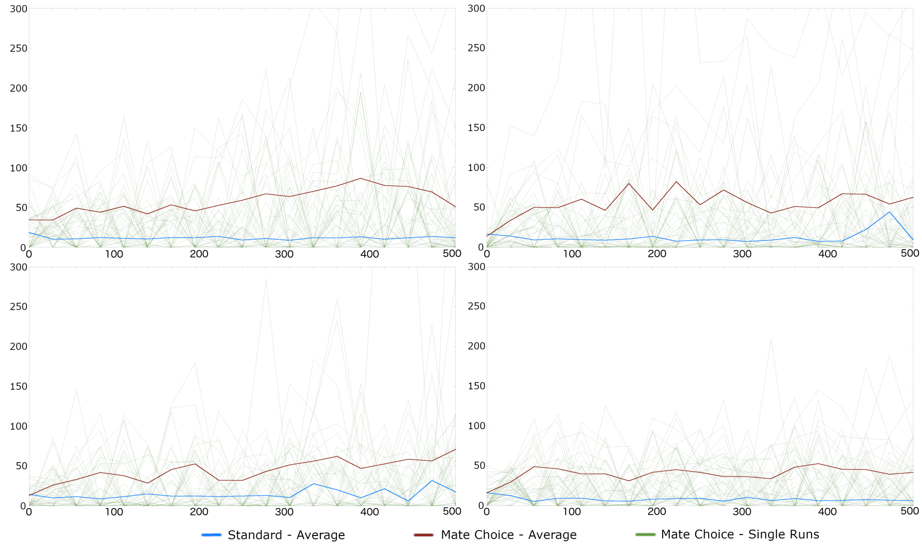

Figure 6.24: Edit distance from male parent for female individuals considered as outlier from previous population's female individuals distribution. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

impact on future generations through their higher growth rate. As a result, not only is genetic diversity promoted in female populations but there's also a chance for genetic drift towards new areas of the search space where potentially better candidate solutions can be exploited.

Such a scenario is benefiting for the search effort but would be rather difficult without contributions from the male populations. When looking at associated data, two observations come to mind: i) the overall growth rate of males is slightly smaller than those of females; ii) the variation in growth rates between less and more innovative individuals is less significant. The first observation can be explained by the larger size of the male group shown in Figure 6.5, which causes growth to be further divided between more individuals. The second observation should be interpreted taking into account the overall gender dynamics. As discussed and shown in Figure 6.18, the male population shows an overall leaning for drifting, pushed by preferences, and making innovation differences less relevant. Nonetheless, the differences are still there, and show that diverging yet attractive individuals are favored over others in regards to survivability. This is in-line with the runaway behavior discussed in regards to diversity and distances between paired partners. In the end, despite the survival of such individuals, a question remains regarding how much they can contribute towards feeding the female gender with genetic variation and ecological opportunities.

While such a linkage between the male and female genders can be complex, Figures 6.21 to 6.24 aim at showing how they can work in cooperation, particularly towards escaping local optima or drifting. This capability is an important part of what is expected from exploration, whereas exploitation can be safely left assured by the fitness based selection operator. Figure 6.21 shows the cumulative number of selected females that may be considered to be escaping the previous female population's genotypical neighborhood by being placed more than 1.5 IQRs over its third quartile. Figure 6.22 focuses on such individuals that also improve on the best fitness found so far. In both cases, populations are sampled at every 25 generations, therefore individuals in each population are compared to the previous one's distribution. Figure 6.21 shows that both approaches are capable of continuously producing individuals that are placed outside the established interval, although at quite different rates (with only a few runs of PIMP being stuck at near zero values). The impact of such individuals is quite different. Regarding the Standard approach, the IQR is likely small, and escaping individuals are making small contributions as demonstrated by Figure 6.19, but which can accumulate towards meaningful ones, as suggested by Figure 6.22. On the other hand, PIMP is less capable of contributing individuals that escape local optima but that are more likely of introducing very diverging solutions. These are more likely to result in drastic drifts in the search space rather than small continuous ones. However, Figure 6.22 suggests that, with the exception of korns-2 (where the Standard approach performs particularly sub-par), those contributions are relevant in the beginning of the search process but rare after the initial period.

While this is in-line with the general idea that exploration has a more important role in the early generations, it would be benefiting to keep up contributions throughout the evolutionary process, combining high exploratory capabilities with the ability to profit from the genes being introduced. Figures 6.23 and 6.24 give some insight on the nature of the escapee individuals, showing that they are increasingly more distant from both parents but more so from their mothers, highlighting on the one hand how exploratory males can contribute to the reproduction of offspring that are competitive while divergent, but on the other hand, suggesting that such ecological opportunities can represent large jumps in the search space rather than a slow but continuous drift.

Given the unbounded nature of the male runaway process, it's reasonable that male contributions, despite introducing diversity and novelty through negative assortative mating, end up being too far away to provide females with a steady rate of cumulative contributions, rather than punctuated disruptions, which impact the search effort but not to its full potential.

6.5 CMP-GP: Behavioural Analysis

Following the methodology used for the analysis of PIMP, and the discussion in Section 6.2.2, the next subsections will focus on empirically showing the behaviors introduced by Mate Choice with free evolving dimensionality and complexity, as well as its effects on the evolutionary process. While the same metrics will be used as in the previous discussion, and which have been discussed in Section 6.2.2, their interpretation is now subjected to the assumptions of CMP-GP. This is particularly relevant for genotypic metrics and for the analysis of perception. The analysis will be again split into three topics, that may at times overlap: i) selection analysis; ii) perception analysis; iii) effects analysis. As a note, including the analysis of all 52 functions through graphics would be impossible, therefore, the same four functions as before are considered: nguyen-4 (1 variable), korns-2 (5 variables), keijzer-3 (1 variable), and vladislavleva-7 (2 variables).

6.5.1 Selection Analysis

Similarly to the discussion in PIMP, analyzing what happens at each selection step provides important insight, potentially confirming that the model, paired with the assumptions of CMP-GP, is capable of emergent Mate Choice. Moreover, the data is important to study the character of choice and extend the analysis to a population level. The metrics involved in this discussion have been properly introduced in Section 6.2.2 and results have been summarized in Figures 6.25 to 6.28.

Just like in PIMP, the first analysis goal is to validate the emergence of Mate Choice by empirically showing its underlying engine: the self reinforcement of mating preferences through runaway processes and the resulting feedback loop between traits and preferences. As discussed, the effect provides unequivocal evidence of the emergence of Mate Choice while abiding by the proposed assumptions. Figure 6.25 shows the discussed genotypic metric while Figure 6.26 shows the phenotypic metric. Both illustrate how often individuals select mating partners that are consistent in choice with themselves, however, as previously mentioned, each has its particularities. The genotypic metric is quite conservative as it uses binary comparisons that count only selected pairs whose mating preferences are exact matches, which may be an overstrict view of consistent choice. The phenotypical metric overcomes such an issue although being potentially subject to a (quite small) chance of false positives.

Overall, both figures show an expressive tendency for self reinforcement, mapped by the increase of the average value from a close to zero value to a final close to one value. The tendency is a clear indication of the feedback loop between mating preferences, whose role is the cornerstone of emergent and sustained Mate Choice. A closer analysis of all 50 runs and the dispersion of the collected data should provide for further insights on the behavior, as well as for comparisons with the behavior achieved by PIMP. In each figure, dispersion is more perceptible below the average line, however, its also noticeable that there are many runs that reach the maximum value on each

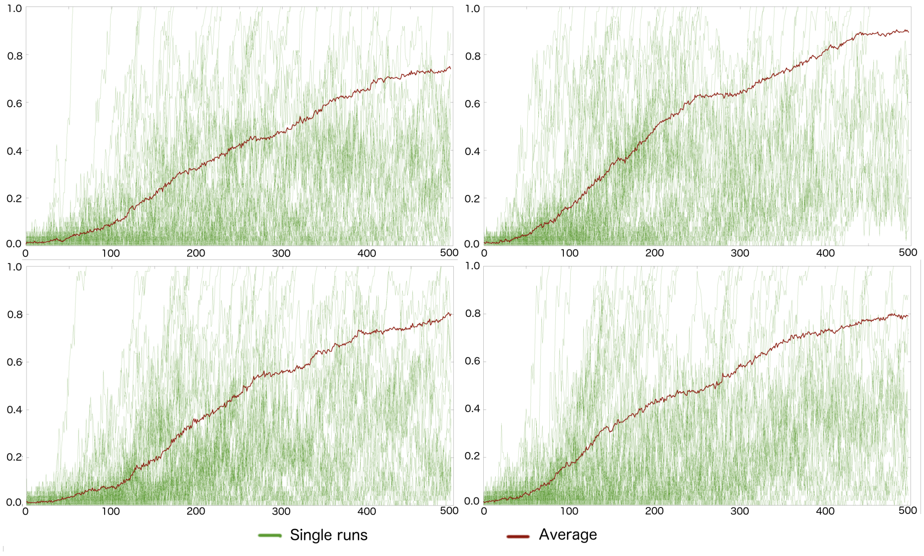

Figure 6.25: Evolution of the ratio of mating pairs that share the exact same preferences genotype. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

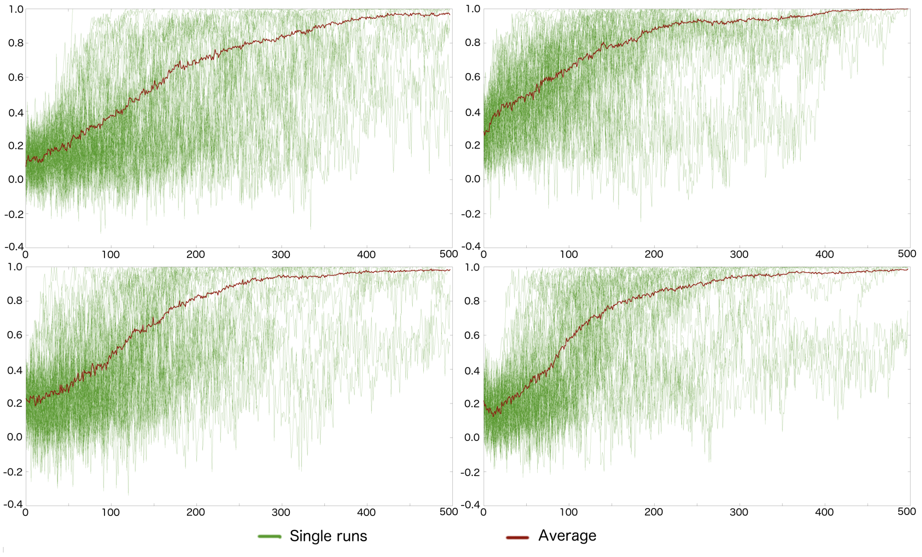

Figure 6.26: Evolution of the Spearman's correlation between phenotypic attractiveness rankings obtained by mating pairs. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

function, thus having a less visual impact in the color map but being reflected upon the average value. Just like in PIMP, the absence of mutation maintains such runs on an equilibrium where agreeing preferences have spread through the whole population. However, the same reasons discussed in the analysis of PIMP regarding why not all runs reach a full equilibrium scenario remain relevant for CMP-GP, such as the impact of initial conditions, candidate pools randomness, multiple competing preferences and so on.

Still, in comparison, CMP-GP seems to result in less dispersion. Additionally, average values of ratio (Figure 6.25) and correlation (Figure 6.26) reach closer to one despite starting closer to zero, which suggests that the initial response in CMP-GP is more similar to random behavior than what is achieved in PIMP. This difference may seem small but in regards to choice consistency, a positive correlation can give an important boost to preferences in initial populations, giving PIMP an advantage that is well expressed by the evolution of the average correlation in the initial few generations. On the other hand, the runaway effect seems on average to kick off later in CMP-GP, but due to a greater momentum (which can be seen in the slope of average values), reaches a stronger correlation not only in regards to the average value, but more often in the run set. Such distinctions are supported by differences between preference landscapes, both in size and character. Whereas the landscape for PIMP is similar for both chromosomes, the landscape in CMP-GP depends on the terminal and non-terminal sets. Arguably, smaller sets would allow for self-reinforcement to commence sooner and stronger, while larger sets should slow down consistent choice but introduce complexity, given that a random-like initialization process is maintained. Comparing between approaches, the behavior of CMP-GP is more consistent with a less rough landscape with larger basins of attraction that allow for runaway processes to last longer, thus resulting in higher correlation values. Reduced dispersion between runs is also in agreement with a smoother landscape. Arguably, by changing the terminal and non-terminal set sizes and compositions, the self-reinforcement process can be tuned and adjusted, which, as will be seen, can hold interesting potential.

Figure 6.27 shows Spearman's correlation between attractiveness and fitness rankings among individuals in the same mating pool, which further expands on the character of evolving mating preferences. Similarly to PIMP, the tendency of the metric goes towards a negative correlation on all four functions, even though there appears to be an initial bias towards positive correlations. This outcome is not fitting with a Wallacean good sense view of Mate Choice but is very fitting with a Fisherian good taste model. Focusing on the assumptions of each model, Fisherian processes can result on ornamentation that are either agreeing or disagreeing with fitness valued characteristics, making it so that the process is undoubtedly Fisherian by rejection of the Wallacean assumptions. Despite the central tendency of the metric, there's some dispersion in individual runs, significantly more than observed in PIMP across all four problem instances. In PIMP, such a behavior was mostly seen on one function, and it has been suggested that it may be due to function specific particularities. However, the same can't be said for CMP-GP, where runs with a high correlation between attractiveness and fitness (sometimes very high) are more widespread. There are a few interesting remarks to be made regarding such a behavior: the representation used in PIMP was known to be able to closely represent the fitness function, thus being certainly capable of evolving in the same direction; with that being true, the conditions to do so seem quite challenging, with most runs evolving in the opposite or neutral directions; the representation used in CMP-GP freely evolves an evaluation function that accesses a much more limited amount of information, which it combines through interactions; it

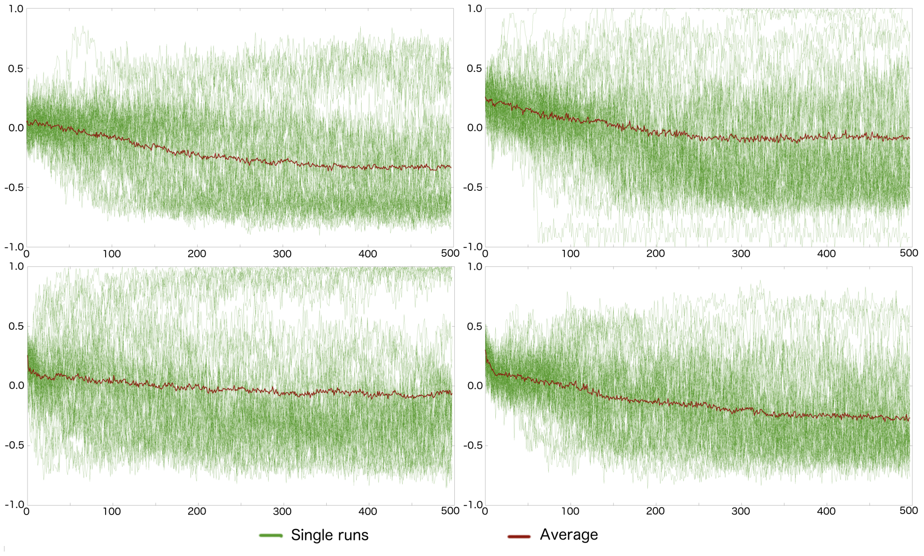

Figure 6.27: Evolution of Spearman's correlation between phenotypic attractiveness rankings obtained by each acting female and the fitness rankings of it's mating candidates. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

was not a given that such a representation would be able to evolve evaluation functions that correlate with fitness.

Despite showing such an ability, the observation does not imply in any way that the evolved attractiveness functions are similar to the fitness function, nor that the model has such capabilities. It does however suggest that given appropriate conditions, the representation is capable of perceiving and selecting mating partners through honest indicators of fitness. This doesn't mean that such a behavior should be the preferred outcome (PIMP results suggest otherwise), an argument that is likely to strongly depend on population status and dynamics. Nonetheless, the contrast between the two approaches is quite interesting, and suggests a greater freedom of choice (at least regarding its correlation with fitness) achieved by CMP-GP, even if relying on less information on mating candidates. An increased freedom should contribute positively to the role of Mate Choice and to its wandering or exploratory character.

Further analysis based on this data alone is difficult, but a few remarks are worth being summarized about the CMP-GP model , in comparison to the previous one: i) as described in Chapter 5, the model makes no assumptions on the character of preferences, which is empirically demonstrated by their ability to emerge in various directions; ii) agreeing attractiveness and fitness rankings are more common in CMP-GP than in PIMP, showing the representation's influence on the character of Mate Choice; iii) initial conditions definitely have an impact on the outcome of evolving mating preferences, with evolving mating functions having an increased freedom when compared to an ideal partner representation; iv) just like before, agreeing metrics may result from conditions being favorable for preferences to match the rankings of fitness or due to an ecological pull on females towards the space favored by pre-existing preferences; v) the emergence of varying choices seems to be less dependent on function specific characteristics than what was observed with PIMP.

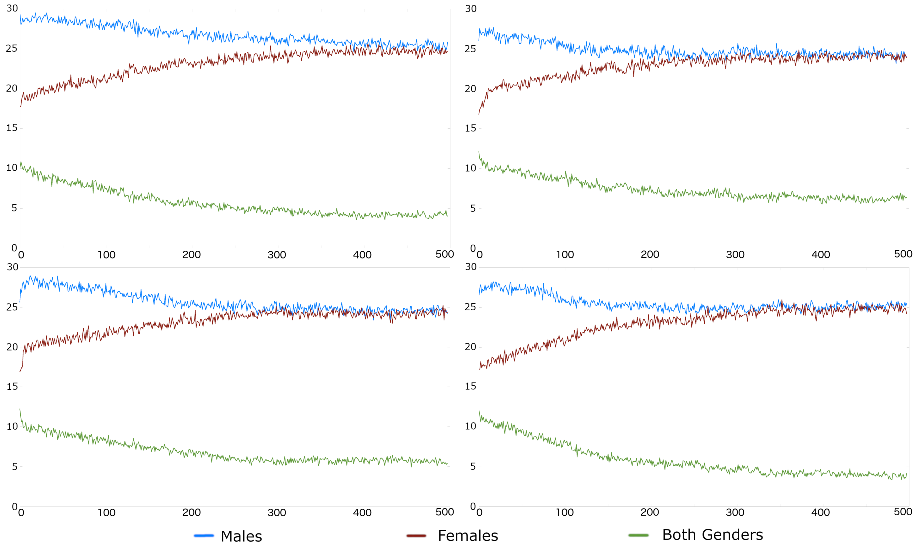

Figure 6.28: Evolution of average population composition by gender. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

Gender distribution analysis can further contribute with insights on a population level. Figure 6.28 shows the following data: i) average number of individuals who are exclusively selected as females; ii) average number of individuals who are exclusively selected as males; iii) average number of individuals who are selected simultaneously as females and males. The same remarks regarding the pool randomness discussed in the analysis of PIMP apply here. The conclusions are quite similar and are also transverse to the studied functions, showing the same increased separation of genders in the population, with individuals specializing in being selected through a specific role, for an increased competitive chance. The same analysis as before maintains for CMP-GP, being summarized as such: a subset of the population is able to be selected for the female role by achieving good enough fitness during evaluation on the target problem (females and hermaphrodites); male selection is initially likely to be random so all individuals have fair chance to be selected (males and hermaphrodites); as self-reinforcement builds pressure on male selection towards a subset of preferences, fewer and fewer individuals are able to compete for that role, reducing both the size of the males-only group and the intersection group; as a side effect, the size of the females-only group increases due to the intersecting group being emptied, even though selection pressure is likely to promote competitiveness among females. In comparison with PIMP, there's a similar tendency in the composition of the groups, however, CMP-GP seems to assert higher pressure on the selection of males, causing its group size to decrease more visibly (which is inline with the increased momentum shown in Figure 6.26). Interestingly, a balance in average pressure in the selection of individuals for each role seems to be achieved at the end of the evolutionary processes.

In summary, similarly to the discussion regarding PIMP, this analysis validates that the model and its assumptions are suitable for emerging Mate Choice, through the self-reinforcement of mating preferences alone. Moreover, the results are compatible with a Fisherian view, with preferences having the liberty to evolve in any direction. When compared with PIMP, CMP-GP suggests a higher degree of freedom, potentially due to differences in representation. While the central tendency of evolving preferences are to have a neutral or opposing correlation with fitness, there is a wider presence of varying behaviors, which can't be disregarded as a particularity of a given function or other factors. Regarding population composition, there seems to be a balance in selection pressure for each role towards the end of the evolutionary process, and a specialization of individuals into one of the two roles for an increased competitive edge. In comparison with PIMP, this effect seems to emerge with increased strength, showing a higher pressure in the operation of selecting males.

6.5.2 Perception Analysis

Complexity and Dimensionality analysis, as discussed, is strongly subjected to the assumptions of each approach. Whereas on PIMP, the second chromosome represents an ideal mating partner, and therefore gathered metrics are related to that representation, in CMP-GP the second chromosome represents an evaluation function, and so the interpretation of complexity and dimensionality is that for which they were initially designed. Dimensionality relates to perception of signals in mating candidates and complexity relates to interactions between such signals resulting in an attractiveness value. As introduced, such features freely evolve within the second chromosome along the evolutionary process. While for each particular approach the metrics are valuable in their own way, potential comparisons are limited by different interpretations and assumptions. Despite the limitations, they are still highly valuable for the behavioral analysis of CMP-GP an should be capable of providing relevant insight. To support the analysis, Figure 6.31 allows for a view of how each metric evolves on average for the four studied functions, while Figure 6.29 and Figure 6.30 show a pairwise comparison of entropy and contrast obtained through attractiveness and fitness in each selection step, averaged over the whole sample.

Focusing on entropy first, which reflects the ability to distinguish between mating candidates thus making it a requirement for Mate Choice, it is expected for the evolving evaluation functions to compete with the fitness metric. Unless mating candidates are similar, in which case the entropy on any evaluation function is zero, it is expected that entropy remains above zero for attractiveness, or far away from -1 in the average pairwise comparison in the graphs in Figure 6.29. Having an entropy difference of -1 would imply that the evolving evaluation functions were incapable of distinguishing between mating candidates when they should, thus making the choice operation comparable to random selection. Although it was already hinted in previous graphs that such would be unlikely, Figures 6.29 and 6.31 offer proof that the approach succeeds in doing so competitively with the fitness function on most runs and on average. While this was more or less a given in PIMP, the outcome is particularly relevant for CMP-GP as females access only a few pieces of information on each mating candidate, which may or may not be used in a relevant way to rank them, in contrast to what happens during fitness evaluation and in PIMP, where whole information is used in a way that is human designed.

As expected, the behavior is different from what is observed in PIMP. Initialization of mating preferences abides by different rules (which carry the issue of erroneous evaluations as infinity but makes it very unlikely) but more importantly, an healthy initial diversity makes it likely that assessing a few data points as signals is sufficient to assemble evaluation functions that distinguish between mating candidates just as well (or closely) as the fitness function. This effect is seen in Figure 6.29 both regarding the

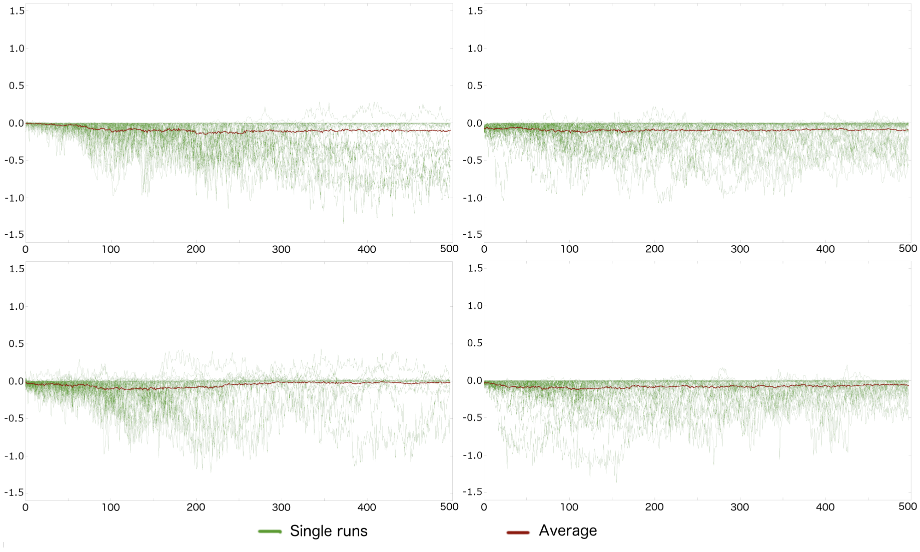

Figure 6.29: Evolution of Evaluation Entropy differences between using Mate Choice or Fitness base selection. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

average difference value and each particular run. However, as the population evolves and potentially converges, distinction of mating candidates must rely on fewer differences, which makes the task increasingly more difficult. As shown in Figure 6.29, entropy differences slowly decay and dispersion between runs becomes more noticeable. Interestingly, the decaying effect is not ongoing throughout the whole process, with the average tendency changing direction towards more competitive values in all four functions. Dispersion is also seen to reduce in later generations after an initial period. While the differences decay can be traced to an initial yet minimal decrease in average attractiveness entropy, as shown in Figure 6.31, the later recovery is more likely a result of a drop of fitness entropy than an ability for the evolutionary process to increase average attractiveness entropy. Since the evaluation function is static, that drop is a result of candidates convergence, so that differences are zeroed for any metric.

A few points are worth mentioning: i) it's likely that for the current setup, the initialization procedure allows for close to maximum average entropy to be achieved in initial populations (as shown in Figure 6.31, leaving very little to improve on the metric; ii) as fitness entropy drops, attractiveness shows sturdiness (probably due to interactions between signals) which allows it to regain some ground; iii) often, differences are zeroed or reduced on average to residual values; iv) a more distinctive ranking of mating candidates is sometimes achieved by the evolved mate evaluation functions, on different functions and on different stages of the evolutionary process, which shows the approach's ability to do so under certain conditions. Arguably, given the opportunity for more signals to be accessed on candidates and for larger trees to be maintained, attractiveness could potentially hold closer or surpass fitness in regards to entropy, specially for the korns-2 and the vladislavleva-7 functions, which are multidimensional and should represent a larger search space. In the end, while attractiveness didn't achieve a positive average entropy difference often, it was able to perform closely to the fitness function ,which has been designed by hand rather than built and evolved

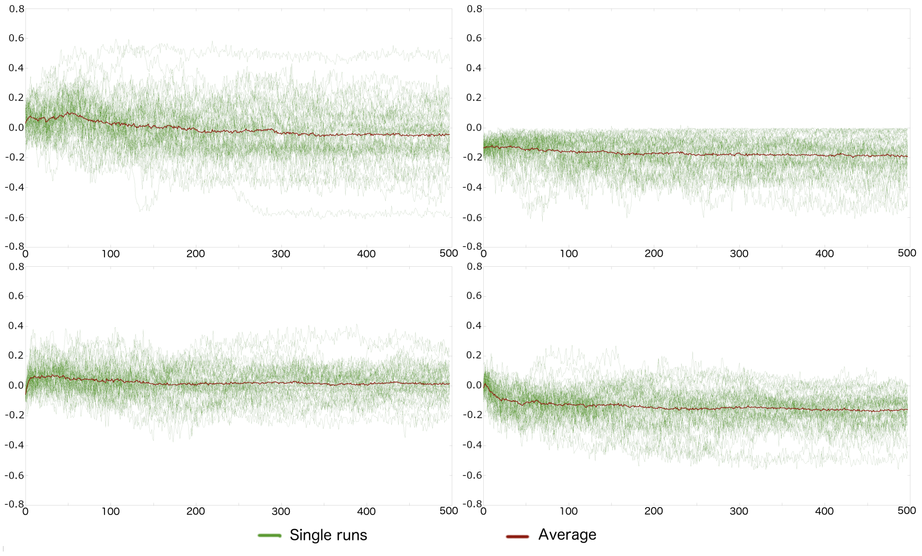

Figure 6.30: Evolution of Evaluation Contrast differences between using Mate Choice or Fitness base selection. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

based on rather restricted node sets.

Contrast, as previously discussed, is a way to measure how candidates distance from each other according to a given metric. While for fitness the metric depends solely on their location in the search space, attractiveness through complex evaluation functions uses more than an aggregation of signals to determine distances between individuals, resulting on non-linear relations. Therefore, the fitness and attractiveness differences of contrast between two individuals is very unlikely to be zero unless the two individuals are similar. On the one hand, fitness (or PIMP) contrast can rely on all available data points, but on the other hand, contrast in CMP-GP can profit from operations between signals to model comparisons between individuals. Still, its characteristics hold: while being more sensible to distances, it's still a less relevant metric than entropy in regards to its significance on a tournament like operator; may be skewed as a central representation of distances within a sample of individuals; the squashing function mitigates disproportionate differences but may also scale up small ones.

A look into the graphs in Figures 6.30 and 6.31 allows for some relevant observations: i) there's a general tendency for attractiveness contrast to decay slowly along the generations; ii) regarding average contrast differences, the effect is more significant in multi-variable functions, whereas on 1-variable ones differences are mostly positive; iii) while the effect on entropy is subtle, there seems to be a linkage between better performing average entropy differences and positive average contrast differences. These observations fall into what would be expected from freely evolved mate evaluation functions with non-linear pairwise contrasts. After all, such characteristics are due to promote a higher variation in attractiveness values, which results in the dispersion between runs that can be seen in Figure 6.30. Perhaps also interesting are the evidences that the established conditions for evolving mate evaluation functions are more appropriate for 1-variable functions, in regards to promoting high contrast between mating candidates, hinting that perhaps the ability to maintain larger mate evaluation functions

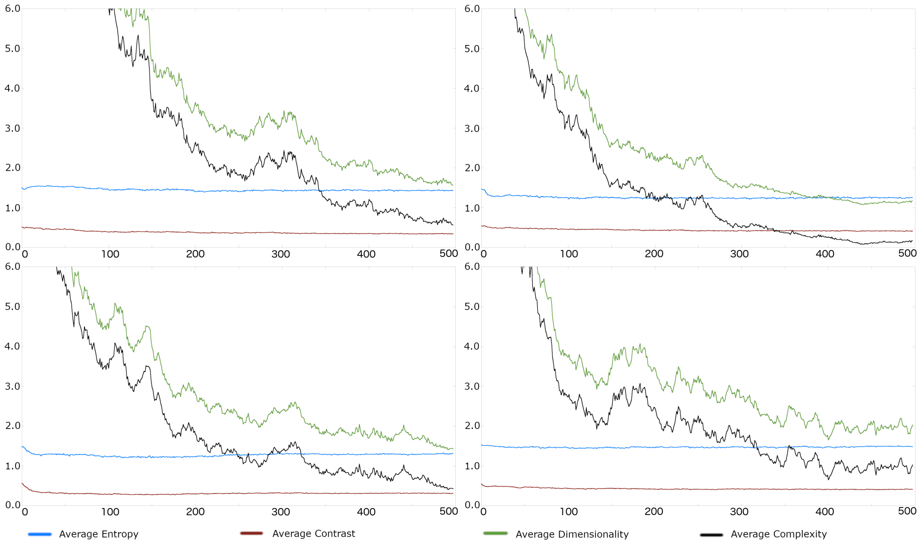

Figure 6.31: Evolution of average Entropy and Contrast as well as average Dimensionality and Complexity. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

or even using larger terminal and non-terminal sets can improve the impact of Mate Choice on multi-dimensional search spaces. This analysis is relevant only in regards to contrast, and may not hold true for population level behaviors.

Just like in PIMP, despite the differences, why there's an evolutionary tendency towards simpler mate evaluation functions is a relevant question. Notice that with this particular representation, the discussion on preferences genotype complexity has a whole different context from PIMP, with interactions and signals being directly encoded in the second chromosome. Nonetheless, the discussion on PIMP as to why simpler preference trees are less volatile by destructive crossover also applies here, and partly explains their competitive edge. Still, it's important to see how dimensionality and complexity impact entropy and contrast in search for differences that can further explain the spreading of simpler mate evaluation functions. For the purpose, Figures 6.32 and 6.33 show how such features influence the outcome of evaluating mating partners in a rather straightforward way, and in a different detail attained by Figure 6.31. In short, they allow for a comparison between multiple dimensionality and complexity values, competing among themselves as a byproduct of Mate Choice. While they don't offer information on the central tendency of the features, or their distribution, the figures provide means to compare each particular structure with their respective outcome in regards to entropy and contrast (Figure 6.32 and Figure 6.33 respectively). In each graph, information from all active females in the first 150 generations of all 50 runs are clustered together and organized by dimensionality and complexity. As a result, each represented dot aggregates information from many choice steps where mate evaluation functions share the same dimensionality and complexity (not necessarily other features). For each dot, its color represents the average value obtained by all selection steps that it represents. Color ranges are adjusted for each particular function to better fit the data rather than using a fixed range, to better display differences.

Looking at Figure 6.32 first, a few general observations can be made: i) with the ex-

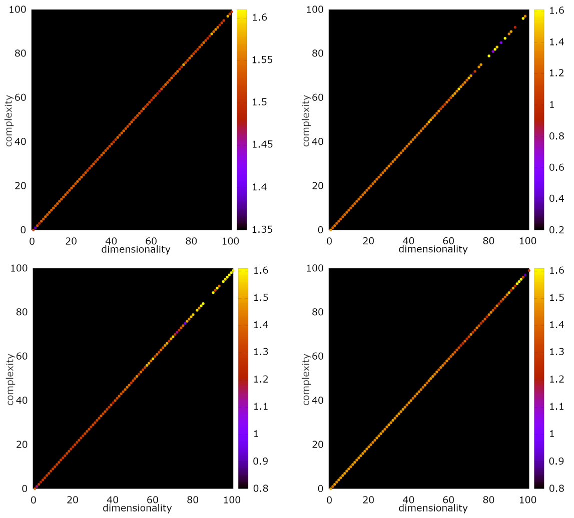

Figure 6.32: Relation between Entropy, Dimensionality and Complexity in the first 150 generations of all runs. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

ception of a few settings, entropy seems to maintain reasonably high values throughout the sample; ii) a closer look shows more extreme values towards the top right corner, with a higher density of particularly high entropy values clustered in that area; iii) the effect is more evident on some functions such as in keijzer-3 than in others. When taking contrast into account, Figure 6.33 shows a higher sensibility, with differences being easier to spot: i) functions keijzer-3 and vladislavleva-7 show an indisputable increase associated with higher dimensionality and complexity; ii) on function korns-2, variation is very subtle but still within the expected behavior; iii) in the nguyen-4 function, extreme values gather at the top right corner, with the remaining area showing a slow but stable degrading towards to bottom left. While this analysis is relevant, a more careful look into Figure 6.31 suggest that individuals contributing to the samples reproduced in Figures 6.32 and 6.33 are not equally distributed, populating mostly the bottom left area of each graph. This skewness may account for the presence of more extreme behaviors associated with higher dimensionality and complexity, which may be more visible due to smaller sample sizes. Therefore, while as a whole the relation of highest entropy or contrast with large dimensionality and complexity seems sufficiently clear, a conservative analysis should contribute to better sustained conclusions. For the purpose, the remaining discussion will focus on instances ranging up to approximately 60 interactions and signals, where the contributing sample of mate evaluating functions is denser. If one focuses on such a subset, the behaviors observed in all functions are more in agreement with each other, both regarding entropy and contrast.

Regarding contrast first, the graphs show that for the large majority of dots, their color represents a higher value than the neighborhood to their left even though differences are subtle, on a well defined scale from lower to higher contrast (particularities of each function affect each scale in their own way). Regarding entropy, because of its rank based nature, the visualized scale is more homogeneous but still present, with differences being much less visible due to a many-to-one relationship between dis-

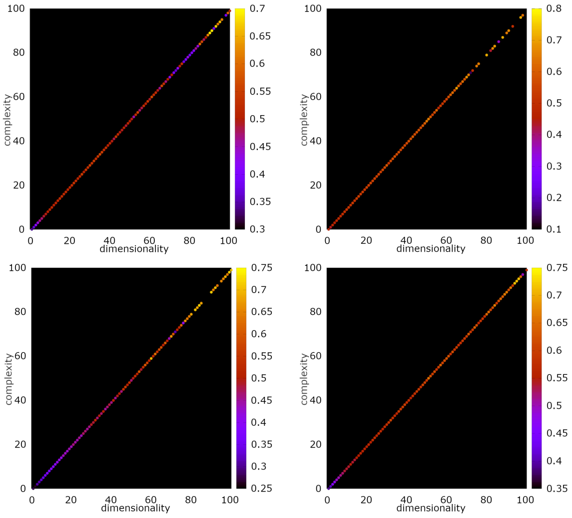

Figure 6.33: Relation between Contrast, Dimensionality and Complexity in the first 150 generations of all runs. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

tances and ranks. A few considerations are worthy of being highlighted: i) despite the association of higher entropy with higher dimensionality and complexity, small mate evaluation functions maintain entropy competitively high, so that the gains of maintaining high dimensionality and complexity is residual or plainly non-advantageous; ii) due to the tournament-like dynamic of the operator, the ability to distinguish one individual from the others may be sufficient for self-sustained Mate Choice, as an extreme case; iii) contrast allows for a more detailed illustration on how dimensionality and complexity may contribute to choice consistency (in contrast to random choice) if given the opportunity to make a difference.

The above observations while suggesting a relation between higher dimensionality and complexity with larger values of entropy and contrast, show that on this particular context, differences may be too small to leverage benefits for maintaining such features. Therefore, they argue in favor of low dimensionality and complexity having a fair chance of competing to thrive in the population through sufficiently high entropy, although contrast sustains the theoretical value of mate evaluation functions with higher dimensionality and complexity to provide better means to distinguish between mating candidates. Such differences have no chance of truly impacting the tournament-like operator in a significant way and are thus not directly selected for. Smaller sized trees have therefore a proper chance at maintaining choice consistency thus explaining the central tendencies of average metrics in Figure 6.31.

In summary, higher entropy and contrast seem more likely among individuals with mate evaluation functions of higher dimensionality and complexity. However, on top of such individuals being less frequent in the studied sample, their gains in entropy and contrast don't seem to be sufficiently meaningful to give them evolutionary advantage. Because simpler trees are able to maintain entropy at sufficiently high levels to successfully compete, and due to being boosted by higher resistance to destructive crossover, mate evaluation functions of lower dimensionality and complexity spread through the

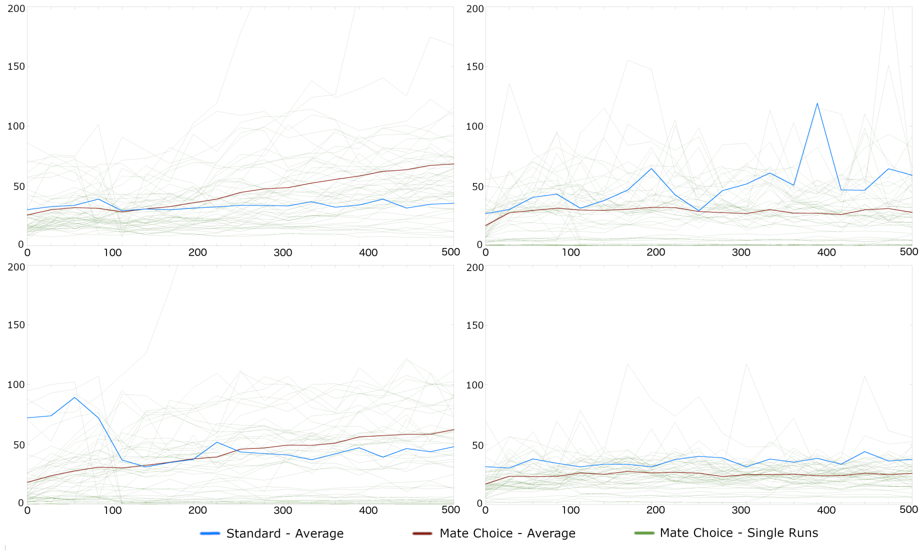

Figure 6.34: Population edit tree diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

population more easily. The effect is not due to a lack of ability of preference trees of higher dimensionality and contrast to promote higher entropy and contrast but rather due to simpler ones being capable of maintaining competitiveness. Still, differences in entropy and specially contrast, although sometimes subtle, have been documented.

6.5.3 Effects Analysis

Selection and perception analysis have provided insight into the inner workings of Mate Choice through evolving mate evaluation functions but have contributed tangentially to understanding population dynamics and how the process influences search efforts on a higher level. The current section will expand on that topic, by covering genotypic and phenotypic measures of diversity within populations and genders as well as by addressing the algorithm's ability to promote and maintain innovation. Figures 6.34 to 6.47 will provide backing materials for the discussion, tackling particular and relevant topics. Moreover, comparisons are going to be made with PIMP, to highlight both similarities and differences introduced by the two diverging representations.

The importance of diversity maintenance on search optimization has been previously discussed. For analysis purposes, an overview of how CMP-GP relates to population diversity can be found in Figure 6.34, including each particular run and the overall average tendency. Moreover, the figure includes the average value for the Standard approach as a mean for comparison. A first look at the results allows for a few observations that are worth highlighting: i) the behaviors are different between the four functions; ii) in functions nguyen-4 and keijzer-3 the average edit tree diversity increases over time and overcomes the results of the Standard approach; iii) contrarily, despite an initial boost, the average metric remains more or less stable in functions korns-2 and vladislavleva-7 at levels below those achieved by the Standard approach. Comparisons with PIMP add important details, through similarities and differences: i)

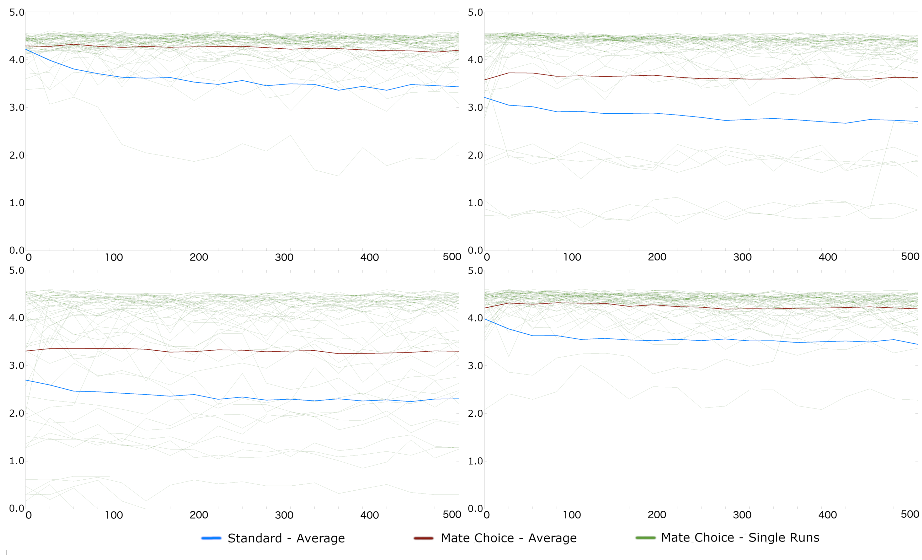

Figure 6.35: Population entropy diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

overall, there's smaller variation between runs, with CMP-GP being more conservative with how large population diversity can get, suggesting a less daring character or less propensity for exploration; ii) the number of runs where the population diversity remains close to zero is slightly larger than seen in the analysis of PIMP. Together, these factors have a relevant impact on the average edit tree diversity. In korns-2, both factors are particularly relevant, reinforcing the modest average value, whereas in keijer-3, the variability, although smaller in CMP-GP, is sufficient to offset the second factor. The first factor is also largely relevant in vladislavleva-7 while nguyen-4 allows for the behavior to be more similar to PIMP.

The reasons behind these observations and the differences between Mate Choice approaches require a deep analysis on the impacts of CMP-GP. Moreover, the analysis will help contextualizing and interpreting the results in Figure 6.11 by addressing the following topics: i) trees may be bloated by no-value sub-trees that don't translate into phenotypes but are still considered relevant by edit tree distances; ii) the use of a pivot to measure edit distance diversity can be subject to skewness, depending on how the pivot positions itself in the population; iii) the observed metric takes into account the whole population, including those individuals that have no impact on future generations by not being selected; iv) gender dynamics can interfere with population diversity and potentially boost it by increasing their distance, reducing its value as an accurate metric for diversity. Each of this factors can and will be addressed to some extent and as independently as possibly for proper insight on diversity. Moreover, the analysis should shed some light on the differences between PIMP and CMP-GP, and suggest root causes for the discrepancies regarding their effect on population dynamics.

Without relying on the troublesome and demanding work of analyzing each individual independently, or making pairwise comparisons in an attempt to address the first two points of discussion, there are alternative methods that can provide clues. For instance, one may look and compare the behaviors of genotypic and phenotypic diversity and seek validation. Ideally, genetic diversity should translate into phenotypic diversity, particularly when using an evaluation function sensible to small changes, which Sections 6.4.2 and 6.5.2 suggest to be the case. Following the analysis in PIMP, Figure 6.35 provides data on fitness entropy within each population and on average for CMP-GP, as well as the average value for the Standard approach. Differences between genotypic and phenotypic diversity are quite noticeable for both plotted approaches. Firstly, as discussed before, the apparent maintenance of average edit tree diversity in the Standard approach is not matched by the same behavior regarding fitness entropy, which declines over time in a converging behavior. This difference suggests that the apparent genotypic diversity and particularly its stability, can be partially boosted by the two first presented factors, questioning the approach's true ability to maintain diversity. Regarding CMP-GP, the observed behaviour is the opposite, with the average fitness entropy remaining on average quite close to maximum value and stable along most runs on all functions. There are however a few other particularities worth bringing up: i) entropy results on korns-2 and keijzer-3 functions reflect the presence of instances with small average diversity, both through individual runs and the average value, however, with the exception of very few runs on the keijzer-3 function, the results discard the possibility of full phenotypic convergence; ii) on all other instances, even on those functions where the average edit-tree diversity was subpar to the Standard approach, results suggest that differences translate better into the phenotypic form. While this offers no definite proof for improved diversity among CMP-GP experiments, it suggests that while the genetic differences span over a smaller interval for CMP-GP when compared to the other two approaches, individuals are distinct and vary within that interval. As a side note, entropy analysis offers some advantages such as not considering potential non-relevant sub-trees and not relying on a pivot for comparisons, or reflecting distances such as those potentially found between genders, offering a non-distorted view of the population.

Regarding the third and forth discussion points, contributions can be made by assessing inner-gender behaviors. Figures 6.36 and 6.38 show how individuals in CMP-GP contribute to each gender's edit-tree diversity. Figures 6.37 and 6.39 show phenotypic data. For each graph, the collected samples are those individuals who have been selected for either reproductive role, thus focusing on their impact rather than on non-competitive individuals in the population. Regarding the Standard approach plotted for comparison purposes, the selected samples are the same has discussed in the analysis of PIMP, being sufficient to say that because similar rules apply to each tournament operator, the selected individuals are representative of the same asexual population, which is reflected by mirroring behaviors in the female or male related figures.

Overall, the figures allow for further distinctions between CMP-GP and each of the other approaches. Interestingly, despite details that will be addressed below, the behaviors are much in agreement with what was observed along the analysis of PIMP. Summarizing the observations regarding the Standard approach for reference, the observed population diversity tendency does not extend into the selected individuals, which, through the combined selective force of the tournament operators, end up having a smaller and smaller average diversity. These results are supported by the data in all four figures (on genotypic and phenotypic measures) and suggest that a part of the population contributing to higher diversity has no chance to reproduce for not being sufficiently fit. In comparison, CMP-GP shows a quite different behavior, one that is for the most part in-line with what was observed with PIMP. Focusing on females first, the diversity is kept considerably higher than on the Standard approach, even on the two functions where population edit-tree diversity was inferior. This is supported by

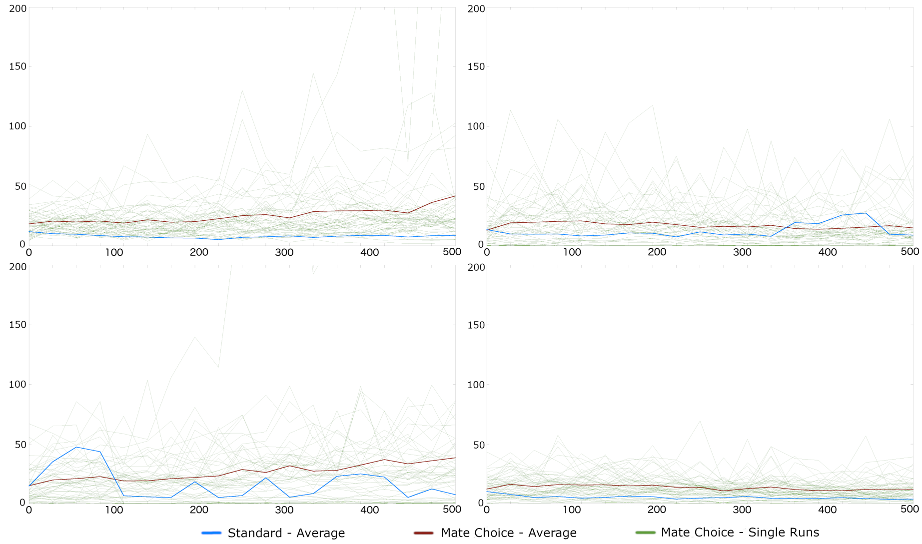

Figure 6.36: Females edit tree diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

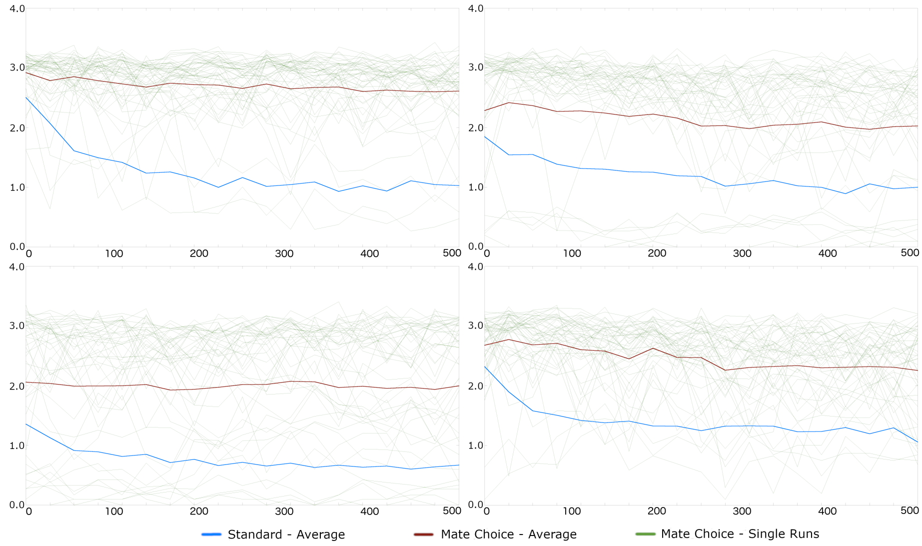

Figure 6.37: Females entropy diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

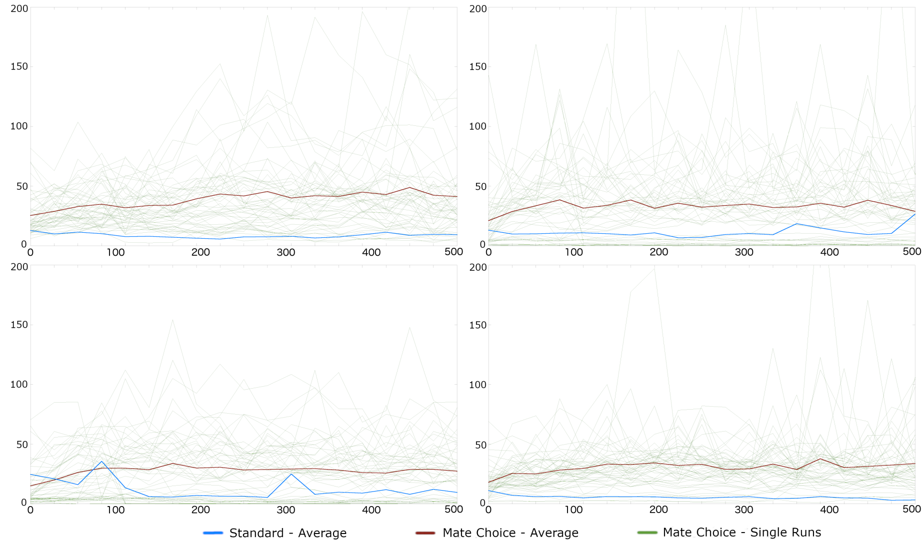

Figure 6.38: Males edit tree diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

both Figure 6.36 and Figure 6.37 and suggests an healthier distribution of reproductive opportunities among candidates for female roles, allowing a wider variety of genes to pass on to future generations.

There are however a few remarks that should be brought forward. CMP-GP shows a slight increase on average edit-tree diversity over the evolutionary process in the nguyen-4 and keijzer-3 functions, similarly to PIMP, however, it also shows a slight decrease for the korns-2 and the vladislavleva-7 functions. There's also likely an impact from close to zero runs on korns-2 and keijzer-3, which becomes more noticeable when entropy levels are considered. Moreover, the entropy analysis highlights the lower diversity on the korns-2 and vladislavelva-7 functions, and perhaps more importantly, a decay in phenotypic diversity on all functions (but more noticeably on these last two) when compared to PIMP. This last observation is new to CMP-GP and may represent a starting point to explain the differences in population diversity among the two Mate Choice approaches. Several interlinked factors may be considered: i) it's possible that unlike PIMP, CMP-GP can't completely counteract the selective pressure put on females by the fitness based selection operator; ii) the introduction of disruptive individuals through interactions with males is smaller and thus less impacting than in PIMP; iii) such individuals have a higher chance of being hermaphrodites, thus having a greater take over effect in the population.

Continuing the discussion on gender dynamics, analyzing diversity among males can further make contributions which are also important to address these questions. Similarly to the female gender, the male population has a considerably higher edit-tree diversity than seen in the whole population analysis and also in comparison to the Standard approach. This outcome is analogous to the one achieved by PIMP, despite representing a higher difference from the female population. Also, just like in PIMP, variability between runs is quite high on all functions, as an impact of self-evolving mate evaluation functions and their unpredictability. As a side note, there's still a

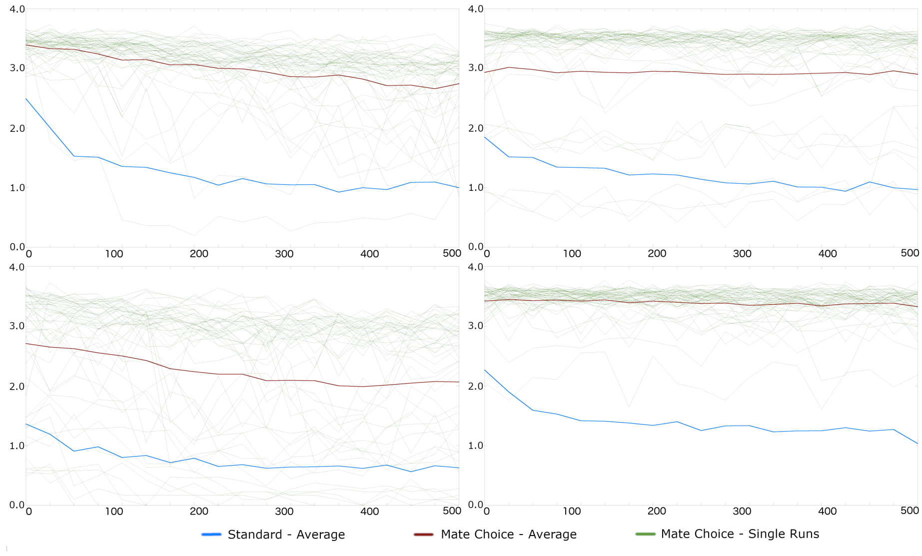

Figure 6.39: Males entropy diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

higher impact of instances with close to zero diversity in both the korns-2 and keijzer-3 functions. When looking at fitness entropy, differences between the approaches become much more visible, particularly on the korns-2 and the vladislavleva-7 functions. On all four functions the initial and overall value is higher for males than for females but, while on the other two functions results are in-line with those seen in PIMP, in these two functions the average entropy decay is very subtle.

As previously explained, a higher initial edit tree diversity and fitness entropy in males compared to females can be straightforwardly explained through the initial random character of Mate Choice. However, explaining the sustainable increase in male edit-tree diversity requires at least one of two behaviors to take place: i) competing mate evaluation functions favor two or more lines of evolution in males, whose distance contributes to the increase in diversity; ii) mate evaluation functions give preference for extreme features, selecting the most diverging individuals and thus increasing male inner diversity. Arguably, both behaviors, as long as they introduce selective pressure on males can account for the drop in fitness entropy, however in order to account for the differences between the two observed behaviors (in functions ngyuen-4 and keizjer-3 and in functions korns-2 and vladislavleva-7), further discussion is needed. Figure 6.40 addresses the first point by showing the average diversity among mating evaluation functions, which leads to the conclusion that despite occasional variations, the hypothesis can be rebuked, as preferences strongly converge into an agreeing structure. Secondly, Figure 6.41 plots the average distance between paired parents, and while showing an overall tendency for increasing pairing distances, the results show function-wise differences and meaningful evidence to explain the behavior differences seen previously.

Focusing on the nguyen-4 function first, the observed behavior is very similar to that generally produced in PIMP, with preferences convincingly acting in a negative assortative mating fashion, and consequently fueling the male population diversity which

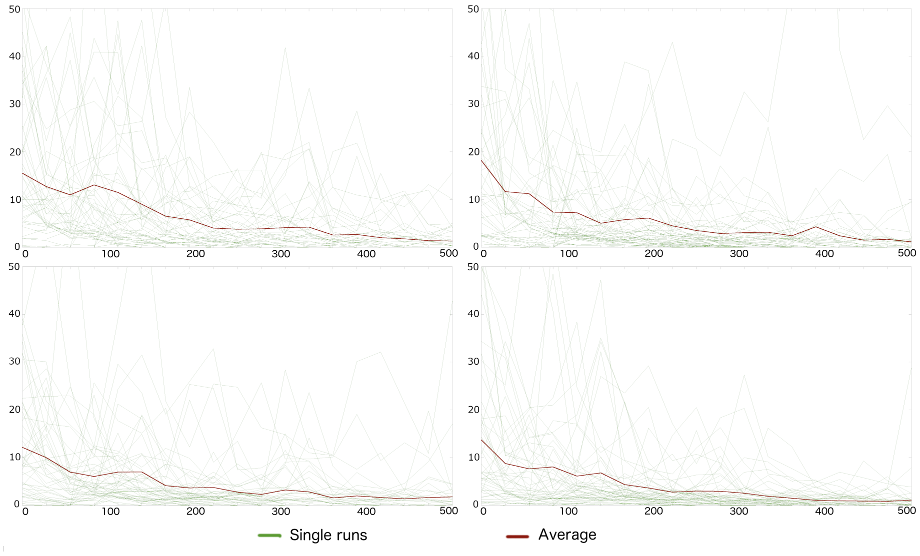

Figure 6.40: Female preferences edit tree diversity at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

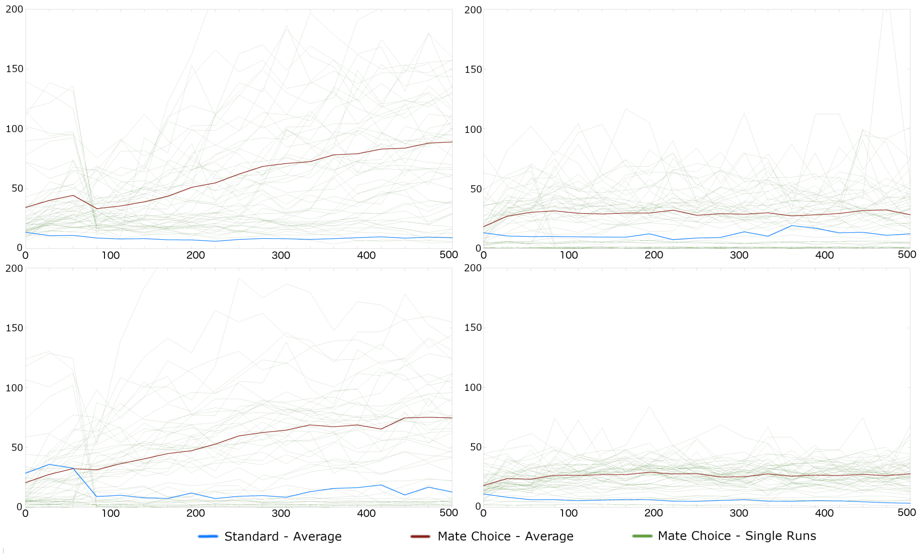

Figure 6.41: Edit tree distance between pairs at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

also helps introducing new genetic material in the female one. As a side effect, the increasing distance between genders is noticeable in the overall population diversity. In the keijzer-3 function, the behavior is overall similar, however, as previously suggested in Figure 6.27 through the presence of positive correlations between attractiveness and fitness, evaluation functions can benefit similar thus fit individuals in some runs, in a somewhat positive assortative mating way. Figure 6.41 shows therefore two strategies, with the preference for extreme individuals still being capable to offset the other. However, the impact can still be seen in both female and male populations, where some instance end up with very little diversity, even though the consequences are smaller in the comparatively higher average male population diversity. Due to the female population being bounded by the fitness based operator, the effect takes a higher toll by contributing to all three suggested hypothesis regarding why diversity lowers. In few words, benefiting males with very low dimorphism will reduce the chances of having disruptive females, while also allowing individuals to more easily taking over by acting as both genders (Figure 6.28 shows a higher intersection of genders than in the nguyen-4 function). Together they contribute to a higher exposure to selection pressure.

A parallelism between nguyen-4 and vladislavleva-7 as well as between keijzer-3 and korns-2 can be made, particularly in regards to positive correlations in Figure 6.27, however when their full behaviors are compared there's one major difference whose root cause has a lot to do with the distance between mating partners. Whereas in both nguyen-4 and keijzer-3 evolving mate evaluation functions gradually benefit more and more diverging individuals, allowing for a continuously increasing selective pressure on males, Figure 6.41 shows that ability to be somewhat limited in the korns-2 and vladislavleva-7 functions, with distances between mating partners being more conservative and apparently bounded. As a consequence, the runaway effect in preferences and traits that fuels continuous exploration in the nguyen-4 and keijzer-3 pair is limited, substituting an increased selective pressure and associated momentum with an equilibrium between mating preferences and traits, which has a chain effect on all the metrics considered before. Figure 6.39 shows the reduced pressure put on males, with reproductive opportunities being more balanced. Diversity within males can still be maintained but the exploratory factor is contained, as more extreme offspring will likely be discarded. Consequently, the male population can only drift as far as the preferences push it, remaining in relative proximity to the female population. In a way, this hinders it's capacity to explore unbounded, and potentially inject new and ever diverging genetic material in the female population. Curiously, even though it's a side effect of preference representations and tree structure, this control ends up having a similar effect to what would be expected from associating costs to extreme ornaments, pushing males toward an equilibria (imposed by female choice rather than by trait cost). The impact of such a strategy should be similar to assortative mating where preference is given to individuals that distance just right from females. As a result, female diversity is kept lower and slowly decaying when comparing with negative assortative mating examples (such as on the other two functions or on PIMP).

In the end and following this discussion, the relatively small population edit-tree diversity is a result of three factors: i) smaller male diversity; ii) smaller female diversity; iii) smaller distance between females and males, which impacts both of the others. Regarding that last factor, a few things are worthy of note. Firstly, the korns-2 function, as discussed regarding the keijzer-3 function, suffers the same effect caused by positive correlations found in Figure 6.27, with the main difference being that the approach has no chance to counteract its effects on the average metrics, making its impact even more noticeable. Still, it seems more capable of variation than in the vladislavleva-7 func-

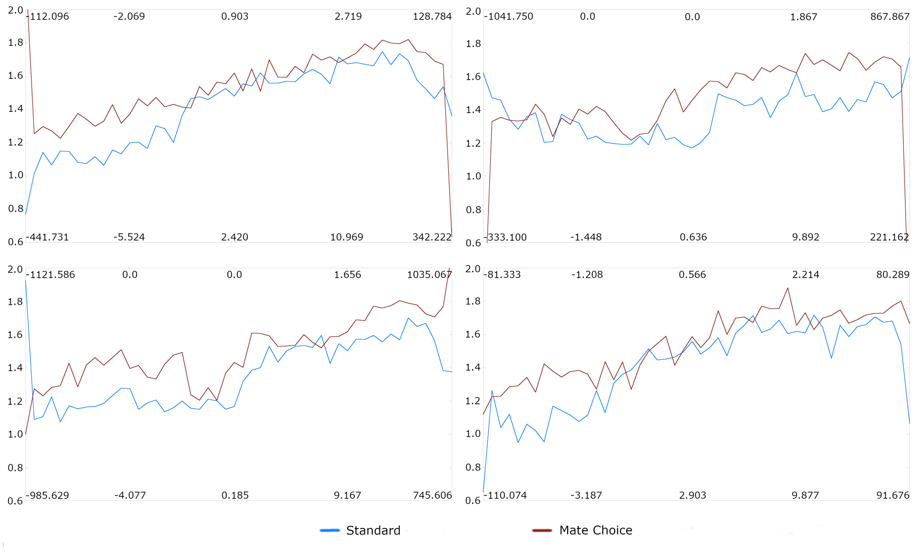

Figure 6.42: Survival rate for females in all 50 runs, bucketed and ordered by innovation rate. Quartile information for CMP-GP shown at the bottom x-axis. Quartile information for the Standard approach included in the top x-axis. Four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

tion. Secondly, the Figure 6.28 also shows the increased intersection between genders for the same reasons regarding keijzer-3. Thirdly, korns-2 and vladislavleva-7 are multidimensional functions (respectively 5 and 2 variables) which reinforces the idea that in respect to the current analysis, the size of terminal and non-terminal sets, as well as the initialization of individual preferences for each signal may not be the most suitable, potentially holding back the results of CMP-GP, specially regarding its exploratory potential. This outcome is likely tied to the previous analysis on perception, particularly regarding the ability of preferences to distinguish between mating candidates (see Section 6.5.2).

Despite the differences between the behaviors produced by CMP-GP, it remains important to assess the neophiliac character of Mate Choice, in order to verify if the evolving mate evaluation functions are capable of contributing to innovating solutions in a sustained effort rather than a fortunate outcome. For the purpose, a similar analysis to the one covered in PIMP will follow, supported by Figures 6.42 to 6.47 and comparisons will be made both with the Standard approach and with PIMP. As a reminder, population conditions are not the same in the three considered scenarios, and has will be seen, are impacted by gender dynamics in meaningful ways, making it so that the analysis needs to be made with such differences in mind.

Figures 6.42 and 6.43 relate innovation to survivability, respectively through the x and y axis. A full description on how the plots were built can be found in Sections 6.2.2 and 6.4.3. In summary, for each approach, females are collected at each 25 generations on all runs into one large sample, which is organized along the x-axis according to how they distance to the their previous generation's inner-gender edit-tree distribution. Individuals that are close to zero are in the neighborhood of last generation's average distance, representing therefore as much innovation as the average individual in that population. Those that are placed at negative values are closer than average to

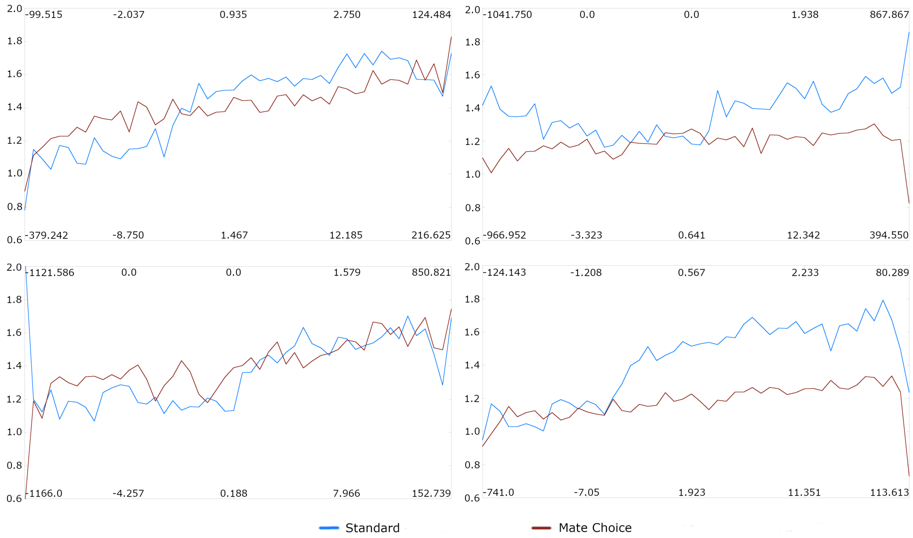

Figure 6.43: Survival rate for males in all 50 runs, bucketed and ordered by innovation rate. Quartile information for CMP-GP shown at the bottom x-axis. Quartile information for the Standard approach included in the top x-axis. Four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

the most reproductive individual, contributing to the exploitation of that search space, while those at the positive side are further than average to the most reproductive individual, likely exploring diverging solutions. For each function, the collected sample is ordered and bucketed into 50 groups, 48 of which have equal size (more than 500 individuals each) and the remaining 2 groups split the surplus individuals, having a size of 24 or less individuals each. These 2 groups include the most extreme subjects at either end of the ordered sample, helping control outliers. As it is, the x-axis alone includes information regarding the distribution of innovation, summarized in a five number summary included along the x-axis, on the bottom for CMP-GP and on top for the Standard approach. Regarding the y-axis, it corresponds to the growth rate, or survivability of each bucketed group over two generations. A few characteristics are worth remembering: i) because in each figure only the selected females (Figure 6.42) and the selected males (Figure 6.43) are studied, unsuccessful individuals are mostly left out; ii) production of two offspring gives a chance of exponential growth over two generations; iii) rates are measured for each bucket, potentially balancing individuals with either none or an outstanding number of grandchildren; iv) the size of the buckets varies between approaches and genders, on the one hand influenced by gender distributions as shown in Figure 6.28, and on the other hand influenced by particularities of sampled generations; v) finally, the metric is defined in the $]-1,\infty[$ interval. As a result, conclusions regarding growth rates are safe within each approach or gender, but potentially complex between them.

Regarding the five number summaries, Figures 6.42 and 6.43 show very different distributions between approaches, with the Standard showing IQRs in the range of ≈ 1.66 to ≈ 4.79 while CMP-GP ranges from ≈ 11.34 to ≈ 20.94. Variation in the Standard approach has been previously discussed, bringing up its exploitative character through the fact that most of the sampled individuals introduce small innovations

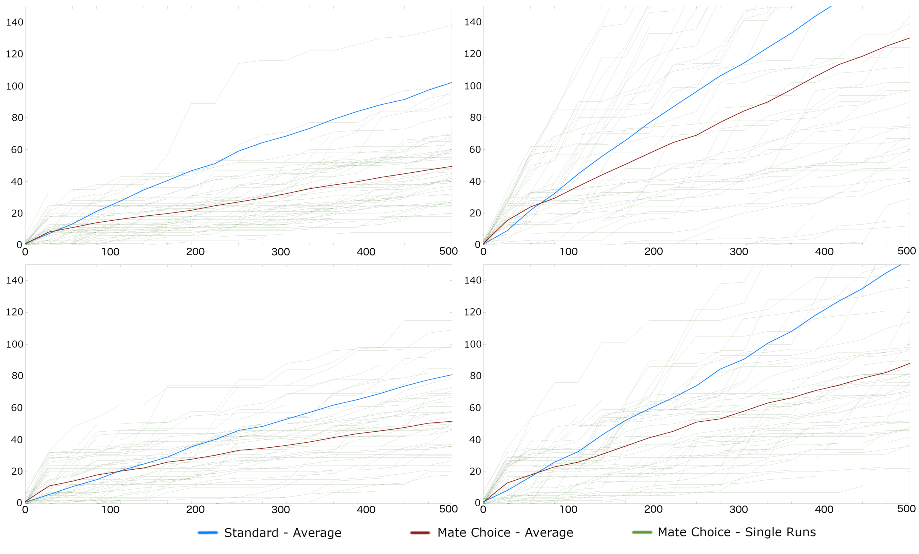

Figure 6.44: Cumulative number of female individuals considered as outlier from previous population's female individuals distribution, measured at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

at best. The summary for CMP-GP distances itself from such a stranglehold, in-line with what was discussed regarding PIMP. However, as expected in light of the discussion on diversity, the sample's variation for CMP-GP is lower than for PIMP, which ranged between ≈ 17.44 and ≈ 26.46. In comparison to the other two approaches, the following can be said regarding CMP-GP: i) the median in all functions is positive and larger than in the Standard approach but smaller than in PIMP, showing that at least 50% of selected individuals follow an exploratory character, but on a slightly smaller proportion than on PIMP; ii) a wider IQR than in the Standard approach reinforces the exploratory character of CMP-GP, suggesting that even the most reproductive individual can be distant from the remaining individuals, however more moderately than on PIMP; iii) the distance from the median to the third quartile is always larger than to the first quartile, suggesting a tendency for exploratory individuals to venture further away than exploitative ones, in similarity to what was observed in PIMP. However, differences in the nguyen-4 function are very small. These characteristics hold true for both females and males, but whereas the females hold a quite steady IQR across functions in PIMP, the same can't be said regarding CMP-GP.

When survivability is considered, further differences are noticeable, but so are important similarities. It should be recalled for the purpose of the discussion that growth rates are relevant within each approach and function, and that direct comparisons between values are not appropriate. Still, insight on their overall behavior and tendency can be used for comparisons. On a first analysis, the same observations made for the two other approaches hold true: the average growth rates, despite being contained, show a tendency for favoring innovative solutions in both genders of CMP-GP, similarly to what is seen in Approach 1 and the Standard approach. The extent of those innovations are distinctively larger than what is achieved by the Standard approach, but more moderate than on PIMP, representing nonetheless ecological opportunities

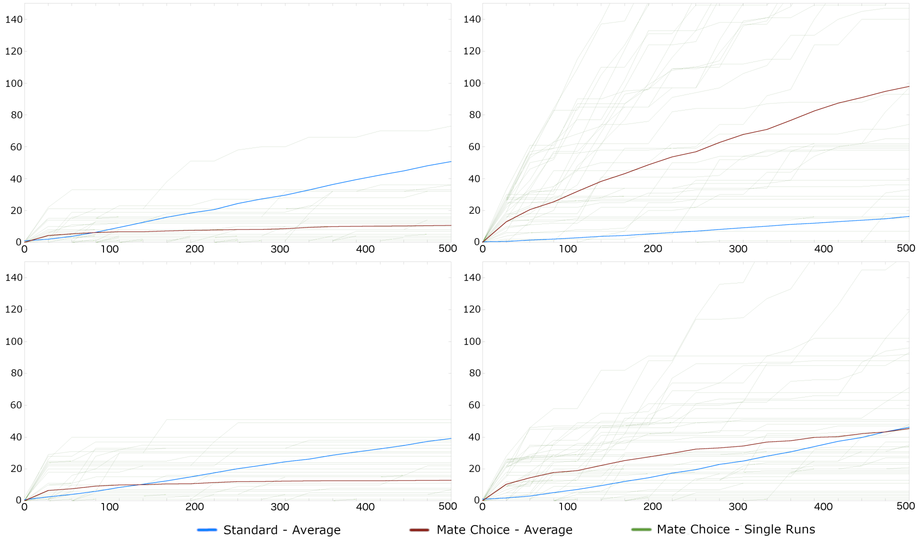

Figure 6.45: Cumulative number of female individuals considered as outlier from previous population's female individuals distribution while also surpassing its best fitness value, measured at every 25 generations. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

for exploratory individuals to act both as females or males and successfully establish a lineage by producing children that are themselves competitive. This data doesn't mean that all individuals that are disruptive will have higher chances of being selected, but rather that those that are both competitive and disruptive have an edge over the others, with many others being discarded along the way for sure.

The impact seems more relevant for females, who are bound to be selected by fitness, and who are more likely to benefit from the ability to absorb and exploit disruptive genes, potentially increasing their diversity or allowing genetic drift towards new areas of the search space. This behavior requires however contributions from males. When looking at the associated data two observations made about PIMP hold generally true also in CMP-GP: i) the overall growth rate of males is smaller than those of females; ii) the variation in growth rates between less and more innovative individuals is less significant. Their explanation is similar to that shown when discussing PIMP. However, some differences are worthy highlighting. Due to the relatively smaller selection pressure on males in functions korns-2 and vladislavleva-7, reproductive opportunities are more equally spread, resulting in an noticeably smaller overall growth rate (due to each bucket representing more individuals) as well on even less differences between innovation levels. Still, it's important to keep in mind that the population by itself, independently of its inner differences, has an exploratory character, drifting to meet preferences for as far as they push. The bias for innovation shown reflects that effort which allows the male population to keep contributing to female genetic variation and search efforts.

Figures 6.44 to 6.47 help illustrate this inter-linkage between males and females, and how males can contribute to females escaping local optima and drifting in the search space. Figure 6.44 shows the cumulative number of females that through the IQR method may be regarded as outside the previous generation's female population

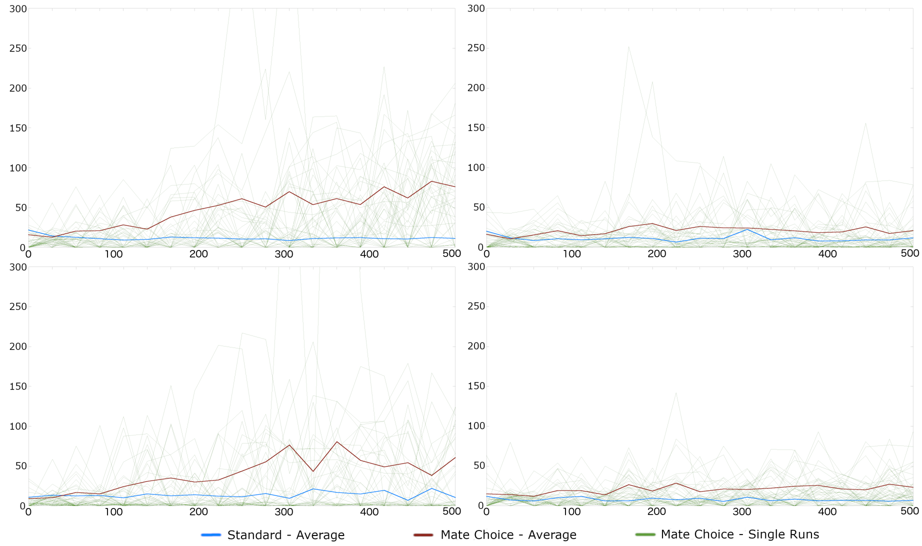

Figure 6.46: Edit distance from female parent for female individuals considered as outlier from previous population's female individuals distribution. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

distribution through a higher tree edit distance. In addition, Figure 6.45 shows those individuals that are both outsiders and fitter than the previous best solution, being thus in a better position to contribute to drifts in the population by having a higher chance of reproducing. As discussed previously, the Standard approach may be at an advantageous position in this analysis, due to having a quite small IQR. Both PIMP and CMP-GP, on the other hand, face a much harder challenge. Still, they are both capable of contributing with a continuous flow of innovative females. Although doing so on a smaller rate, these individuals have a higher chance of representing larger leaps in the search space.

In both Mate Choice approaches, as shown in Figure 6.45 the impact seems more relevant on the beginning of the runs, with new fitness peaks being found more often. By definition, finding higher and higher fitness peaks becomes a challenge that grows in difficulty over time. While PIMP performs competitively on initial generations, it soon falls into stagnation. This brings up differences between PIMP and CMP-GP that are important to address. While the behaviour of both approaches is quite similar in the nguyen-4 and keijzer-3 functions, both Figures 6.44 and 6.45 show important differences in the korns-2 and vladislavleva-7 functions. In the first one, CMP-GP is able to remain much more competitive with the Standard approach, despite the much larger IQR, and on the second one, it shows its capability to continuously find better and better fitness peaks, avoiding the stagnation found in PIMP. This is achieved through the equilibrium imposed by the evolved mate evaluation functions, which keep males closer to females (but not on convergence like in the Standard approach), allowing the provision of genes that are more easily valuable for the female effort. These contributions while being small, show how cumulative innovations can contribute to fitness gains continuously and in opposition to drastic changes imposed by males that are lead further and further away by negative assortative mating. This analysis is supported by

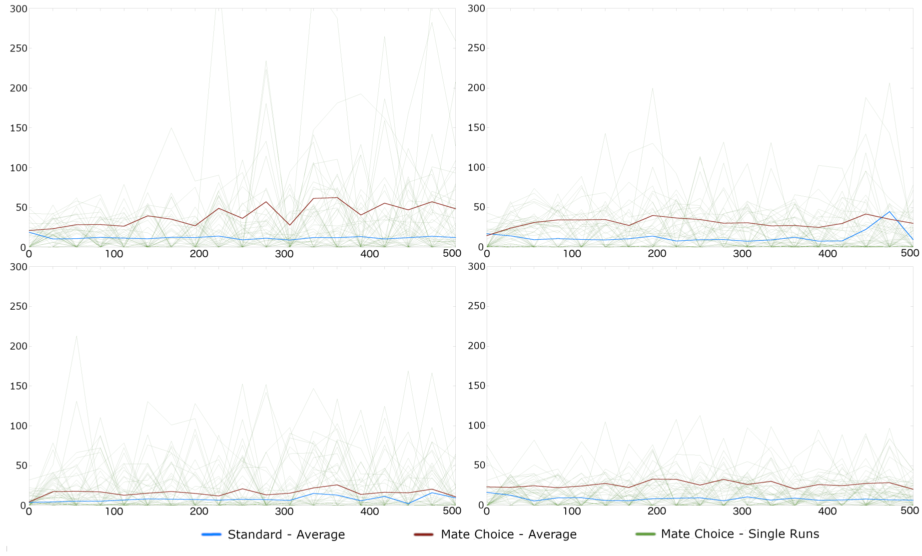

Figure 6.47: Edit distance from male parent for female individuals considered as outlier from previous population's female individuals distribution. Results shown for four functions: nguyen-4 (top left); korns-2 (top right); keijzer-3 (bottom left); vladislavleva-7 (bottom right).

Figures 6.46 and 6.47 which, for functions nguyen-4 and keijzer-3 shows that disruptive females are on average more and more distant from their mothers than from their fathers, while in the other two functions, the distances are smaller and more balanced, and slightly higher for fathers than for mothers.

6.6 Summarized Comparison of PIMP and CMP-GP

The two discussed Mate Choice approaches have shown to, through their own assumptions, be capable of emergent Mate Choice. When looking at the resulting behaviors, there are plenty of agreeing phenomena between the two, but there are also particularities that are characteristic of each one and can't be generalized. This section aims at briefly summarizing the findings, but most importantly it links behaviors with design choices, clarifying differences and justifying outcomes. For lack of a more complete analysis, the four studied functions will have to do, supported by the results achieved by each approach on the analysis set. It should be recalled that no statistically significant differences between the two approaches were found on the four studied functions but that PIMP statistically outperformed the Standard approach on the korns-2 function while CMP-GP statistically surpassed the Standard approach on the keijzer-3 and vladislavleva-7 functions. Both approaches successfully statistically distanced themselves from the Standard in the nguyen-4 function.

Regarding selection analysis, Mate Choice was shown to emerge by cheer force of competition and the self-reinforcement of mating preferences. PIMP seems to be in initial advantage in regards to consistent choice, guiding preferences smoothly towards close to convergence in a few generations, but CMP-GP shows strong capabilities to kick off the feedback loop, even if later, and reach higher choice consistency. Additionally, both approaches show a Fisherian character and the ability for preferences to push in different directions, either in a way converging with the fitness function or in diverging ways. While, by design, it was known that the representation of mating preferences in PIMP was capable of reproducing the target function (even though it can be a tough task), the same was not a given for the representation of CMP-GP. Interestingly, the latter shows a higher propensity for guiding search through Mate Choice towards the same direction as the fitness function (still on a small subset of runs), which not only illustrates the capacity for mate evaluation functions to freely lead mating partners in diverging directions but also highlights the representation's tendency for an open-ended search effort. The impact of initial conditions as well as the particularities of each search landscape are relevant for the resulting outcome.

Perception analysis is absolutely dependent on the assumptions of each approach and, particularly regarding genotypic metrics, their interpretations are quite different and difficult to compare. Nonetheless, entropy and contrast for PIMP remains remarkably close to that of the fitness function, as was expected since they both access the same amount of data, which is combined in the same way. There are however slight frailties, mostly associated with the chance of preferences tending to infinity. Regarding CMP-GP, the amount of data accessed is much less than that used in the fitness function or on PIMP. The perceived signals are measured against individual preferences and their relation combined through interactions. The resulting entropy is on times smaller than the fitness function, but overall is kept at competitive levels. Contrast variation is larger, showing higher capabilities on 1-var functions whereas in multi-var functions the amount of information, initialization of preferences, or the means to combine them into an attractiveness value seems insufficient in comparison to the fitness function. Still, both approaches maintain average entropy close to maximum levels, and definitely at sufficiently high levels to promote consistent choice. Interestingly, that is achieved while favoring simpler representations of preferences or mate evaluation functions, whose average number of terminals and non-terminals drops consistently on average throughout the evolutionary process. A comparison between competing dimensionality and complexity levels shows that while higher entropy and contrast is often associated with larger preference trees in either approach, simpler ones successfully maintain a competitive edge that allows them to spread through the population. This is true for both approaches despite interpretation differences.

Finally, effects analysis shows the impact on the evolutionary process on a population level. Firstly, both approaches result in a form of speciation through gender, with individuals being competitive either for female or male roles in detriment of simultaneously competing as hermaphrodites. This separation is fueled by the self-reinforcing of mating preferences and the driving of the male population away from the female one. PIMP systematically introduces a runaway process of negative assortative mating which continuously increases the distance between genders, in a swiping motion through the search space. CMP-GP is capable of the same behavior but only on certain conditions, otherwise, mate evaluation functions have shown to push males only a certain distance away from the females, reaching a form of equilibra, imposed by preferences rather than fitness costs. Arguably, this effect generalizes to all functions but depending on the characteristics of the search space, it may be more or less visible, suggesting that at times the point of equilibria is simply not reached. The exploitative character of females and the exploratory tendency of males is well illustrated in both approaches, with freely evolving preferences leading males to wander in the search space, hopefully landing on areas that represent ecological opportunities. Such individuals, by being competitive fitness-wise, have reproductive chances as females, injecting new genetic material that can further fuel evolution and result on genetic drifts. In both approaches and genders, innovative individuals benefit from a higher survivability, backing up their relevance on upcoming generations, on inner-gender diversity, and on each gender's particular role. Overall, this dynamic between genders contributes to escaping local optima, but with significant differences between behaviors. In instances where an unbounded runaway process is underway, individuals pushing females to escape their local neighborhoods are likely highly disruptive, being closer to their male parent than to the female, consequently introducing large tunneling behaviors between fitness peaks and punctuated gains in the female population. In contrast, instances where traits are pushed to an equilibria suggest a more continuous effort of small changes and gains that accumulate and fuel drift in a more controlled and sustainable way, while still introducing high levels of innovation.

The similarities shown by both approaches suggest that under the right assumptions and independently of the representations, self-adaptive preferences can introduce Mate Choice and its underlying behaviors without particular troubles. However, the evolution of mate evaluation functions, with adaptive dimensionality and complexity can bring forth relevant advantages. Comparing the representations, PIMP is designed to work at full capacity, profiting from access to full information on each mating candidate, a human-designed function, and tailored build sets for each function. On the other hand, CMP-GP has limited access to signals, and a general purpose build set. It may be feasible for PIMP, with further customization, to introduce balances between traits and preferences rather than a growing tendency for extremes, potentially improving on the benefits brought by exploration, but as it is, CMP-GP shows higher control to introduce a wider variety of behaviors, even if sometimes risking some of its perception abilities. Arguably, with special focus on a target function, the terminal and non-terminal sets as well as build rules can be adjusted to provide customized setups, potentially improving on results. Furthermore, mechanisms to maintain higher dimensionality and complexity may allow for valuable return.

In the end, statistical differences between the Mate Choice approaches are difficult to find in the full test set, but in comparison to the Standard approach, evolving mate evaluation functions seems to take the lead, with much more room for further improvements. As it turns out, deviating from a goal oriented search effort where fitness is promoted through higher reproductive chances, can introduce behaviors that are beneficial on a population level, even if the male half of the population is entirely focused on adapting to a goal that is likely to be completely outside of the scope of the fitness function (unless preferences take a Wallacean character). Interestingly, that behavior is not imposed by any rule that promotes exploration or exploitation, but simply by the selfishness of genes, including those representing preferences, whose aim is to replicate and survive by reproducing sexy sons, in disregard of their contributions to fitness.

6.7 Effects of Mutation: Performance and Statistical Analysis

Mate Choice following the proposed assumptions was shown to deeply impact the behavior of evolutionary algorithms, introducing search dynamics that emerge through self-adaptive mechanisms. Moreover, the changes in behavior have repercussions on the algorithm's performance, which have been discussed in Section 6.3.2. During the corresponding experimental setup, mutation was left out in order to reduce noise and aid in matching design choices to results with as much precision as possible. However, mutation is regarded as an important part of evolutionary algorithms, an operator that can introduce variation in a population with simplicity, despite it's canonical blindness. From a performance point of view, mutation may result in meaningful gains for the Standard approach, which are worth addressing. In regards to Mate Choice, mutation can also have important impacts, potentially bringing benefits through the introduction of variation in preferences or traits. While a full behavioral analysis, following the research questions and methodology suggested in Section 6.2.2, would greatly bloat the current study, performance impacts can easily be addressed. The following subsections will address the impact of mutation on each Mate Choice approach, exploring the application of the operator on each or both chromosomes. Moreover, the effects will be compared to the Standard approach, with and without mutation.

6.7.1 Impacts on Mate Choice

The full extent of the analysis can be found in Appendixes B and C, with results being summarized in Tables 6.12 and 6.13. Both a best-overall or a pairwise analysis of the different setups on each particular function can bring forth interesting details, but the summarized information in this section is sufficient to highlight deep differences in performance and compare the impact of mutation through each setup. Overall, the data shows in a straightforward way that both Mate Choice approaches can benefit immensely from the introduction of mutation, specially on both chromosomes simultaneously, easily overcoming the results achieved by the base setup or any of the other mutation setups, both regarding sample medians and hit rates. A closer look at each approach will allow to further explore how that is achieved.

Looking at the two setups where mutation is exclusively applied to one of the two chromosomes, a few observations are worth listing regarding PIMP: i) mutation on the first chromosome outperforms the base approach on $\approx 81\%$ of the instances, and on $\approx 44\%$ with statistical significant gains; ii) mutation on the second chromosome achieves better outcomes than the base approach on $\approx 56\%$ of the problems but only gets statistically significant differences on $\approx 4\%$; iii) mutation on both chromosomes improves on base results in all but one function (which is a tie between all setups), corresponding to a gain of $\approx 21\%$ and $\approx 76\%$ over each of the single approaches respectively; iv) regarding statistical significant gains, the last setup achieves better results than the base on $\approx 56\%$, corresponding to gains of $\approx 26\%$ and 1350% over each of the single mutation approaches; v) pairwise comparisons between mutation setups follow suit with the results obtained individually in relation to the base setup. These results suggest that, within the assumptions of PIMP, mutation of traits is far more important than mutation of preferences, outperforming the base approach on over two thirds of the test instances and showing statistical gains on more than half. The results achieved by mutation of preferences alone are more moderate. While better results are achieved on almost half the test set, their relevance is shorter, only being statistically relevant on a very small subset.

The performance changes shown in CMP-GP are quite similar to those discussed regarding PIMP: i) mutation on the first chromosome increases performance on $\approx 77\%$ of the instances when compared to the base approach, with statistical differences in $\approx 44\%$; ii) regarding the second chromosome, mutation boosts results on $\approx 54\%$ of the problems, and statistically significant gains are found on $\approx 2\%$ instances; iii) when applied on both chromosomes, mutation outperforms the base setup on $\approx 75\%$ of the times, which represent gains of $\approx -3\%$ and $\approx 39\%$ when compared to both other mu-

Table 6.12: Comparison between different Mutation setups for the PIMP Approach. Summary of the results observed in the full extent of the performance analysis.

Median

	Base	Mutation 1	Mutation 2	Mutation Both
Base		9	21	
Mutation 1	42		36	
Mutation 2	29	15		
Mutation Both	51	51	51	

IQR

	Base	Mutation 1	Mutation 2	Mutation Both
Base		21	26	15
Mutation 1	31		36	23
Mutation 2	26	16		13
Mutation Both	37	29	39	

Mann-Whitney

	Base	Mutation 1	Mutation 2	Mutation Both
Base			2	
Mutation 1	23		21	1
Mutation 2	2	1		1
Mutation Both	29	3	26	

Hit Rate

	Base	Mutation 1	Mutation 2	Mutation Both
Base		4	3	6
Mutation 1	12		9	6
Mutation 2	11	6		5
Mutation Both	12	9	12	

Taillard

	Base	Mutation 1	Mutation 2	Mutation Both
Base				
Mutation 1	2		2	
Mutation 2	1			1
Mutation Both	4	2	3	

Table 6.13: Comparison between different Mutation setups for the CMP-GP Approach. Summary of the results observed in the full extent of the performance analysis.

Median

	Base	Mutation 1	Mutation 2	Mutation Both
Base		11	23	12
Mutation 1	40		42	18
Mutation 2	28	10		9
Mutation Both	39	33	43	

IQR

	Base	Mutation 1	Mutation 2	Mutation Both
Base		17	25	13
Mutation 1	35		36	22
Mutation 2	27	16		15
Mutation Both	39	30	37	

Mann-Whitney

	Base	Mutation 1	Mutation 2	Mutation Both
Base				
Mutation 1	23		20	1
Mutation 2	1			
Mutation Both	28	4	26	

Hit Rate

	Base	Mutation 1	Mutation 2	Mutation Both
Base		4	8	3
Mutation 1	10		12	6
Mutation 2	8	4		5
Mutation Both	15	10	13	

Taillard

	Base	Mutation 1	Mutation 2	Mutation Both
Base			1	
Mutation 1	1		3	2
Mutation 2	1	1		
Mutation Both	2	1	4	

tation setups; iv) regarding statistically significant differences, the setup outperforms the base on $\approx 54\%$ instances, corresponding to gains of $\approx 22\%$ over mutating the first chromosome and $\approx 2700\%$ over mutating the second chromosome; v) pairwise comparisons between mutation setups are in agreement with this analysis. These results reinforce that mutation of traits can be more valuable in regards to performance than mutation of preferences, extending the analysis to the assumptions of CMP-GP. It is likely that independently of the representation, the differences in relevance generalize to Mate Choice as a strategy. As a side note, comparisons between PIMP and CMP-GP are not viable through these tables as they each compare to their own base setups. As shown in Table 6.11 regarding base setups, CMP-GP gains over PIMP in median differences with and without statistical significance. The base is therefore likely tougher to beat, but a useful comparison will be included in the next subsection.

Comparisons between mutation setups are nonetheless important to discuss further. The differences in mutation relevance in either chromosome is expected and comparisons on which one performs better are unfair. After all, mutation on the first chromosome can directly influence the quality of solutions and potentially introduce new, better performing individuals, which will likely impact the behavior of the female gender. As a consequence, if preferences are yet to converge, shifts in the process of reinforcement can occur. Moreover, mutation can introduce diversity into the male population, potentially unlocking periods of stasis and rebooting competition for attractiveness, or even introducing traits that make pre-existent preferences relevant. On the other hand, mutation on preferences has at best an indirect impact on solution quality. Still, they can have meaningful effects. They can slow the process of self-reinforcement or even shift its direction but perhaps more importantly, they can interrupt equilibra and reintroduce competition. Moreover, they can make traits that were overlooked be relevant or the other way around. Likely, mutation on preferences will impact the exploratory character of males which may consequently impact female exploitation through gender synergies. The results show however that the simultaneous introduction of both mutation operators provides best gains. The results clearly shows that adding mutation on the first chromosome to a setup where mutation exists on the second chromosome can boost results many-fold but, it's also important to mention that the opposite scenario bring gains in between $\approx 20\%$ and $\approx 30\%$, which are not residual. Interestingly, when mutation on the second chromosome is added, gains seem to be larger on setups that already have mutation on the first chromosome than when adding to the base setup, which shows that both operators can cooperate towards a better outcome.

As a side note, the samples IQR range is also impacted by the introduction of mutation, following different behaviors: i) regarding the introduction of mutation in the first chromosome, there's smaller variation on about two thirds of the functions, suggesting higher consistency among results; ii) in relation to mutation on the second chromosome, variation reduces on about approximately one half of the functions and increases on the other half, showing no special tendency for higher consistency, ultimately depending on the function; iii) when both are introduced, variation reduces in nearly three quarters of the function, again suggesting a reinforcement of consistency brought by the application of both operators simultaneously. In regards to hit rates, improvements are brought following the same tendency as results on median, although in some cases results are already difficult to beat, making differences hard to come by.

6.7.2 Comparison with impacts on Standard Approach

Extending the study on mutation, it's useful to look at results in perspective of how they can improve those of the Standard approach, with a few questions in mind: i) what gains can mutation bring to the Standard approach; ii) how does Mate Choice, using the base setup, perform as an alternative to mutation; iii) how do the Mate Choice approaches, in their best setup, compare with each other and with the Standard approach with mutation. In order to address these questions, the initial study comparing the three base approaches shown in Section 6.3.2 will be broadened with additional information. The full studied information has been organized in Appendix D and summarized in Table 6.14. In answer to the first question, mutation does a reasonable job in improving the Standard approach, overcoming the base setup in $\approx 62\%$ of the instances, but only with statistical significance in $\approx 10\%$ of the test set. As an alternative, PIMP without mutation improves on the Standard base approach on $\approx 75\%$ of the test set, including $\approx 27\%$ where statistical significant gains were found, whereas CMP-GP (also without mutation) brings improvements on $\approx 88\%$ instances, with statistical significant improvements being found on $\approx 31\%$ of them. In comparison to using mutation, Mate Choice therefore represents gains in regards to median values of $\approx 22\%$ for PIMP and $\approx 44\%$ for CMP-GP. When statistical significant differences are considered, the gains are $\approx 180\%$ and $\approx 220\%$ respectively. Overall, the results show that Mate Choice can provide a viable and alternative strategy to improve search efforts.

Tables 6.12 and 6.13 show that the best performing setup used mutation on both chromosomes, which therefore improve even further the gains shown when compared to the Standard approach with and without mutation. When comparing between the two Mate Choice approaches, differences are more dim: i) performance wins are distributed as $\approx 38\%$ for PIMP and $\approx 60\%$ for CMP-GP; ii) when statistical differences are considered, PIMP outperforms CMP-GP on $\approx 6\%$ instances while the opposite happens on $\approx 15\%$; iii) when measuring against the Standard approach without mutation, statistical significant gains are found on $\approx 62\%$ of instances for PIMP and on $\approx 71\%$ for CMP-GP; iv) a similar comparison to the Standard approach with mutation shows gains on $\approx 71\%$ for PIMP and on $\approx 69\%$ for CMP-GP. Regarding hit rates, both Mate Choice approaches show close results that distance themselves from those achieved by the Standard approach, and on a relevant subset showing statistically significant differences.

In summary, Mate Choice has been shown not only to be a viable alternative to mutation but also to improve on its performance, approximately doubling its gains on both approaches. No doubt, this is a direct impact of its ability to maintain a higher diversity and of gender synergies, which materialize in a higher exploration and the feeding of exploitative efforts. Moreover, rather than used as an alternative, Mate Choice can be paired with mutation, in which case it has been shown to profit from the induced variability and reach significant performance gains that further improve its performance. Among the tested setups, introducing mutation on both chromosomes shows the best gains. Between the two Mate Choice approaches, both show competitiveness, with CMP-GP taking the lead by a slight margin, in agreement to the same comparison regarding Mate Choice without mutation, but showing nonetheless a larger difference than before. In conclusion, in the context scoped by this study, Mate Choice improves on search performance, and is a stronger alternative than mutation. In combination, their performance gains are very significant, and, if a Mate Choice approach has to be chosen, then CMP-GP seems to be a safer, higher performing choice.

Table 6.14: Comparison between Standard Approach with and without Mutation and both Mate Choice approaches with Mutation on both chromosomes. Summary of the results observed in the full extent of the performance analysis.

Median

	Standard	Mutation	PIMP	CMP-GP
Standard		19	3	4
Mutation	32		5	3
PIMP	49	46		20
CMP-GP	48	48	31	

IQR

	Standard	Mutation	PIMP	CMP-GP
Standard		24	14	1
Mutation	28		11	1
PIMP	38	41		9
CMP-GP	51	51	43	

Mann-Whitney

	Standard	Mutation	PIMP	CMP-GP
Standard				
Mutation	5			
PIMP	32	37		3
CMP-GP	37	36	8	

Hit Rate

	Standard	Mutation	PIMP	CMP-GP
Standard		11	3	2
Mutation	5		2	0
PIMP	13	15		7
CMP-GP	15	16	10	

Taillard

	Standard	Mutation	PIMP	CMP-GP
Standard		1		
Mutation	3		1	
PIMP	8	9		3
CMP-GP	11	10	3	

Chapter 7

Conclusions

The research conducted for this thesis has an exploratory character and focuses on the role of Mate Choice as a self-adaptive model that allows individuals to choose mating pairs following their own preferences. It promotes a higher degree of autonomous evolution through partner interactions, and therefore introduces a chance of following self-regulated diverging evolutionary paths, in a combination of open-ended evolution with the goal-focused character of optimization algorithms. The study aims at the development of a framework to model Mate Choice based on a strong theoretical background. It clarifies assumptions and requirements to keep applications simple yet powerful and discusses likely impacts and potential advantages. For the purpose of representation of mating preferences, Genetic Programming trees are considered and two approaches are introduced, one that represents preferences ideal mating partners to which candidates proximity is measured (PIMP), and one that profits from explicitly encoding a perception system, corresponding signals and preferences, and means to combine simple evaluations into complex functions (CMP-GP).

7.1 Summary

The thesis offers strong theoretical background behind the mechanisms of Sexual Selection, and particularly Mate Choice, in Chapter 2, by following historical steps from early views to a modern synthesis. It starts by introducing Darwin's good taste and Wallace's good sense schools of thought, how they aim at explaining the emergence of conspicuous traits (or other relevant aspects), their strengths, and their caveats. It further explores contributions made to both views, progressively filling the gaps left behind by both Darwin and Wallace, towards a modern overview of Sexual Selection. The growing discussion clarifies the place of Sexual Selection in evolutionary theory and its relation with Natural Selection, in a synthesis that profited from both Darwin and Wallace aligned ideas. So as to clarify modern interpretations of Sexual Selection and particularly Mate Choice, inner processes are discussed in a structured manner, focusing on conditions for Sexual Selection, principles of adaptive Mate Choice, and relevant aspects of mating preferences.

The thesis moves on to bridging between theoretical knowledge and evolutionary models in Chapter 3. It discusses the first genetic models used for mathematical validation of Mate Choice, both for Darwin's and for Wallace's views. Respectively, the two-locus and the three-locus models are introduced, along with their assumptions and resulting observations. Together, they provide extra knowledge on the genetic relation between preferences and traits, and comparatively, they further explore the proximity between both models, despite diverging assumptions. A parallelism is made between genetic models for the studying of natural behaviors and evolutionary algorithms for the purpose of optimization, and how principles can be transferred. With its behaviors being demonstrated, Mate Choice as an operator for optimization is discussed, covering its design steps and impacts: i) how to build female and male selection pools; ii) how to select each female from the corresponding pool; iii) how to select a set of mating candidates from the available pool; iv) how to evaluate each male candidate following the active females preferences; v) how to select the best candidate for reproduction.

The subject of complex evaluation of mating candidates is finally introduced, moving away from few-locus models and steadily introducing more and more features. In the end, the self-adaptation of mate evaluation functions is discussed, as a representation that allows for the simultaneous evolution of dimensions and complexity along preferences, while emulating a variety of relevant behaviors that are difficult to model otherwise. The paradigm imposes serious changes in the way the search space is explored, which is discussed in detail, as are the potential benefits and impacts of Mate Choice, particularly regarding: i) reducing the error of Natural Selection; ii) increasing contrast between similar individuals; iii) escaping local optima; iv) emergence of complex innovations; v) spontaneous sympatric speciation.

Having covered relevant theoretical knowledge on Sexual Selection through Mate Choice as an important topic in natural sciences, as well as having addressed the incremental introduction of more and more complete gene-centered, self-adaptive operators in Evolutionary Algorithms, this thesis moves on to cover existing practical applications of Mate Choice in optimization as well as other relevant operators and contexts, in Chapter 4. It offers a structured and thorough look at the state of the art, providing insight on the different sources of inspiration for Sexual Selection related behaviors for optimization, on the wide range of design choices and applications, but most importantly, on the innovations brought by the proposed model by contrast with other studies. It completes the previous theoretical analysis on Mate Choice with a full description of what can be found in relevant literature, on the one hand showing how similarly they follow the discussed ideas, but on the other hand showing also how they deviate.

Within the context laid out so far, Chapter 5 contributes with a general framework for the modeling of Mate Choice as a selection operator, clarifying what assumptions and requirements should absolutely be present but also discussing those that are sometimes found in the literature but don't need to be enforced. It also establishes the framework's underlying evolutionary steps, particularly regarding representation of ornamentation and mating preferences, evaluation of mating candidates, inheritance and evolving forces, and design choices. By doing so, it synthesizes the discussion so far and clears up what are in fact the needs of a Mate Choice model to introduce appropriate freedom of choice and autonomous evolution.

On top of the proposed framework, two approaches for the representation of mating preferences and evaluation of mating candidates are proposed: i) the representation of mating preferences through an ideal mating partner to which candidates are measured against (PIMP); ii) the explicit representation of signals, preferences and their complex interactions towards an attractiveness value (CMP-GP). For each approach, full descriptions are provided regarding representation and evaluation, as well as specific assumptions and considerations on how each of them impacts perception, context interpretation, aggregation function / mate evaluation function, preference interactions, and complexity. Furthermore, proof of concept is provided on different hard optimization problems, with performance being compared to a Standard Approach and an approach where mating partners are selected randomly. The results and behaviors are briefly analyzed but only as a validation of the proposed approaches, rather than focusing on answering the declared hypothesis or research questions.

That particular effort has been made on its own well defined application and experimental setup, laid out in Chapter 6. Both approaches have been tested on a set of 52 Symbolic Regression instances and compared to a Standard Approach. In order to limit noise, the base scenario avoids the use of mutation, which is later introduced, independently on traits and preferences and simultaneously on both, in order to study its impact and relation with Mate Choice. Specifics for each approach on the context of Symbolic Regression are also described and justified. The means for analysis are extensively discussed, both regarding performance and behavior. While performance analysis follows well known metrics, behavioral analysis presents multiple challenges. Each research question regarding behavior is addressed in turn, and the means and metrics used for analysis are discussed in detail.

Finally, the discussed performance metrics are used to compare the Mate Choice approaches along with a Standard approach. Furthermore, each Mate Choice approach is extensively discussed in regards to behavior, focusing on three scopes: selection, perception, and effects. Comparisons are made when possible, even thought the interpretation of metrics is sometimes dependent on the assumptions of each approach. Finally, mutation is introduced and comparisons in regards to performance are made, within each Mate Choice approach, so as to single out the impacts of mutation and its relation with traits and preferences. Comparisons are also made between PIMP and CMP-GP with mutation and a Standard approach with and without mutation.

7.2 Declared Hypothesis and Experimental Outcomes

The main hypothesis brought up by this thesis is that Evolutionary Algorithms coupled with proper Mate Choice mechanisms can improve on optimization by adopting a widening perspective on search and the relaxation of objectives. This study focuses on the modeling of mating preferences through Genetic Programming trees, applied to the context of Symbolic regression, which itself relies on a Genetic Programming representation. For the purpose of proof of concept, Approach 2 has also been tested on problems combining Genetic Algorithms and Genetic programming representations and operators. On the one hand, the study falls short on testing Mate Choice, as set out by the described assumptions, on the full range of available algorithms and representations (which is a growing range). On the other hand, it offers supporting evidence that the emergence of Mate Choice should hold independently of the representation, by being the product of sheer self-reinforcement, as long as the assumptions are followed.

With that in mind, increasing the range of problems targeted by Mate Choice would provide growing evidence to address performance. Nonetheless, along the different stages of this study, families of hard optimization problems have been discussed, which account for a wide range of test instances corresponding to search landscapes with varying roughness, from smooth to rigged with local optima, and deep multiple-funnel characters. Globally, Mate Choice has been empirically shown to represent a safer choice for optimization, consistently showing performance improvements across the test instances. Particularly on Symbolic Regression, improvements have been found on most of the 52 test instances, and statistically significant gains on nearly a third of them, when the base setup is considered. When mutation is introduced, the number of instances where statistically significant gains can be found grows to over two thirds. This analysis holds true for both Mate Choice approaches, although small variations are found between the two, in which case Approach 2 seems to take the lead.

Despite the discussed shortcoming on the range of the study, the presented results confirm the declared hypothesis as far as the scope of this thesis goes. Moreover, the behavioral analysis on both Mate Choice approaches suggests that performance gains are a result of a self-regulated widening search effort, attained by promoting the reproduction of individuals that abide to mating preferences rather than to the objective function. For the purpose, the self-adaptive character of mating preferences provides means for a degree of open-ended evolution that ultimately leads to an (almost always) diverging selective force. In combination with Natural Selection, Mate Choice affects the exploratory effort of the algorithm and the contributions made to the exploitative one, through the emergence of genders and the synergies between them.

To achieve such behaviors and results, the representation of mating preferences, following PIMP and CMP-GP, have been demonstrated to provide appropriate models. They have been extensively discussed in Sections 6.4 and 6.5 by means of the research questions introduced in Section 6.2.2. They have been compared and discussed in Section 6.6, showing many similarities but also important differences. Despite those differences, both models have shown to be appropriate for Mate Choice, each under its own assumptions for the representation of preferences and the evaluation of mating candidates. The behavioral analysis suggests so, particularly in regards to selection analysis. There are nonetheless potential shortcomings, discussed mostly in the analysis of perception, but in any case, the global results and the effects analysis together confirm the secondary hypothesis declared, that multidimensional mating preferences can be appropriately modeled using Genetic Programming representations. In order to better understand potential shortcomings as well as unexplored aspects of Mate Choice, future work should be considered.

7.3 Future work

The subject of Mate Choice is immensely vast and ever growing. In natural sciences, its mechanisms and impacts are yet not fully understood and continuous contributions are likely to be seen in the future. On top of studies on natural populations and evidences, the integration of growing amounts of knowledge in computational models for validation is likely to take place. Apart from these behavioral focused studies, there's room for the transference of knowledge into optimization algorithms, even if the resulting models are non-aligned with a standard, canonical view of goal focused evolution. When that happens, a methodology similar to that taking place in this thesis can be beneficial, by not focusing solely on the algorithm's outcome, but also on studying the inner workings of the algorithm and the potential impacts of Mate Choice, whatever the involved assumptions may be.

Focusing on this particular framework, and the discussed approaches, there are also good opportunities for future work besides the obvious need to apply and validate the models on more contexts and families of problems, both from academia and with practical applications. The most important return on that effort, other than testing performance, would be to assess how easily terminal and non-terminal sets can be built for CMP-GP, and how often is PIMP viable. Perhaps more interestingly, it would be particularly relevant to test the framework as a setup for multi-objective optimization and on dynamic problems. Regarding multi-objective optimization, the evolution of mate evaluation functions using single objectives as terminals should be easy to setup and gives the algorithms a self-regulated chance to build complex functions that behave differently from traditional evaluation means. There are many particularities on that topic worth addressing, specially considering the relation between single objectives and fitness. In regards to dynamic problems, the emergence of diverging evolutionary forces may give the algorithm an edge for adapting faster to changes in the fitness landscape, which is worth exploring.

Stepping away from specific applications, there should also be value in further studying the relation of Sexual Selection and Natural Selection. For the purpose, multiple research venues should be considered. Firstly, the application of Mate Choice on open-ended evolution, thus totally or partly removing the impacts of Natural Selection, should provide further means to study the relation between the two evolutionary forces, how they balance or restrict each other. Secondly, a parametric study on the size of candidates pools, for the roles of females and males, should be considered, thus adjusting the pressure put by fitness or attractiveness on the population. Additionally, other selection operators could be considered, potentially mimicking behaviors that diverge from the lek-like character of tournament selection, which potentially impacts selection pressure. Finally, the combination of fitness and attractiveness for the selection of males, as a metaphor of male competition, should be further studied and the impacts for optimization considered.

In regards to the setups analyzed in this study, further work should be considered. First of all, a full grid-search of parameters and operators should be considered, not only regarding pool sizes (as discussed above) but taking into account the whole design choices described in Sections 6.1.1 to 6.1.3. The benefits may be two-fold: i) finding the configuration that performs better on the target problem or specifically for each instance; ii) providing empirical data to study the behavior of each Mate Choice approach on a wide range of setups, allowing for behavioral comparisons and potentially overcoming drawbacks. Perhaps a more detailed analysis should be considered regarding the terminal and non-terminal sets for CMP-GP as well, testing different sizes as well as operators with different characteristics, such as combining more than two inputs. As a follow up, the initialization of preferences in CMP-GP may also need further analysis.

Such an analysis should provide a way to look more thoroughly at dimensionality and complexity. The behaviors described in this thesis in regards to these topics, while being properly justified, suggest that there may be much room for improvements. A detailed analysis on the topic may benefit from the already mentioned parameterization effort but other aspect should be fruitful to cover. It's important to understand under which conditions does high entropy and contrast become differentiating aspects and when do individuals with high perception capabilities achieve evolutionary advantages. The lack of that behavior may simply be the result of the search landscape, but it may also be due to operators or other design choices. Finding and testing setups that can be regarded as fairer for competition between multiple dimensionality and complexity values should provide valuable insights into the true value of modeling and self-adapting those features.

Moreover, the research questions should be extended to include a few aspects that are relevant for optimization efforts. For instance in the context of Symbolic Regression, it should be valuable to assess the size of the resulting solutions, as an additional metric for performance. It has been shown that the quality of the solutions is globally better, but they may also be bloated, or surprisingly more simple than the ones developed by a Standard approach. Also in regards to performance, the evolution of average and best fitness should be considered, in order to have a sense of how soon are good quality solutions found. Perhaps Mate Choice takes a large number of generations to surpass the Standard Approach, doing so later in the runs, or perhaps high quality solutions can often be found sooner in the run, potentially allowing for fewer generations to be used with little impact on performance. Visualization tools such as Elicit [55] can contribute not only to this analysis but to the discussion of all research questions by allowing views on different levels, from population to individual levels, or even on each particular chromosome. Population level visualizations can provide additional evidence of self-reinforcement, or the effects of Mate Choice, while more detailed views can allow for an individual by individual analysis that would otherwise demand an outstanding effort.

Finally, the computational costs of Mate Choice should be studied in depth, which due to representation and evaluation issues, is not a simple subject. It's undeniable that at each selection step, Mate Choice introduces overhead, through the evaluation of mating candidates. However, particularly for CMP-GP, how much overhead is involved is highly depended on a number of characteristics: the size of terminal and non-terminal sets, the size of evaluation trees, the range of active traits and preferences in the populations, diversity among preferences and male candidates, among others. Regarding PIMP, as discussed, the number of data points used for comparison between phenotypes and preferences can also be tuned, although statically rather than dynamically as an effect of the evolutionary process. These reasons make it so that calculating the overhead is more than simply measuring the number of evaluated individuals, and requires therefore a better weighted methodology.

Appendix A

Full experimental results

Table A.1: Best Fitness, MBF and sample Standard Deviation obtained by the Standard Approach on 50 runs tackling each of the 52 Symbolic Regression instances (First part).

	Standard		
	Best	MBF	StDev
koza-1	0.00E+00	1.66E-03	3.72E-05
koza-2	2.46E-08	3.18E-03	7.22E-05
koza-3	0.00E+00	5.21E-04	2.41E-06
nguyen-1	0.00E+00	8.29E-04	4.34E-06
nguyen-2	0.00E+00	1.51E-03	1.01E-05
nguyen-3	0.00E+00	3.80E-03	2.20E-04
nguyen-4	0.00E+00	2.66E-03	2.50E-05
nguyen-5	1.12E-07	1.39E-03	3.55E-05
nguyen-6	0.00E+00	1.34E-02	4.94E-04
nguyen-7	0.00E+00	1.99E-03	1.06E-04
nguyen-8	1.53E-12	1.45E-02	2.74E-03
nguyen-9	0.00E+00	1.05E-02	1.61E-04
nguyen-10	0.00E+00	1.45E-02	5.18E-04
pagie-1	5.14E-04	7.03E-02	4.11E-03
pagie-2	7.88E-03	1.92E-01	3.54E-03
korns-1	2.75E-01	8.46E+04	3.02E+10
korns-2	1.83E+04	2.57E+08	2.76E+18
korns-3	2.37E+03	1.92E+11	7.45E+23
korns-4	6.83E-05	1.61E-01	1.96E-01
korns-5	4.87E+29	5.00E+29	2.20E+55
korns-6	4.90E+29	5.01E+29	2.28E+55
korns-7	3.49E+23	1.55E+26	6.07E+51
korns-8	4.91E+29	5.00E+29	2.36E+55
korns-9	7.64E+29	7.75E+29	1.49E+55
korns-10	7.10E+03	3.90E+11	7.51E+24
korns-11	5.93E+01	6.11E+01	6.73E+00
korns-12	1.08E+00	1.13E+00	2.24E-02
korns-13	3.56E+07	1.96E+14	1.67E+30
korns-14	5.37E+05	3.92E+09	6.44E+20
korns-15	5.82E+29	5.93E+29	1.98E+55

Table A.2: Best Fitness, MBF and sample Standard Deviation obtained by the Standard Approach on 50 runs tackling each of the 52 Symbolic Regression instances (Second part).

		Standard	
	Best	MBF	StDev
keijzer-1	3.88E-05	6.85E-03	1.57E-05
keijzer-2	9.39E-03	4.81E-02	1.36E-04
keijzer-3	9.35E-02	1.23E-01	1.60E-04
keijzer-4	7.63E-03	8.11E-02	6.17E-04
keijzer-5	6.17E-05	8.33E-02	9.18E-03
keijzer-6	3.55E-05	1.90E-01	9.03E-02
keijzer-7	1.73E-03	4.20E-01	1.70E-01
keijzer-8	0.00E+00	0.00E+00	0.00E+00
keijzer-9	2.07E-04	6.82E-01	2.43E-01
keijzer-10	3.83E-03	2.72E-02	5.80E-05
keijzer-11	2.07E-02	8.41E-01	3.49E+00
keijzer-12	2.50E+00	1.26E+02	3.27E+04
keijzer-13	1.75E-01	5.49E+00	9.38E+00
keijzer-14	1.27E-01	5.81E-01	6.30E-02
keijzer-15	1.66E-01	3.62E+00	3.01E+00
vladislavleva-1	8.58E-04	1.65E-02	7.31E-05
vladislavleva-2	3.73E-04	4.20E-02	7.32E-04
vladislavleva-3	4.14E-01	9.54E-01	4.39E-02
vladislavleva-4	1.91E-02	4.58E-02	1.32E-03
vladislavleva-5	1.21E-02	2.15E-01	1.16E-02
vladislavleva-6	7.92E-01	5.31E+00	5.04E+00
vladislavleva-7	9.66E-01	6.79E+00	7.53E+00
vladislavleva-8	7.83E-02	1.08E+00	5.98E-01

Table A.3: Best Fitness, MBF and sample Standard Deviation obtained by the PIMP Approach on 50 runs tackling each of the 52 Symbolic Regression instances (First part).

	PIMP		
	Best	MBF	StDev
koza-1	0.00E+00	6.56E-03	8.49E-04
koza-2	0.00E+00	8.09E-05	2.26E-08
koza-3	0.00E+00	2.81E-04	1.19E-06
nguyen-1	0.00E+00	1.56E-02	3.19E-03
nguyen-2	0.00E+00	3.52E-04	7.02E-07
nguyen-3	0.00E+00	6.43E-04	1.72E-06
nguyen-4	0.00E+00	1.34E-03	1.46E-05
nguyen-5	0.00E+00	4.53E-04	5.50E-07
nguyen-6	0.00E+00	7.13E-03	3.69E-04
nguyen-7	0.00E+00	3.64E-02	4.64E-03
nguyen-8	0.00E+00	2.07E-03	1.71E-05
nguyen-9	0.00E+00	3.60E-03	2.99E-05
nguyen-10	0.00E+00	8.33E-03	8.81E-05
pagie-1	9.21E-04	6.49E-02	3.59E-03
pagie-2	4.19E-02	1.75E-01	2.61E-03
korns-1	7.54E-05	5.44E+04	2.21E+10
korns-2	1.85E+02	1.76E+07	1.30E+16
korns-3	3.09E+03	1.23E+12	4.28E+25
korns-4	8.35E-03	8.50E-03	9.24E-09
korns-5	4.86E+29	5.00E+29	3.05E+55
korns-6	4.85E+29	4.99E+29	2.97E+55
korns-7	3.34E+25	1.74E+26	6.12E+51
korns-8	4.86E+29	5.01E+29	3.20E+55
korns-9	7.65E+29	7.77E+29	1.59E+55
korns-10	2.27E+04	8.33E+11	3.45E+25
korns-11	5.86E+01	6.17E+01	1.75E+01
korns-12	1.08E+00	1.11E+00	1.31E-04
korns-13	3.47E+07	3.26E+11	2.81E+24
korns-14	3.42E+05	7.59E+08	1.36E+19
korns-15	5.83E+29	5.95E+29	2.69E+55

Table A.4: Best Fitness, MBF and sample Standard Deviation obtained by the PIMP Approach on 50 runs tackling each of the 52 Symbolic Regression instances (Second part).

	PIMP		
	Best	MBF	StDev
keijzer-1	7.70E-04	6.72E-03	1.59E-05
keijzer-2	1.06E-02	4.75E-02	1.03E-04
keijzer-3	5.85E-02	1.16E-01	3.45E-04
keijzer-4	1.52E-02	7.49E-02	6.54E-04
keijzer-5	2.45E-06	9.06E-02	1.07E-02
keijzer-6	4.29E-04	1.76E-01	8.47E-02
keijzer-7	6.82E-04	2.31E-01	1.37E-01
keijzer-8	0.00E+00	0.00E+00	0.00E+00
keijzer-9	5.34E-03	5.78E-01	2.73E-01
keijzer-10	9.96E-04	2.61E-02	4.32E-05
keijzer-11	4.44E-02	6.90E-01	1.45E+00
keijzer-12	2.04E+00	1.22E+02	3.36E+04
keijzer-13	3.78E-01	5.47E+00	5.63E+00
keijzer-14	1.78E-01	6.06E-01	6.52E-02
keijzer-15	2.56E-01	4.08E+00	4.10E+00
vladislavleva-1	2.11E-03	1.64E-02	7.22E-05
vladislavleva-2	2.88E-03	4.25E-02	7.35E-04
vladislavleva-3	2.20E-01	9.25E-01	3.77E-02
vladislavleva-4	2.69E-02	3.71E-02	3.09E-05
vladislavleva-5	6.05E-03	1.95E-01	9.73E-03
vladislavleva-6	1.46E+00	5.38E+00	4.92E+00
vladislavleva-7	1.12E+00	4.69E+00	4.30E+00
vladislavleva-8	7.64E-02	1.11E+00	7.56E-01

Table A.5: Best Fitness, MBF and sample Standard Deviation obtained by the CMP-GP Approach on 50 runs tackling each of the 52 Symbolic Regression instances (First part).

		CMP-GP	
	Best	MBF	StDev
koza-1	0.00E+00	1.71E-03	1.33E-04
koza-2	0.00E+00	6.60E-05	7.86E-09
koza-3	0.00E+00	9.89E-05	6.86E-08
nguyen-1	0.00E+00	1.07E-02	1.25E-03
nguyen-2	0.00E+00	3.63E-04	1.10E-06
nguyen-3	0.00E+00	1.03E-03	1.10E-05
nguyen-4	0.00E+00	9.19E-04	4.59E-06
nguyen-5	0.00E+00	5.22E-04	2.62E-06
nguyen-6	0.00E+00	1.54E-02	8.08E-04
nguyen-7	6.57E-07	1.96E-02	2.69E-03
nguyen-8	0.00E+00	2.74E-03	2.31E-05
nguyen-9	0.00E+00	3.77E-03	2.41E-05
nguyen-10	0.00E+00	9.17E-03	3.85E-04
pagie-1	6.26E-04	4.69E-02	2.63E-03
pagie-2	4.19E-02	1.71E-01	2.40E-03
korns-1	9.00E-04	4.62E+04	1.89E+10
korns-2	1.40E+04	1.21E+07	2.83E+15
korns-3	2.25E+04	4.87E+13	1.18E+29
korns-4	6.15E-04	1.56E-01	6.24E-01
korns-5	4.84E+29	5.00E+29	2.63E+55
korns-6	4.90E+29	5.00E+29	2.49E+55
korns-7	3.59E+25	1.66E+26	6.54E+51
korns-8	4.90E+29	4.99E+29	2.03E+55
korns-9	7.65E+29	7.76E+29	1.95E+55
korns-10	2.21E+04	4.10E+12	8.41E+26
korns-11	6.00E+01	6.09E+01	2.10E-01
korns-12	1.07E+00	1.11E+00	1.42E-04
korns-13	1.89E+07	2.12E+10	7.07E+21
korns-14	5.10E+05	7.97E+09	3.02E+21
korns-15	5.87E+29	5.95E+29	2.07E+55

Table A.6: Best Fitness, MBF and sample Standard Deviation obtained by the CMP-GP Approach on 50 runs tackling each of the 52 Symbolic Regression instances (Second Part).

	CMP-GP		
	Best	MBF	StDev
keijzer-1	3.43E-05	6.15E-03	3.70E-05
keijzer-2	1.63E-02	4.80E-02	1.17E-04
keijzer-3	6.82E-02	1.18E-01	2.41E-04
keijzer-4	1.05E-02	7.06E-02	7.00E-04
keijzer-5	5.75E-06	8.10E-02	7.25E-03
keijzer-6	2.80E-05	2.58E-01	1.11E-01
keijzer-7	2.88E-04	3.14E-01	1.66E-01
keijzer-8	0.00E+00	0.00E+00	0.00E+00
keijzer-9	3.69E-03	6.07E-01	2.71E-01
keijzer-10	5.57E-04	2.64E-02	5.39E-05
keijzer-11	8.62E-02	6.35E-01	1.31E+00
keijzer-12	8.61E-01	1.08E+02	4.16E+04
keijzer-13	3.50E-01	4.62E+00	8.36E+00
keijzer-14	1.18E-01	5.79E-01	7.43E-02
keijzer-15	4.85E-01	3.68E+00	3.12E+00
vladislavleva-1	1.27E-03	1.55E-02	8.21E-05
vladislavleva-2	1.29E-03	2.56E-02	7.03E-04
vladislavleva-3	2.02E-01	9.38E-01	6.15E-02
vladislavleva-4	2.43E-02	3.81E-02	2.33E-04
vladislavleva-5	8.85E-03	1.79E-01	1.18E-02
vladislavleva-6	1.53E+00	4.89E+00	2.94E+00
vladislavleva-7	1.48E+00	4.57E+00	4.90E+00
vladislavleva-8	5.91E-02	9.56E-01	6.40E-01

Table A.7: Full 5 number quartile information for the Standard Approach on each of the 51 Symbolic Regression test instances (First part).

			Standard		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0.00E+00	1.69E-05	2.66E-04	6.40E-04	4.21E-02
koza-2	2.46E-08	6.89E-06	1.32E-04	2.88E-04	3.31E-02
koza-3	0.00E+00	5.62E-06	2.67E-05	1.44E-04	7.38E-03
nguyen-1	0.00E+00	0.00E+00	9.71E-06	3.98E-04	1.23E-02
nguyen-2	0.00E+00	2.09E-05	4.25E-04	1.39E-03	1.91E-02
nguyen-3	0.00E+00	6.74E-06	8.36E-05	1.35E-03	1.02E-01
nguyen-4	0.00E+00	9.25E-05	3.96E-04	3.09E-03	2.85E-02
nguyen-5	1.12E-07	2.73E-05	1.25E-04	8.48E-04	4.22E-02
nguyen-6	0.00E+00	9.02E-05	5.24E-04	1.84E-02	8.96E-02
nguyen-7	0.00E+00	4.87E-05	1.19E-04	5.33E-04	7.28E-02
nguyen-8	1.53E-12	4.88E-05	1.01E-03	4.42E-03	2.89E-01
nguyen-9	0.00E+00	4.72E-04	5.01E-03	1.47E-02	5.20E-02
nguyen-10	0.00E+00	1.18E-04	1.78E-03	2.13E-02	9.81E-02
pagie-1	5.14E-04	1.35E-02	4.86E-02	1.19E-01	2.30E-01
pagie-2	7.88E-03	1.61E-01	1.99E-01	2.35E-01	3.10E-01
korns-1	2.75E-01	7.65E+01	7.80E+01	1.10E+03	4.56E+05
korns-2	1.83E+04	8.89E+04	2.12E+05	7.26E+05	1.17E+10
korns-3	2.37E+03	3.19E+07	7.70E+08	1.51E+10	5.65E+12
korns-4	6.83E-05	8.47E-03	8.56E-03	1.78E-02	2.07E+00
korns-5	4.87E+29	4.98E+29	5.00E+29	5.03E+29	5.13E+29
korns-6	4.90E+29	4.98E+29	5.01E+29	5.04E+29	5.13E+29
korns-7	3.49E+23	9.06E+25	1.69E+26	2.17E+26	2.75E+26
korns-8	4.91E+29	4.97E+29	4.99E+29	5.03E+29	5.11E+29
korns-9	7.64E+29	7.73E+29	7.75E+29	7.78E+29	7.84E+29
korns-10	7.10E+03	1.86E+05	1.07E+07	2.31E+08	1.94E+13
korns-11	5.93E+01	6.03E+01	6.07E+01	6.11E+01	7.82E+01
korns-12	1.08E+00	1.10E+00	1.11E+00	1.12E+00	2.15E+00
korns-13	3.56E+07	6.22E+08	2.35E+09	1.44E+10	9.11E+15
korns-14	5.37E+05	3.28E+06	7.91E+06	8.44E+07	1.79E+11
korns-15	5.82E+29	5.90E+29	5.93E+29	5.96E+29	6.01E+29

Table A.8: Full 5 number quartile information for the Standard Approach on each of the 51 Symbolic Regression test instances (Second part).

			Standard		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	3.88E-05	2.65E-03	8.04E-03	1.18E-02	1.31E-02
keijzer-2	9.39E-03	4.09E-02	5.59E-02	5.59E-02	5.80E-02
keijzer-3	9.35E-02	1.12E-01	1.30E-01	1.30E-01	1.52E-01
keijzer-4	7.63E-03	5.97E-02	9.22E-02	1.01E-01	1.22E-01
keijzer-5	6.17E-05	1.85E-02	6.51E-02	7.78E-02	3.19E-01
keijzer-6	3.55E-05	1.01E-02	1.85E-02	2.37E-01	8.37E-01
keijzer-7	1.73E-03	3.06E-02	1.35E-01	8.53E-01	9.10E-01
keijzer-8	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
keijzer-9	2.07E-04	2.18E-02	1.01E+00	1.03E+00	1.22E+00
keijzer-10	3.83E-03	2.26E-02	2.75E-02	3.16E-02	4.05E-02
keijzer-11	2.07E-02	3.68E-01	4.08E-01	4.97E-01	1.19E+01
keijzer-12	2.50E+00	8.08E+00	6.72E+01	1.19E+02	7.42E+02
keijzer-13	1.75E-01	2.72E+00	5.83E+00	7.59E+00	1.30E+01
keijzer-14	1.27E-01	4.03E-01	6.01E-01	7.37E-01	1.15E+00
keijzer-15	1.66E-01	2.61E+00	3.81E+00	4.79E+00	6.74E+00
vladislavleva-1	8.58E-04	1.16E-02	1.62E-02	2.30E-02	3.36E-02
vladislavleva-2	3.73E-04	1.03E-02	5.26E-02	5.51E-02	9.65E-02
vladislavleva-3	4.14E-01	7.74E-01	9.63E-01	1.18E+00	1.18E+00
vladislavleva-4	1.91E-02	3.27E-02	3.68E-02	4.00E-02	2.36E-01
vladislavleva-5	1.21E-02	1.18E-01	1.96E-01	3.18E-01	4.00E-01
vladislavleva-6	7.92E-01	3.49E+00	5.45E+00	6.88E+00	1.04E+01
vladislavleva-7	9.66E-01	5.05E+00	7.45E+00	8.97E+00	1.11E+01
vladislavleva-8	7.83E-02	4.65E-01	9.80E-01	1.62E+00	3.62E+00

Table A.9: Full 5 number quartile information for the PIMP Approach on each of the 51 Symbolic Regression test instances (First part).

			PIMP		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0.00E+00	0.00E+00	6.37E-05	6.53E-04	1.94E-01
koza-2	0.00E+00	2.55E-06	1.49E-05	1.08E-04	8.86E-04
koza-3	0.00E+00	1.05E-06	1.09E-05	5.91E-05	7.39E-03
nguyen-1	0.00E+00	0.00E+00	0.00E+00	1.46E-03	3.30E-01
nguyen-2	0.00E+00	0.00E+00	3.62E-05	2.85E-04	4.94E-03
nguyen-3	0.00E+00	0.00E+00	1.44E-05	6.02E-04	6.92E-03
nguyen-4	0.00E+00	3.52E-05	1.58E-04	7.97E-04	2.28E-02
nguyen-5	0.00E+00	9.89E-06	7.43E-05	6.05E-04	2.72E-03
nguyen-6	0.00E+00	0.00E+00	6.37E-06	9.09E-05	8.03E-02
nguyen-7	0.00E+00	2.27E-05	1.70E-04	2.82E-02	2.40E-01
nguyen-8	0.00E+00	4.51E-05	2.61E-04	2.36E-03	1.84E-02
nguyen-9	0.00E+00	0.00E+00	7.74E-04	6.18E-03	1.87E-02
nguyen-10	0.00E+00	2.09E-04	1.34E-03	1.88E-02	2.54E-02
pagie-1	9.21E-04	1.04E-02	4.28E-02	1.22E-01	2.37E-01
pagie-2	4.19E-02	1.43E-01	1.80E-01	2.31E-01	2.49E-01
korns-1	7.54E-05	1.19E+01	6.96E+01	7.75E+01	4.57E+05
korns-2	1.85E+02	3.14E+04	7.00E+04	3.59E+05	8.05E+08
korns-3	3.09E+03	2.62E+07	2.25E+08	3.85E+09	4.36E+13
korns-4	8.35E-03	8.46E-03	8.48E-03	8.53E-03	9.06E-03
korns-5	4.86E+29	4.96E+29	4.99E+29	5.04E+29	5.13E+29
korns-6	4.85E+29	4.95E+29	4.99E+29	5.03E+29	5.09E+29
korns-7	3.34E+25	1.06E+26	1.85E+26	2.41E+26	2.92E+26
korns-8	4.86E+29	4.98E+29	5.00E+29	5.04E+29	5.15E+29
korns-9	7.65E+29	7.75E+29	7.78E+29	7.79E+29	7.86E+29
korns-10	2.27E+04	9.34E+05	7.22E+06	4.03E+07	4.15E+13
korns-11	5.86E+01	6.05E+01	6.08E+01	6.11E+01	7.91E+01
korns-12	1.08E+00	1.10E+00	1.11E+00	1.11E+00	1.14E+00
korns-13	3.47E+07	2.79E+08	1.26E+09	4.54E+09	1.09E+13
korns-14	3.42E+05	1.97E+06	8.31E+06	2.33E+07	2.45E+10
korns-15	5.83E+29	5.92E+29	5.95E+29	5.98E+29	6.07E+29

Table A.10: Full 5 number quartile information for the PIMP Approach on each of the 51 Symbolic Regression test instances (Second part).

			PIMP		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	7.70E-04	2.72E-03	8.04E-03	1.18E-02	1.22E-02
keijzer-2	1.06E-02	4.10E-02	4.81E-02	5.59E-02	5.90E-02
keijzer-3	5.85E-02	1.00E-01	1.30E-01	1.30E-01	1.45E-01
keijzer-4	1.52E-02	5.45E-02	6.66E-02	1.01E-01	1.20E-01
keijzer-5	2.45E-06	1.01E-02	6.27E-02	8.07E-02	3.38E-01
keijzer-6	4.29E-04	4.58E-03	1.01E-02	1.90E-01	7.15E-01
keijzer-7	6.82E-04	1.20E-02	3.06E-02	6.31E-02	1.02E+00
keijzer-8	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
keijzer-9	5.34E-03	1.76E-02	1.01E+00	1.01E+00	1.32E+00
keijzer-10	9.96E-04	2.15E-02	2.67E-02	3.05E-02	4.43E-02
keijzer-11	4.44E-02	3.66E-01	4.67E-01	5.34E-01	7.88E+00
keijzer-12	2.04E+00	8.63E+00	5.74E+01	1.48E+02	9.07E+02
keijzer-13	3.78E-01	4.00E+00	5.89E+00	7.25E+00	9.27E+00
keijzer-14	1.78E-01	3.67E-01	5.86E-01	7.78E-01	1.23E+00
keijzer-15	2.56E-01	2.86E+00	4.17E+00	5.41E+00	8.76E+00
vladislavleva-1	2.11E-03	1.05E-02	1.51E-02	2.26E-02	4.10E-02
vladislavleva-2	2.88E-03	1.49E-02	5.32E-02	5.40E-02	1.01E-01
vladislavleva-3	2.20E-01	8.32E-01	9.27E-01	1.02E+00	1.18E+00
vladislavleva-4	2.69E-02	3.33E-02	3.71E-02	3.95E-02	5.40E-02
vladislavleva-5	6.05E-03	9.05E-02	2.16E-01	2.65E-01	3.98E-01
vladislavleva-6	1.46E+00	4.08E+00	5.30E+00	6.73E+00	1.06E+01
vladislavleva-7	1.12E+00	2.97E+00	4.51E+00	6.42E+00	9.23E+00
vladislavleva-8	7.64E-02	4.92E-01	8.66E-01	1.51E+00	3.84E+00

Table A.11: Full 5 number quartile information for the CMP-GP on each of the 51 Symbolic Regression test instances (First part).

			CMP-GP		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0.00E+00	0.00E+00	1.38E-07	7.91E-05	8.15E-02
koza-2	0.00E+00	4.69E-06	3.37E-05	1.04E-04	4.31E-04
koza-3	0.00E+00	4.45E-06	7.99E-06	2.97E-05	1.16E-03
nguyen-1	0.00E+00	0.00E+00	0.00E+00	3.50E-04	2.25E-01
nguyen-2	0.00E+00	0.00E+00	1.75E-05	1.55E-04	6.62E-03
nguyen-3	0.00E+00	0.00E+00	3.96E-05	3.72E-04	1.71E-02
nguyen-4	0.00E+00	0.00E+00	9.61E-05	5.58E-04	1.05E-02
nguyen-5	0.00E+00	1.44E-05	5.21E-05	3.52E-04	1.12E-02
nguyen-6	0.00E+00	7.26E-06	1.10E-04	1.44E-02	1.10E-01
nguyen-7	6.57E-07	2.79E-05	1.08E-04	2.65E-03	2.14E-01
nguyen-8	0.00E+00	1.11E-04	4.74E-04	1.73E-03	1.69E-02
nguyen-9	0.00E+00	3.09E-05	1.30E-03	5.64E-03	1.59E-02
nguyen-10	0.00E+00	1.94E-05	4.74E-04	1.83E-02	1.29E-01
pagie-1	6.26E-04	2.90E-03	2.02E-02	1.15E-01	1.42E-01
pagie-2	4.19E-02	1.40E-01	1.60E-01	2.33E-01	2.49E-01
korns-1	9.00E-04	1.32E+01	3.33E+01	7.83E+01	4.61E+05
korns-2	1.40E+04	3.66E+04	1.11E+05	1.29E+06	3.62E+08
korns-3	2.25E+04	7.44E+06	1.34E+08	8.67E+09	2.42E+15
korns-4	6.15E-04	8.45E-03	8.52E-03	8.57E-03	5.30E+00
korns-5	4.84E+29	4.97E+29	5.00E+29	5.03E+29	5.14E+29
korns-6	4.90E+29	4.96E+29	5.00E+29	5.03E+29	5.12E+29
korns-7	3.59E+25	8.50E+25	1.67E+26	2.40E+26	2.85E+26
korns-8	4.90E+29	4.95E+29	4.99E+29	5.01E+29	5.10E+29
korns-9	7.65E+29	7.74E+29	7.77E+29	7.80E+29	7.85E+29
korns-10	2.21E+04	7.80E+05	7.28E+06	6.86E+07	2.05E+14
korns-11	6.00E+01	6.06E+01	6.09E+01	6.13E+01	6.22E+01
korns-12	1.07E+00	1.10E+00	1.10E+00	1.11E+00	1.13E+00
korns-13	1.89E+07	1.84E+08	6.36E+08	3.25E+09	5.64E+11
korns-14	5.10E+05	2.39E+06	5.92E+06	1.79E+07	3.89E+11
korns-15	5.87E+29	5.91E+29	5.95E+29	5.98E+29	6.05E+29

Table A.12: Full 5 number quartile information for the CMP-GP on each of the 51 Symbolic Regression test instances (Second part).

			CMP-GP		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	3.43E-05	2.52E-03	4.27E-03	8.21E-03	4.05E-02
keijzer-2	1.63E-02	3.99E-02	5.59E-02	5.59E-02	6.63E-02
keijzer-3	6.82E-02	1.08E-01	1.30E-01	1.30E-01	1.33E-01
keijzer-4	1.05E-02	4.51E-02	6.49E-02	1.01E-01	1.01E-01
keijzer-5	5.75E-06	3.88E-02	5.68E-02	7.68E-02	3.27E-01
keijzer-6	2.80E-05	3.76E-03	1.02E-02	6.78E-01	8.71E-01
keijzer-7	2.88E-04	1.98E-02	3.43E-02	8.53E-01	1.21E+00
keijzer-8	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
keijzer-9	3.69E-03	1.74E-02	1.01E+00	1.01E+00	1.69E+00
keijzer-10	5.57E-04	2.22E-02	2.55E-02	2.97E-02	4.53E-02
keijzer-11	8.62E-02	3.80E-01	4.40E-01	4.89E-01	8.05E+00
keijzer-12	8.61E-01	4.73E+00	2.09E+01	1.04E+02	9.54E+02
keijzer-13	3.50E-01	2.11E+00	4.76E+00	6.42E+00	1.29E+01
keijzer-14	1.18E-01	4.05E-01	5.30E-01	8.10E-01	1.21E+00
keijzer-15	4.85E-01	2.33E+00	3.74E+00	5.02E+00	7.43E+00
vladislavleva-1	1.27E-03	1.00E-02	1.44E-02	2.21E-02	3.52E-02
vladislavleva-2	1.29E-03	7.49E-03	1.12E-02	5.29E-02	1.01E-01
vladislavleva-3	2.02E-01	8.23E-01	9.72E-01	1.18E+00	1.18E+00
vladislavleva-4	2.43E-02	3.22E-02	3.56E-02	3.97E-02	1.39E-01
vladislavleva-5	8.85E-03	9.99E-02	1.80E-01	2.61E-01	3.76E-01
vladislavleva-6	1.53E+00	3.52E+00	4.61E+00	6.37E+00	8.67E+00
vladislavleva-7	1.48E+00	2.84E+00	4.00E+00	5.93E+00	9.77E+00
vladislavleva-8	5.91E-02	3.70E-01	7.91E-01	1.25E+00	3.88E+00

Table A.13: Median and interquartile range information obtained by the Standard Approach on all 51 instances of Symbolic Regression problems (First part).

	Standard	
	Median	IQR
koza-1	2.66E-04	6.23E-04
koza-2	1.32E-04	2.81E-04
koza-3	2.67E-05	1.38E-04
nguyen-1	9.71E-06	3.98E-04
nguyen-2	4.25E-04	1.37E-03
nguyen-3	8.36E-05	1.34E-03
nguyen-4	3.96E-04	3.00E-03
nguyen-5	1.25E-04	8.21E-04
nguyen-6	5.24E-04	1.83E-02
nguyen-7	1.19E-04	4.84E-04
nguyen-8	1.01E-03	4.37E-03
nguyen-9	5.01E-03	1.42E-02
nguyen-10	1.78E-03	2.12E-02
pagie-1	4.86E-02	1.05E-01
pagie-2	1.99E-01	7.38E-02
korns-1	7.80E+01	1.03E+03
korns-2	2.12E+05	6.37E+05
korns-3	7.70E+08	1.50E+10
korns-4	8.56E-03	9.37E-03
korns-5	5.00E+29	5.20E+27
korns-6	5.01E+29	6.50E+27
korns-7	1.69E+26	1.26E+26
korns-8	4.99E+29	6.60E+27
korns-9	7.75E+29	4.47E+27
korns-10	1.07E+07	2.30E+08
korns-11	6.07E+01	8.37E-01
korns-12	1.11E+00	1.86E-02
korns-13	2.35E+09	1.38E+10
korns-14	7.91E+06	8.11E+07
korns-15	5.93E+29	5.96E+27

Table A.14: Median and interquartile range information obtained by the Standard Approach on all 51 instances of Symbolic Regression problems (Second part).

	Standard	
	Median	IQR
keijzer-1	8.04E-03	9.16E-03
keijzer-2	5.59E-02	1.50E-02
keijzer-3	1.30E-01	1.82E-02
keijzer-4	9.22E-02	4.11E-02
keijzer-5	6.51E-02	5.92E-02
keijzer-6	1.85E-02	2.27E-01
keijzer-7	1.35E-01	8.22E-01
keijzer-8	0.00E+00	0.00E+00
keijzer-9	1.01E+00	1.01E+00
keijzer-10	2.75E-02	9.07E-03
keijzer-11	4.08E-01	1.29E-01
keijzer-12	6.72E+01	1.11E+02
keijzer-13	5.83E+00	4.86E+00
keijzer-14	6.01E-01	3.34E-01
keijzer-15	3.81E+00	2.18E+00
vladislavleva-1	1.62E-02	1.13E-02
vladislavleva-2	5.26E-02	4.47E-02
vladislavleva-3	9.63E-01	4.06E-01
vladislavleva-4	3.68E-02	7.23E-03
vladislavleva-5	1.96E-01	2.00E-01
vladislavleva-6	5.45E+00	3.40E+00
vladislavleva-7	7.45E+00	3.92E+00
vladislavleva-8	9.80E-01	1.16E+00

Table A.15: Median and interquartile range information obtained by the PIMP Approach on all 51 instances of Symbolic Regression problems (First part).

	PIMP	
	Median	IQR
koza-1	6.37E-05	6.53E-04
koza-2	1.49E-05	1.05E-04
koza-3	1.09E-05	5.81E-05
nguyen-1	0.00E+00	1.46E-03
nguyen-2	3.62E-05	2.85E-04
nguyen-3	1.44E-05	6.02E-04
nguyen-4	1.58E-04	7.62E-04
nguyen-5	7.43E-05	5.95E-04
nguyen-6	6.37E-06	9.09E-05
nguyen-7	1.70E-04	2.81E-02
nguyen-8	2.61E-04	2.31E-03
nguyen-9	7.74E-04	6.18E-03
nguyen-10	1.34E-03	1.86E-02
pagie-1	4.28E-02	1.12E-01
pagie-2	1.80E-01	8.83E-02
korns-1	6.96E+01	6.56E+01
korns-2	7.00E+04	3.28E+05
korns-3	2.25E+08	3.82E+09
korns-4	8.48E-03	7.16E-05
korns-5	4.99E+29	7.90E+27
korns-6	4.99E+29	8.20E+27
korns-7	1.85E+26	1.35E+26
korns-8	5.00E+29	5.70E+27
korns-9	7.78E+29	3.90E+27
korns-10	7.22E+06	3.94E+07
korns-11	6.08E+01	6.14E-01
korns-12	1.11E+00	1.45E-02
korns-13	1.26E+09	4.26E+09
korns-14	8.31E+06	2.14E+07
korns-15	5.95E+29	6.19E+27

Table A.16: Median and interquartile range information obtained by the PIMP Approach on all 51 instances of Symbolic Regression problems (Second part).

	PIMP	
	Median	IQR
keijzer-1	8.04E-03	9.09E-03
keijzer-2	4.81E-02	1.50E-02
keijzer-3	1.30E-01	2.97E-02
keijzer-4	6.66E-02	4.62E-02
keijzer-5	6.27E-02	7.07E-02
keijzer-6	1.01E-02	1.85E-01
keijzer-7	3.06E-02	5.11E-02
keijzer-8	0.00E+00	0.00E+00
keijzer-9	1.01E+00	9.94E-01
keijzer-10	2.67E-02	8.99E-03
keijzer-11	4.67E-01	1.69E-01
keijzer-12	5.74E+01	1.39E+02
keijzer-13	5.89E+00	3.25E+00
keijzer-14	5.86E-01	4.12E-01
keijzer-15	4.17E+00	2.55E+00
vladislavleva-1	1.51E-02	1.21E-02
vladislavleva-2	5.32E-02	3.91E-02
vladislavleva-3	9.27E-01	1.91E-01
vladislavleva-4	3.71E-02	6.22E-03
vladislavleva-5	2.16E-01	1.75E-01
vladislavleva-6	5.30E+00	2.65E+00
vladislavleva-7	4.51E+00	3.44E+00
vladislavleva-8	8.66E-01	1.01E+00

Table A.17: Median and interquartile range information obtained by the CMP-GP Approach on all 51 instances of Symbolic Regression problems (First part).

	CMP-GP	
	Median	IQR
koza-1	1.38E-07	7.91E-05
koza-2	3.37E-05	9.93E-05
koza-3	7.99E-06	2.52E-05
nguyen-1	0.00E+00	3.50E-04
nguyen-2	1.75E-05	1.55E-04
nguyen-3	3.96E-05	3.72E-04
nguyen-4	9.61E-05	5.58E-04
nguyen-5	5.21E-05	3.38E-04
nguyen-6	1.10E-04	1.44E-02
nguyen-7	1.08E-04	2.62E-03
nguyen-8	4.74E-04	1.62E-03
nguyen-9	1.30E-03	5.61E-03
nguyen-10	4.74E-04	1.83E-02
pagie-1	2.02E-02	1.12E-01
pagie-2	1.60E-01	9.23E-02
korns-1	3.33E+01	6.51E+01
korns-2	1.11E+05	1.26E+06
korns-3	1.34E+08	8.66E+09
korns-4	8.52E-03	1.16E-04
korns-5	5.00E+29	6.10E+27
korns-6	5.00E+29	7.60E+27
korns-7	1.67E+26	1.55E+26
korns-8	4.99E+29	6.00E+27
korns-9	7.77E+29	5.68E+27
korns-10	7.28E+06	6.79E+07
korns-11	6.09E+01	6.74E-01
korns-12	1.10E+00	1.62E-02
korns-13	6.36E+08	3.06E+09
korns-14	5.92E+06	1.56E+07
korns-15	5.95E+29	6.74E+27

Table A.18: Median and interquartile range information obtained by the CMP-GP Approach on all 51 instances of Symbolic Regression problems (Second part).

	CMP-GP	
	Median	IQR
keijzer-1	4.27E-03	5.69E-03
keijzer-2	5.59E-02	1.60E-02
keijzer-3	1.30E-01	2.26E-02
keijzer-4	6.49E-02	5.57E-02
keijzer-5	5.68E-02	3.80E-02
keijzer-6	1.02E-02	6.74E-01
keijzer-7	3.43E-02	8.33E-01
keijzer-8	0.00E+00	0.00E+00
keijzer-9	1.01E+00	9.92E-01
keijzer-10	2.55E-02	7.52E-03
keijzer-11	4.40E-01	1.09E-01
keijzer-12	2.09E+01	9.90E+01
keijzer-13	4.76E+00	4.31E+00
keijzer-14	5.30E-01	4.05E-01
keijzer-15	3.74E+00	2.69E+00
vladislavleva-1	1.44E-02	1.21E-02
vladislavleva-2	1.12E-02	4.54E-02
vladislavleva-3	9.72E-01	3.60E-01
vladislavleva-4	3.56E-02	7.48E-03
vladislavleva-5	1.80E-01	1.61E-01
vladislavleva-6	4.61E+00	2.85E+00
vladislavleva-7	4.00E+00	3.08E+00
vladislavleva-8	7.91E-01	8.85E-01

Appendix B

Impacts of Mutation on PIMP

Table B.1: Best Fitness, MBF and sample Standard Deviation obtained by the PIMP Approach with mutation on the first chromosome on 50 runs tackling each of the 51 Symbolic Regression instances (First Part).

	Mutation 1		
	Best	MBF	StDev
koza-1	0,00E+00	4,20E-04	9,15E-07
koza-2	0,00E+00	1,37E-04	2,27E-07
koza-3	0,00E+00	2,33E-04	9,92E-07
nguyen-1	0,00E+00	3,99E-03	1,44E-04
nguyen-2	0,00E+00	3,57E-04	1,02E-06
nguyen-3	0,00E+00	5,03E-04	1,31E-06
nguyen-4	0,00E+00	6,71E-04	3,13E-06
nguyen-5	4,20E-09	2,39E-04	2,59E-07
nguyen-6	0,00E+00	5,94E-04	6,19E-06
nguyen-7	1,00E-07	1,51E-03	3,02E-05
nguyen-8	0,00E+00	1,88E-03	1,74E-05
nguyen-9	0,00E+00	1,63E-03	6,56E-06
nguyen-10	0,00E+00	1,20E-03	1,81E-05
pagie-1	2,10E-03	3,98E-02	1,91E-03
pagie-2	2,18E-02	1,52E-01	2,52E-03
korns-1	1,75E-01	3,96E+03	2,60E+08
korns-2	1,82E+02	4,63E+06	8,97E+14
korns-3	1,65E+03	5,36E+12	9,58E+26
korns-4	7,47E-05	7,15E-03	8,62E-06
korns-5	4,86E+29	4,99E+29	2,09E+55
korns-6	4,89E+29	4,99E+29	2,65E+55
korns-7	1,62E+20	1,37E+26	4,72E+51
korns-8	4,89E+29	5,00E+29	2,30E+55
korns-9	7,68E+29	7,75E+29	1,26E+55
korns-10	1,22E+04	2,88E+09	2,28E+20
korns-11	5,95E+01	6,06E+01	2,85E-01
korns-12	1,08E+00	1,11E+00	1,73E-04
korns-13	2,77E+07	1,27E+12	7,50E+25
korns-14	3,79E+05	1,59E+08	9,58E+17
korns-15	5,86E+29	5,94E+29	3,05E+55

Table B.2: Best Fitness, MBF and sample Standard Deviation obtained by the PIMP Approach with mutation on the first chromosome on 50 runs tackling each of the 51 Symbolic Regression instances (Second part).

	Mutation 1		
	Best	MBF	StDev
keijzer-1	8,36E-04	3,84E-03	5,82E-06
keijzer-2	1,52E-02	3,88E-02	9,10E-05
keijzer-3	6,14E-02	1,07E-01	1,73E-04
keijzer-4	1,39E-02	6,46E-02	6,30E-04
keijzer-5	1,31E-05	1,20E-02	2,60E-04
keijzer-6	6,11E-05	9,18E-03	2,29E-04
keijzer-7	1,71E-04	3,86E-02	1,51E-02
keijzer-8	0,00E+00	0,00E+00	0,00E+00
keijzer-9	3,45E-04	1,50E-01	1,08E-01
keijzer-10	5,33E-04	1,88E-02	1,07E-04
keijzer-11	4,35E-02	5,13E-01	7,48E-01
keijzer-12	5,33E-03	2,94E+01	5,22E+03
keijzer-13	2,61E-01	3,76E+00	5,46E+00
keijzer-14	2,45E-02	4,16E-01	7,79E-02
keijzer-15	3,71E-01	2,75E+00	2,68E+00
vladislavleva-1	1,04E-03	7,60E-03	2,48E-05
vladislavleva-2	3,57E-04	2,77E-02	5,61E-04
vladislavleva-3	1,54E-01	8,07E-01	3,99E-02
vladislavleva-4	2,31E-02	3,39E-02	2,69E-05
vladislavleva-5	1,20E-02	1,67E-01	7,19E-03
vladislavleva-6	2,04E+00	4,77E+00	3,66E+00
vladislavleva-7	1,55E+00	4,87E+00	5,03E+00
vladislavleva-8	2,38E-01	8,63E-01	2,41E-01

Table B.3: Best Fitness, MBF and sample Standard Deviation obtained by the PIMP Approach with mutation on the second chromosome on 50 runs tackling each of the 51 Symbolic Regression instances (First part).

	Mutation 2		
	Best	MBF	StDev
koza-1	0,00E+00	3,45E-04	8,26E-07
koza-2	0,00E+00	2,65E-04	1,57E-06
koza-3	0,00E+00	3,67E-04	2,74E-06
nguyen-1	0,00E+00	6,13E-03	1,90E-04
nguyen-2	0,00E+00	5,22E-03	5,75E-04
nguyen-3	0,00E+00	2,67E-03	1,27E-04
nguyen-4	0,00E+00	3,95E-03	5,19E-04
nguyen-5	0,00E+00	2,58E-04	2,86E-07
nguyen-6	0,00E+00	1,04E-02	6,34E-04
nguyen-7	4,37E-07	2,70E-02	3,01E-03
nguyen-8	0,00E+00	2,16E-03	2,45E-05
nguyen-9	0,00E+00	5,17E-03	4,53E-05
nguyen-10	0,00E+00	1,30E-02	2,83E-04
pagie-1	2,43E-04	4,95E-02	2,44E-03
pagie-2	2,61E-02	1,88E-01	2,51E-03
korns-1	2,04E-06	1,27E+05	4,21E+10
korns-2	9,93E+02	1,15E+07	3,33E+15
korns-3	2,88E+03	3,15E+12	4,77E+26
korns-4	1,09E-05	9,28E-03	2,55E-05
korns-5	4,89E+29	4,99E+29	2,59E+55
korns-6	4,90E+29	5,00E+29	2,09E+55
korns-7	1,02E+23	1,36E+26	6,39E+51
korns-8	4,90E+29	4,99E+29	2,83E+55
korns-9	7,63E+29	7,76E+29	2,41E+55
korns-10	5,09E+04	4,86E+11	1,02E+25
korns-11	5,97E+01	6,11E+01	6,17E+00
korns-12	1,09E+00	1,13E+00	1,99E-02
korns-13	3,66E+07	4,17E+12	8,62E+26
korns-14	1,16E+06	1,72E+10	9,07E+21
korns-15	5,83E+29	5,95E+29	3,03E+55

Table B.4: Best Fitness, MBF and sample Standard Deviation obtained by the PIMP Approach with mutation on the second chromosome on 50 runs tackling each of the 51 Symbolic Regression instances (Second part).

	Mutation 2		
	Best	MBF	StDev
keijzer-1	4,15E-04	6,76E-03	1,34E-05
keijzer-2	1,57E-02	4,43E-02	1,59E-04
keijzer-3	5,00E-02	1,18E-01	3,58E-04
keijzer-4	1,88E-02	7,21E-02	6,04E-04
keijzer-5	3,09E-06	1,15E-01	1,40E-02
keijzer-6	1,64E-04	1,75E-01	8,49E-02
keijzer-7	7,10E-04	3,56E-01	1,83E-01
keijzer-8	0,00E+00	0,00E+00	0,00E+00
keijzer-9	3,59E-03	4,59E-01	2,55E-01
keijzer-10	1,03E-03	2,59E-02	5,22E-05
keijzer-11	8,32E-02	1,04E+00	7,32E+00
keijzer-12	2,37E-03	4,42E+01	1,83E+04
keijzer-13	4,29E-01	5,10E+00	8,69E+00
keijzer-14	9,49E-02	5,62E-01	7,84E-02
keijzer-15	3,60E-01	3,85E+00	4,23E+00
vladislavleva-1	5,08E-04	1,41E-02	6,02E-05
vladislavleva-2	1,27E-03	3,69E-02	7,95E-04
vladislavleva-3	5,05E-01	9,25E-01	3,16E-02
vladislavleva-4	2,60E-02	3,57E-02	2,16E-05
vladislavleva-5	1,12E-02	2,27E-01	1,24E-02
vladislavleva-6	1,33E+00	5,05E+00	4,28E+00
vladislavleva-7	1,28E+00	4,45E+00	4,33E+00
vladislavleva-8	2,08E-01	1,34E+00	9,36E-01

Table B.5: Best Fitness, MBF and sample Standard Deviation obtained by the PIMP Approach with mutation on both chromosomes on 50 runs tackling each of the 51 Symbolic Regression instances (First part).

	Mutation Both		
	Best	MBF	StDev
koza-1	0,00E+00	8,72E-04	1,35E-05
koza-2	0,00E+00	4,36E-05	4,34E-09
koza-3	0,00E+00	4,40E-05	7,67E-09
nguyen-1	0,00E+00	4,72E-04	5,41E-06
nguyen-2	0,00E+00	3,72E-04	6,04E-07
nguyen-3	0,00E+00	2,91E-04	3,54E-07
nguyen-4	0,00E+00	3,77E-04	3,16E-07
nguyen-5	0,00E+00	4,18E-04	4,54E-07
nguyen-6	0,00E+00	5,31E-05	3,06E-08
nguyen-7	9,11E-07	1,60E-04	5,94E-08
nguyen-8	1,45E-07	1,91E-03	1,62E-05
nguyen-9	0,00E+00	1,37E-03	3,97E-06
nguyen-10	0,00E+00	7,42E-04	6,16E-06
pagie-1	3,66E-04	3,04E-02	1,83E-03
pagie-2	4,42E-02	1,51E-01	2,45E-03
korns-1	2,74E-02	6,52E+03	1,35E+09
korns-2	7,29E-02	1,87E+05	5,79E+11
korns-3	9,07E+02	3,26E+16	5,27E+34
korns-4	5,41E-05	8,28E-03	2,33E-05
korns-5	4,87E+29	4,99E+29	2,43E+55
korns-6	4,89E+29	5,01E+29	2,41E+55
korns-7	9,93E+22	1,38E+26	4,49E+51
korns-8	4,93E+29	5,00E+29	1,94E+55
korns-9	7,65E+29	7,76E+29	1,68E+55
korns-10	1,95E+04	9,30E+08	2,42E+19
korns-11	5,92E+01	6,05E+01	3,62E-01
korns-12	1,09E+00	1,11E+00	1,80E-04
korns-13	5,06E+07	6,29E+10	8,68E+22
korns-14	4,74E+05	1,31E+08	2,37E+17
korns-15	5,79E+29	5,93E+29	3,13E+55

Table B.6: Best Fitness, MBF and sample Standard Deviation obtained by the PIMP Approach with mutation on both chromosomes on 50 runs tackling each of the 51 Symbolic Regression instances (Second part).

	Mutation Both		
	Best	MBF	StDev
keijzer-1	2,35E-04	3,91E-03	1,00E-05
keijzer-2	2,63E-02	3,94E-02	5,38E-05
keijzer-3	1,22E-02	1,03E-01	3,54E-04
keijzer-4	1,90E-02	6,51E-02	6,01E-04
keijzer-5	1,76E-05	2,47E-02	3,58E-03
keijzer-6	9,73E-05	4,58E-02	2,60E-02
keijzer-7	3,30E-04	1,68E-02	1,52E-04
keijzer-8	0,00E+00	0,00E+00	0,00E+00
keijzer-9	2,00E-04	1,21E-01	9,27E-02
keijzer-10	1,28E-03	1,63E-02	9,00E-05
keijzer-11	6,83E-02	3,65E-01	1,99E-02
keijzer-12	2,03E-05	1,25E+01	2,94E+02
keijzer-13	2,38E-01	3,29E+00	3,42E+00
keijzer-14	1,14E-02	4,13E-01	7,92E-02
keijzer-15	4,39E-02	1,76E+00	2,84E+00
vladislavleva-1	1,23E-03	7,50E-03	3,52E-05
vladislavleva-2	1,03E-03	3,07E-02	5,49E-04
vladislavleva-3	2,66E-01	8,21E-01	3,19E-02
vladislavleva-4	2,49E-02	3,50E-02	1,85E-05
vladislavleva-5	2,38E-03	1,54E-01	8,59E-03
vladislavleva-6	6,46E-01	4,53E+00	4,56E+00
vladislavleva-7	1,26E+00	4,91E+00	4,70E+00
vladislavleva-8	6,37E-02	7,20E-01	2,26E-01

Table B.7: Full 5 number quartile information for PIMP with mutation on the first chromosome on each of the 51 Symbolic Regression test instances (First part).

			Mutation 1		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0,00E+00	0,00E+00	5,61E-05	2,34E-04	4,33E-03
koza-2	0,00E+00	2,47E-06	2,44E-05	1,29E-04	3,37E-03
koza-3	0,00E+00	4,10E-06	1,93E-05	7,34E-05	6,98E-03
nguyen-1	0,00E+00	0,00E+00	0,00E+00	2,46E-04	5,80E-02
nguyen-2	0,00E+00	0,00E+00	3,00E-05	2,23E-04	6,25E-03
nguyen-3	0,00E+00	0,00E+00	7,36E-05	4,17E-04	6,47E-03
nguyen-4	0,00E+00	3,34E-05	1,14E-04	8,02E-04	1,22E-02
nguyen-5	4,20E-09	8,49E-06	3,22E-05	2,09E-04	2,93E-03
nguyen-6	0,00E+00	0,00E+00	3,06E-07	7,09E-05	1,54E-02
nguyen-7	1,00E-07	2,12E-05	5,37E-05	2,27E-04	2,74E-02
nguyen-8	0,00E+00	3,59E-05	2,09E-04	1,55E-03	1,88E-02
nguyen-9	0,00E+00	0,00E+00	6,74E-04	2,08E-03	1,28E-02
nguyen-10	0,00E+00	8,87E-06	2,54E-04	4,60E-04	2,25E-02
pagie-1	2,10E-03	9,28E-03	2,35E-02	5,15E-02	1,78E-01
pagie-2	2,18E-02	1,25E-01	1,59E-01	1,88E-01	2,42E-01
korns-1	1,75E-01	6,14E+00	1,19E+01	4,68E+01	8,03E+04
korns-2	1,82E+02	2,85E+04	6,56E+04	2,79E+05	2,12E+08
korns-3	1,65E+03	2,31E+06	1,04E+08	1,91E+09	2,18E+14
korns-4	7,47E-05	8,40E-03	8,47E-03	8,52E-03	8,62E-03
korns-5	4,86E+29	4,95E+29	5,00E+29	5,03E+29	5,05E+29
korns-6	4,89E+29	4,96E+29	5,00E+29	5,02E+29	5,09E+29
korns-7	1,62E+20	7,64E+25	1,38E+26	1,96E+26	2,73E+26
korns-8	4,89E+29	4,96E+29	5,01E+29	5,02E+29	5,09E+29
korns-9	7,68E+29	7,72E+29	7,76E+29	7,78E+29	7,84E+29
korns-10	1,22E+04	4,20E+05	4,67E+06	7,02E+07	1,06E+11
korns-11	5,95E+01	6,03E+01	6,06E+01	6,10E+01	6,17E+01
korns-12	1,08E+00	1,10E+00	1,11E+00	1,12E+00	1,14E+00
korns-13	2,77E+07	3,73E+08	1,40E+09	1,10E+10	6,13E+13
korns-14	3,79E+05	1,64E+06	4,80E+06	2,47E+07	6,94E+09
korns-15	5,86E+29	5,89E+29	5,94E+29	5,97E+29	6,09E+29

Table B.8: Full 5 number quartile information for PIMP with mutation on the first chromosome on each of the 51 Symbolic Regression test instances (Second part).

			Mutation 1		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	8,36E-04	2,33E-03	2,99E-03	4,49E-03	1,06E-02
keijzer-2	1,52E-02	3,42E-02	3,82E-02	4,59E-02	5,61E-02
keijzer-3	6,14E-02	1,02E-01	1,10E-01	1,13E-01	1,30E-01
keijzer-4	1,39E-02	4,70E-02	6,16E-02	9,26E-02	1,01E-01
keijzer-5	1,31E-05	5,84E-04	4,88E-03	1,54E-02	7,18E-02
keijzer-6	6,11E-05	1,24E-03	3,94E-03	1,01E-02	8,91E-02
keijzer-7	1,71E-04	5,96E-03	1,19E-02	2,81E-02	8,53E-01
keijzer-8	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
keijzer-9	3,45E-04	1,02E-02	1,74E-02	2,18E-02	1,02E+00
keijzer-10	5,33E-04	1,16E-02	2,01E-02	2,63E-02	3,67E-02
keijzer-11	4,35E-02	3,11E-01	4,36E-01	5,00E-01	6,41E+00
keijzer-12	5,33E-03	1,87E+00	7,06E+00	1,59E+01	4,62E+02
keijzer-13	2,61E-01	1,55E+00	3,59E+00	5,46E+00	9,28E+00
keijzer-14	2,45E-02	2,33E-01	3,84E-01	5,42E-01	1,06E+00
keijzer-15	3,71E-01	1,04E+00	2,71E+00	4,29E+00	5,87E+00
vladislavleva-1	1,04E-03	3,85E-03	6,62E-03	1,06E-02	2,07E-02
vladislavleva-2	3,57E-04	7,78E-03	1,54E-02	5,30E-02	8,54E-02
vladislavleva-3	1,54E-01	7,12E-01	8,54E-01	9,54E-01	1,03E+00
vladislavleva-4	2,31E-02	3,05E-02	3,33E-02	3,79E-02	4,38E-02
vladislavleva-5	1,20E-02	1,03E-01	1,60E-01	2,21E-01	3,67E-01
vladislavleva-6	2,04E+00	3,17E+00	4,42E+00	5,89E+00	9,56E+00
vladislavleva-7	1,55E+00	2,74E+00	4,53E+00	6,62E+00	1,02E+01
vladislavleva-8	2,38E-01	5,01E-01	7,44E-01	1,17E+00	2,19E+00

Table B.9: Full 5 number quartile information for PIMP with mutation on the second chromosome on each of the 51 Symbolic Regression test instances (First part).

	Mutation 2				
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0,00E+00	0,00E+00	3,21E-05	2,39E-04	5,54E-03
koza-2	0,00E+00	6,62E-07	1,16E-05	8,65E-05	8,82E-03
koza-3	0,00E+00	2,48E-07	5,45E-06	4,03E-05	9,23E-03
nguyen-1	0,00E+00	0,00E+00	0,00E+00	3,83E-04	5,48E-02
nguyen-2	0,00E+00	0,00E+00	2,10E-05	5,06E-04	1,28E-01
nguyen-3	0,00E+00	0,00E+00	2,38E-05	3,43E-04	6,63E-02
nguyen-4	0,00E+00	2,09E-06	1,27E-04	6,78E-04	1,61E-01
nguyen-5	0,00E+00	1,43E-06	2,60E-05	1,30E-04	2,18E-03
nguyen-6	0,00E+00	0,00E+00	3,05E-05	9,84E-04	8,82E-02
nguyen-7	4,37E-07	3,26E-05	2,77E-04	2,51E-02	2,00E-01
nguyen-8	0,00E+00	1,03E-05	2,04E-04	1,35E-03	2,41E-02
nguyen-9	0,00E+00	0,00E+00	1,06E-03	1,31E-02	2,38E-02
nguyen-10	0,00E+00	9,50E-05	1,26E-02	2,07E-02	9,76E-02
pagie-1	2,43E-04	3,85E-03	2,64E-02	1,06E-01	1,51E-01
pagie-2	2,61E-02	1,59E-01	1,86E-01	2,33E-01	2,84E-01
korns-1	2,04E-06	2,00E+01	7,73E+01	4,47E+05	4,62E+05
korns-2	9,93E+02	3,09E+04	1,54E+05	5,18E+05	4,02E+08
korns-3	2,88E+03	1,65E+07	8,94E+07	1,59E+09	1,55E+14
korns-4	1,09E-05	8,42E-03	8,49E-03	8,53E-03	3,37E-02
korns-5	4,89E+29	4,96E+29	4,99E+29	5,02E+29	5,09E+29
korns-6	4,90E+29	4,96E+29	5,01E+29	5,04E+29	5,10E+29
korns-7	1,02E+23	6,81E+25	1,26E+26	2,18E+26	2,50E+26
korns-8	4,90E+29	4,94E+29	4,99E+29	5,01E+29	5,12E+29
korns-9	7,63E+29	7,73E+29	7,76E+29	7,79E+29	7,85E+29
korns-10	5,09E+04	1,51E+06	9,57E+06	1,41E+08	2,26E+13
korns-11	5,97E+01	6,04E+01	6,07E+01	6,11E+01	7,79E+01
korns-12	1,09E+00	1,10E+00	1,11E+00	1,12E+00	2,10E+00
korns-13	3,66E+07	3,16E+08	1,39E+09	1,09E+10	2,08E+14
korns-14	1,16E+06	5,79E+06	4,27E+07	3,28E+08	6,59E+11
korns-15	5,83E+29	5,91E+29	5,95E+29	5,98E+29	6,07E+29

Table B.10: Full 5 number quartile information for PIMP with mutation on the second chromosome on each of the 51 Symbolic Regression test instances (Second part).

			Mutation 2		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	4,15E-04	3,05E-03	8,04E-03	8,84E-03	1,27E-02
keijzer-2	1,57E-02	3,67E-02	4,23E-02	5,59E-02	7,76E-02
keijzer-3	5,00E-02	1,05E-01	1,30E-01	1,30E-01	1,38E-01
keijzer-4	1,88E-02	5,52E-02	6,27E-02	1,01E-01	1,11E-01
keijzer-5	3,09E-06	3,72E-02	4,73E-02	2,69E-01	3,24E-01
keijzer-6	1,64E-04	1,01E-02	1,02E-02	6,46E-02	7,19E-01
keijzer-7	7,10E-04	1,75E-02	4,68E-02	8,53E-01	1,11E+00
keijzer-8	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
keijzer-9	3,59E-03	1,74E-02	2,18E-02	1,01E+00	1,08E+00
keijzer-10	1,03E-03	2,18E-02	2,74E-02	3,15E-02	3,56E-02
keijzer-11	8,32E-02	3,91E-01	4,35E-01	4,80E-01	1,52E+01
keijzer-12	2,37E-03	3,60E+00	7,94E+00	2,29E+01	9,36E+02
keijzer-13	4,29E-01	3,05E+00	5,65E+00	7,24E+00	1,31E+01
keijzer-14	9,49E-02	3,60E-01	5,44E-01	7,42E-01	1,22E+00
keijzer-15	3,60E-01	2,27E+00	4,19E+00	5,31E+00	1,01E+01
vladislavleva-1	5,08E-04	9,71E-03	1,20E-02	1,79E-02	3,24E-02
vladislavleva-2	1,27E-03	8,11E-03	4,83E-02	5,35E-02	1,01E-01
vladislavleva-3	5,05E-01	8,32E-01	9,16E-01	1,02E+00	1,18E+00
vladislavleva-4	2,60E-02	3,25E-02	3,51E-02	3,92E-02	4,48E-02
vladislavleva-5	1,12E-02	1,62E-01	2,43E-01	3,29E-01	4,18E-01
vladislavleva-6	1,33E+00	3,45E+00	4,65E+00	6,62E+00	9,50E+00
vladislavleva-7	1,28E+00	2,57E+00	4,40E+00	5,61E+00	9,03E+00
vladislavleva-8	2,08E-01	6,22E-01	1,02E+00	1,87E+00	4,50E+00

Table B.11: Full 5 number quartile information for PIMP with mutation on both chromosomes on each of the 51 Symbolic Regression test instances (First part).

	Mutation Both				
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0,00E+00	0,00E+00	1,15E-04	4,57E-04	2,60E-02
koza-2	0,00E+00	1,78E-06	1,02E-05	6,58E-05	2,79E-04
koza-3	0,00E+00	1,83E-06	6,85E-06	4,11E-05	3,47E-04
nguyen-1	0,00E+00	0,00E+00	0,00E+00	6,88E-05	1,64E-02
nguyen-2	0,00E+00	0,00E+00	3,41E-05	3,70E-04	3,51E-03
nguyen-3	0,00E+00	0,00E+00	6,65E-05	1,92E-04	3,01E-03
nguyen-4	0,00E+00	4,49E-05	1,40E-04	4,83E-04	2,59E-03
nguyen-5	0,00E+00	2,52E-05	9,83E-05	3,24E-04	2,83E-03
nguyen-6	0,00E+00	0,00E+00	0,00E+00	2,08E-05	1,16E-03
nguyen-7	9,11E-07	1,32E-05	6,32E-05	2,20E-04	1,35E-03
nguyen-8	1,45E-07	7,60E-05	3,28E-04	1,37E-03	2,05E-02
nguyen-9	0,00E+00	0,00E+00	1,73E-04	2,08E-03	7,13E-03
nguyen-10	0,00E+00	6,00E-07	7,28E-05	2,47E-04	1,63E-02
pagie-1	3,66E-04	4,54E-03	1,48E-02	3,62E-02	2,19E-01
pagie-2	4,42E-02	1,20E-01	1,59E-01	1,82E-01	2,43E-01
korns-1	2,74E-02	7,55E+00	1,22E+01	5,23E+01	2,52E+05
korns-2	7,29E-02	1,79E+04	3,75E+04	1,34E+05	5,41E+06
korns-3	9,07E+02	5,81E+06	2,44E+07	6,53E+08	1,62E+18
korns-4	5,41E-05	8,43E-03	8,47E-03	8,51E-03	3,76E-02
korns-5	4,87E+29	4,95E+29	4,98E+29	5,02E+29	5,10E+29
korns-6	4,89E+29	4,97E+29	5,01E+29	5,04E+29	5,12E+29
korns-7	9,93E+22	8,19E+25	1,47E+26	1,95E+26	2,62E+26
korns-8	4,93E+29	4,97E+29	5,00E+29	5,02E+29	5,11E+29
korns-9	7,65E+29	7,74E+29	7,75E+29	7,79E+29	7,83E+29
korns-10	1,95E+04	2,02E+05	1,51E+06	8,89E+06	3,40E+10
korns-11	5,92E+01	5,99E+01	6,05E+01	6,10E+01	6,16E+01
korns-12	1,09E+00	1,10E+00	1,11E+00	1,12E+00	1,14E+00
korns-13	5,06E+07	3,88E+08	2,46E+09	1,74E+10	2,07E+12
korns-14	4,74E+05	2,26E+06	5,52E+06	3,67E+07	3,23E+09
korns-15	5,79E+29	5,89E+29	5,94E+29	5,97E+29	6,03E+29

Table B.12: Full 5 number quartile information for PIMP with mutation on both chromosomes on each of the 51 Symbolic Regression test instances (Second part).

	Mutation Both				
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	2,35E-04	1,80E-03	2,48E-03	5,50E-03	1,23E-02
keijzer-2	2,63E-02	3,44E-02	3,99E-02	4,57E-02	5,60E-02
keijzer-3	1,22E-02	9,46E-02	1,05E-01	1,14E-01	1,32E-01
keijzer-4	1,90E-02	4,80E-02	5,72E-02	9,20E-02	1,01E-01
keijzer-5	1,76E-05	4,98E-04	3,55E-03	2,74E-02	3,53E-01
keijzer-6	9,73E-05	1,06E-03	2,66E-03	1,01E-02	6,78E-01
keijzer-7	3,30E-04	5,39E-03	1,37E-02	3,06E-02	5,00E-02
keijzer-8	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
keijzer-9	2,00E-04	8,29E-03	1,74E-02	1,77E-02	1,02E+00
keijzer-10	1,28E-03	8,50E-03	1,66E-02	2,31E-02	3,79E-02
keijzer-11	6,83E-02	2,50E-01	3,86E-01	4,60E-01	6,66E-01
keijzer-12	2,03E-05	2,19E+00	5,84E+00	1,57E+01	7,78E+01
keijzer-13	2,38E-01	1,68E+00	3,20E+00	4,49E+00	7,56E+00
keijzer-14	1,14E-02	1,80E-01	3,77E-01	6,15E-01	1,34E+00
keijzer-15	4,39E-02	4,96E-01	9,71E-01	2,76E+00	6,59E+00
vladislavleva-1	1,23E-03	3,28E-03	5,58E-03	8,36E-03	2,51E-02
vladislavleva-2	1,03E-03	9,16E-03	1,67E-02	5,31E-02	7,89E-02
vladislavleva-3	2,66E-01	7,19E-01	8,68E-01	9,30E-01	1,16E+00
vladislavleva-4	2,49E-02	3,26E-02	3,49E-02	3,80E-02	4,39E-02
vladislavleva-5	2,38E-03	8,07E-02	1,36E-01	2,26E-01	3,73E-01
vladislavleva-6	6,46E-01	2,83E+00	4,40E+00	5,93E+00	1,13E+01
vladislavleva-7	1,26E+00	2,63E+00	4,63E+00	6,88E+00	9,31E+00
vladislavleva-8	6,37E-02	3,29E-01	5,73E-01	1,03E+00	1,90E+00

Table B.13: Median and interquartile range information obtained by PIMP with mutation on the first chromosome on all 51 instances of Symbolic Regression problems (First part).

	Mutation 1	
	Median	IQR
koza-1	5,61E-05	2,34E-04
koza-2	2,44E-05	1,27E-04
koza-3	1,93E-05	6,93E-05
nguyen-1	0,00E+00	2,46E-04
nguyen-2	3,00E-05	2,23E-04
nguyen-3	7,36E-05	4,17E-04
nguyen-4	1,14E-04	7,68E-04
nguyen-5	3,22E-05	2,00E-04
nguyen-6	3,06E-07	7,09E-05
nguyen-7	5,37E-05	2,06E-04
nguyen-8	2,09E-04	1,51E-03
nguyen-9	6,74E-04	2,08E-03
nguyen-10	2,54E-04	4,51E-04
pagie-1	2,35E-02	4,22E-02
pagie-2	1,59E-01	6,26E-02
korns-1	1,19E+01	4,07E+01
korns-2	6,56E+04	2,50E+05
korns-3	1,04E+08	1,91E+09
korns-4	8,47E-03	1,27E-04
korns-5	5,00E+29	7,40E+27
korns-6	5,00E+29	6,20E+27
korns-7	1,38E+26	1,20E+26
korns-8	5,01E+29	6,10E+27
korns-9	7,76E+29	5,21E+27
korns-10	4,67E+06	6,97E+07
korns-11	6,06E+01	6,73E-01
korns-12	1,11E+00	1,52E-02
korns-13	1,40E+09	1,06E+10
korns-14	4,80E+06	2,31E+07
korns-15	5,94E+29	7,97E+27

Table B.14: Median and interquartile range information obtained by PIMP with mutation on the first chromosome on all 51 instances of Symbolic Regression problems (Second part).

	Mutation 1	
	Median	IQR
keijzer-1	2,99E-03	2,15E-03
keijzer-2	3,82E-02	1,17E-02
keijzer-3	1,10E-01	1,12E-02
keijzer-4	6,16E-02	4,56E-02
keijzer-5	4,88E-03	1,48E-02
keijzer-6	3,94E-03	8,89E-03
keijzer-7	1,19E-02	2,21E-02
keijzer-8	0,00E+00	0,00E+00
keijzer-9	1,74E-02	1,16E-02
keijzer-10	2,01E-02	1,47E-02
keijzer-11	4,36E-01	1,89E-01
keijzer-12	7,06E+00	1,40E+01
keijzer-13	3,59E+00	3,91E+00
keijzer-14	3,84E-01	3,09E-01
keijzer-15	2,71E+00	3,24E+00
vladislavleva-1	6,62E-03	6,75E-03
vladislavleva-2	1,54E-02	4,52E-02
vladislavleva-3	8,54E-01	2,41E-01
vladislavleva-4	3,33E-02	7,42E-03
vladislavleva-5	1,60E-01	1,18E-01
vladislavleva-6	4,42E+00	2,72E+00
vladislavleva-7	4,53E+00	3,89E+00
vladislavleva-8	7,44E-01	6,74E-01

Table B.15: Median and interquartile range information obtained by PIMP with mutation on the second chromosome on all 51 instances of Symbolic Regression problems (First part).

	Mutation 2	
	Median	IQR
koza-1	3,21E-05	2,39E-04
koza-2	1,16E-05	8,59E-05
koza-3	5,45E-06	4,00E-05
nguyen-1	0,00E+00	3,83E-04
nguyen-2	2,10E-05	5,06E-04
nguyen-3	2,38E-05	3,43E-04
nguyen-4	1,27E-04	6,76E-04
nguyen-5	2,60E-05	1,29E-04
nguyen-6	3,05E-05	9,84E-04
nguyen-7	2,77E-04	2,51E-02
nguyen-8	2,04E-04	1,34E-03
nguyen-9	1,06E-03	1,31E-02
nguyen-10	1,26E-02	2,06E-02
pagie-1	2,64E-02	1,02E-01
pagie-2	1,86E-01	7,48E-02
korns-1	7,73E+01	4,47E+05
korns-2	1,54E+05	4,87E+05
korns-3	8,94E+07	1,57E+09
korns-4	8,49E-03	1,11E-04
korns-5	4,99E+29	6,20E+27
korns-6	5,01E+29	7,70E+27
korns-7	1,26E+26	1,49E+26
korns-8	4,99E+29	7,10E+27
korns-9	7,76E+29	5,87E+27
korns-10	9,57E+06	1,39E+08
korns-11	6,07E+01	7,52E-01
korns-12	1,11E+00	1,59E-02
korns-13	1,39E+09	1,06E+10
korns-14	4,27E+07	3,22E+08
korns-15	5,95E+29	6,76E+27

Table B.16: Median and interquartile range information obtained by PIMP with mutation on the second chromosome on all 51 instances of Symbolic Regression problems (Second part).

	Mutation 2	
	Median	IQR
keijzer-1	8,04E-03	5,79E-03
keijzer-2	4,23E-02	1,92E-02
keijzer-3	1,30E-01	2,47E-02
keijzer-4	6,27E-02	4,56E-02
keijzer-5	4,73E-02	2,32E-01
keijzer-6	1,02E-02	5,45E-02
keijzer-7	4,68E-02	8,35E-01
keijzer-8	0,00E+00	0,00E+00
keijzer-9	2,18E-02	9,93E-01
keijzer-10	2,74E-02	9,68E-03
keijzer-11	4,35E-01	8,95E-02
keijzer-12	7,94E+00	1,93E+01
keijzer-13	5,65E+00	4,19E+00
keijzer-14	5,44E-01	3,81E-01
keijzer-15	4,19E+00	3,04E+00
vladislavleva-1	1,20E-02	8,21E-03
vladislavleva-2	4,83E-02	4,54E-02
vladislavleva-3	9,16E-01	1,86E-01
vladislavleva-4	3,51E-02	6,71E-03
vladislavleva-5	2,43E-01	1,67E-01
vladislavleva-6	4,65E+00	3,18E+00
vladislavleva-7	4,40E+00	3,04E+00
vladislavleva-8	1,02E+00	1,25E+00

Table B.17: Median and interquartile range information obtained by PIMP with mutation on both chromosomes on all 51 instances of Symbolic Regression problems (First part).

	Mutation Both	
	Median	IQR
koza-1	0,00E+00	4,57E-04
koza-2	1,78E-06	6,40E-05
koza-3	1,83E-06	3,92E-05
nguyen-1	0,00E+00	6,88E-05
nguyen-2	0,00E+00	3,70E-04
nguyen-3	0,00E+00	1,92E-04
nguyen-4	4,49E-05	4,38E-04
nguyen-5	2,52E-05	2,98E-04
nguyen-6	0,00E+00	2,08E-05
nguyen-7	1,32E-05	2,07E-04
nguyen-8	7,60E-05	1,29E-03
nguyen-9	0,00E+00	2,08E-03
nguyen-10	6,00E-07	2,47E-04
pagie-1	4,54E-03	3,17E-02
pagie-2	1,20E-01	6,14E-02
korns-1	7,55E+00	4,47E+01
korns-2	1,79E+04	1,16E+05
korns-3	5,81E+06	6,47E+08
korns-4	8,43E-03	8,85E-05
korns-5	4,95E+29	6,40E+27
korns-6	4,97E+29	7,90E+27
korns-7	8,19E+25	1,13E+26
korns-8	4,97E+29	5,60E+27
korns-9	7,74E+29	5,61E+27
korns-10	2,02E+05	8,69E+06
korns-11	5,99E+01	1,04E+00
korns-12	1,10E+00	2,12E-02
korns-13	3,88E+08	1,70E+10
korns-14	2,26E+06	3,44E+07
korns-15	5,89E+29	8,00E+27

Table B.18: Median and interquartile range information obtained by PIMP with mutation on both chromosomes on all 51 instances of Symbolic Regression problems (Second part).

	Mutation Both	
	Median	IQR
keijzer-1	1,80E-03	3,70E-03
keijzer-2	3,44E-02	1,13E-02
keijzer-3	9,46E-02	1,96E-02
keijzer-4	4,80E-02	4,40E-02
keijzer-5	4,98E-04	2,69E-02
keijzer-6	1,06E-03	9,05E-03
keijzer-7	5,39E-03	2,52E-02
keijzer-8	0,00E+00	0,00E+00
keijzer-9	8,29E-03	9,43E-03
keijzer-10	8,50E-03	1,46E-02
keijzer-11	2,50E-01	2,10E-01
keijzer-12	2,19E+00	1,35E+01
keijzer-13	1,68E+00	2,81E+00
keijzer-14	1,80E-01	4,35E-01
keijzer-15	4,96E-01	2,26E+00
vladislavleva-1	3,28E-03	5,08E-03
vladislavleva-2	9,16E-03	4,39E-02
vladislavleva-3	7,19E-01	2,11E-01
vladislavleva-4	3,26E-02	5,38E-03
vladislavleva-5	8,07E-02	1,45E-01
vladislavleva-6	2,83E+00	3,09E+00
vladislavleva-7	2,63E+00	4,25E+00
vladislavleva-8	3,29E-01	6,96E-01

Table B.19: Comparison between different Mutation setups for the PIMP approach. Instances where the p-value obtained by the Wilcoxon Mann Whitney test was below the 0.05 alpha value are identified (First part).

	Base vs Mutation 1	Base vs Mutation 2	Base vs Mutation Both
koza-3			
nguyen-5			
nguyen-6			
nguyen-7	Mut 1		Mut B
nguyen-9			
nguyen-10	Mut 1		Mut B
pagie-1			Mut B
pagie-2	Mut 1		Mut B
korns-1	Mut 1	Base	Mut B
korns-2			Mut B
korns-7	Mut 1	Mut 2	Mut B
korns-9	Mut 1		
korns-10			Mut B
korns-11			Mut B
korns-14		Base	
keijzer-1	Mut 1		Mut B
keijzer-2	Mut 1		Mut B
keijzer-3	Mut 1		Mut B
keijzer-4	Mut 1		Mut B
keijzer-5	Mut 1		Mut B
keijzer-6	Mut 1		Mut B
keijzer-7	Mut 1		Mut B
keijzer-9	Mut 1		Mut B
keijzer-10	Mut 1		Mut B
keijzer-11			Mut B
keijzer-12	Mut 1	Mut 2	Mut B
keijzer-13	Mut 1		Mut B
keijzer-14	Mut 1		Mut B
keijzer-15	Mut 1		Mut B
vladislavleva-1	Mut 1		Mut B
vladislavleva-2	Mut 1		Mut B
vladislavleva-3	Mut 1		Mut B
vladislavleva-4	Mut 1		
vladislavleva-5			Mut B
vladislavleva-6			Mut B
vladislavleva-8			Mut B

Table B.20: Comparison between different Mutation setups for the PIMP approach. Instances where the p-value obtained by the Wilcoxon Mann Whitney test was below the 0.05 alpha value are identified (Second part).

	Mutation 1 vs Mutation 2	Mutation 1 vs Mutation Both	Mutation 2 vs Mutation Both
koza-3	Mut 2	Mut B	
nguyen-5		Mut 1	Mut 2
nguyen-6	Mut 1		Mut B
nguyen-7	Mut 1		Mut B
nguyen-9			Mut B
nguyen-10	Mut 1		Mut B
pagie-1			
pagie-2	Mut 1		Mut B
korns-1	Mut 1		Mut B
korns-2		Mut B	Mut B
korns-7			
korns-9			
korns-10			Mut B
korns-11			Mut B
korns-14	Mut 1		Mut B
keijzer-1	Mut 1		Mut B
keijzer-2	Mut 1		Mut B
keijzer-3	Mut 1		Mut B
keijzer-4			
keijzer-5	Mut 1		Mut B
keijzer-6	Mut 1		Mut B
keijzer-7	Mut 1		Mut B
keijzer-9	Mut 1		Mut B
keijzer-10	Mut 1		Mut B
keijzer-11			Mut B
keijzer-12			
keijzer-13	Mut 1		Mut B
keijzer-14	Mut 1		Mut B
keijzer-15	Mut 1	Mut B	Mut B
vladislavleva-1	Mut 1		Mut B
vladislavleva-2			
vladislavleva-3	Mut 1		Mut B
vladislavleva-4			
vladislavleva-5	Mut 1		Mut B
vladislavleva-6			
vladislavleva-8	Mut 1		Mut B

Table B.21: Comparison between different Mutation setups for the PIMP approach. Number of runs where the error between the best individual and the optima was below $1E-4$.

	Base	Mutation 1	Mutation 2	Mutation Both
koza-1	27	30	32	24
koza-2	36	35	39	43
koza-3	41	40	43	44
nguyen-1	31	34	36	39
nguyen-2	27	31	30	32
nguyen-3	31	29	28	29
nguyen-4	20	22	23	24
nguyen-5	27	33	33	26
nguyen-6	38	39	29	43
nguyen-7	19	31	20	30
nguyen-8	20	20	19	15
nguyen-9	15	17	16	24
nguyen-10	12	20	13	33
korns-1	1	0	1	0
korns-4	0	1	1	1
keijzer-5	3	5	3	1
keijzer-6	0	2	0	1
keijzer-12	0	0	0	1

Table B.22: Comparison between different Mutation setups for the PIMP approach. Instances where the p-value obtainded by Taillard's proportion's tests was below the 0.05 alpha value are identified.

	Base vs Mutation 1	Base vs Mutation 2	Base vs Mutation Both
koza-2			Mut B
nguyen-1			Mut B
nguyen-6		Mut 2	
nguyen-7	Mut 1		Mut B
nguyen-8			
nguyen-9			Mut B
nguyen-10	Mut 1		

	Mutation 1 vs Mutation 2	Mutation 1 vs Mutation Both	Mutation 2 vs Mutation Both
koza-2		Mut B	Mut 1
nguyen-1			
nguyen-6	Mut 1		Mut B
nguyen-7	Mut 1		Mut B
nguyen-8			
nguyen-9			Mut B
nguyen-10		Mut B	

Appendix C

Impacts of Mutation on CMP-GP

Table C.1: Best Fitness, MBF and sample Standard Deviation obtained by the CMP-GP Approach with mutation on the first chromosome on 50 runs tackling each of the 51 Symbolic Regression instances (First part).

	Mutation 1		
	Best	MBF	StDev
koza-1	0,00E+00	2,58E-04	4,19E-07
koza-2	0,00E+00	4,86E-05	5,89E-09
koza-3	0,00E+00	2,24E-04	7,72E-07
nguyen-1	0,00E+00	1,54E-04	2,31E-07
nguyen-2	0,00E+00	4,79E-04	1,66E-06
nguyen-3	0,00E+00	8,26E-04	5,16E-06
nguyen-4	0,00E+00	9,02E-04	1,21E-05
nguyen-5	6,16E-08	2,55E-04	1,64E-07
nguyen-6	0,00E+00	1,92E-04	5,18E-07
nguyen-7	0,00E+00	7,99E-04	1,17E-05
nguyen-8	0,00E+00	2,66E-03	3,26E-05
nguyen-9	0,00E+00	1,64E-03	3,47E-06
nguyen-10	0,00E+00	4,93E-04	4,71E-07
pagie-1	2,12E-03	5,02E-02	1,90E-03
pagie-2	9,13E-03	1,52E-01	2,42E-03
korns-1	4,03E-02	2,00E+03	1,80E+08
korns-2	5,80E+01	2,62E+05	3,70E+11
korns-3	2,72E+03	8,99E+11	3,40E+25
korns-4	1,07E-05	8,24E-03	2,25E-05
korns-5	4,87E+29	5,00E+29	2,03E+55
korns-6	4,85E+29	4,99E+29	1,81E+55
korns-7	1,53E+25	1,44E+26	6,80E+51
korns-8	4,91E+29	5,00E+29	2,03E+55
korns-9	7,64E+29	7,75E+29	2,31E+55
korns-10	1,48E+04	3,49E+12	3,00E+26
korns-11	5,96E+01	6,06E+01	3,64E-01
korns-12	1,07E+00	1,11E+00	2,04E-04
korns-13	2,20E+07	1,22E+11	1,85E+23
korns-14	3,41E+05	3,79E+07	1,75E+16
korns-15	5,87E+29	5,95E+29	1,85E+55

Table C.2: Best Fitness, MBF and sample Standard Deviation obtained by the CMP-GP Approach with mutation on the first chromosome on 50 runs tackling each of the 51 Symbolic Regression instances (Second part).

	Mutation 1		
	Best	MBF	StDev
keijzer-1	4,65E-04	3,87E-03	7,58E-06
keijzer-2	2,05E-02	3,91E-02	4,88E-05
keijzer-3	7,94E-02	1,04E-01	1,23E-04
keijzer-4	2,01E-02	6,21E-02	4,32E-04
keijzer-5	4,05E-05	3,21E-02	3,46E-03
keijzer-6	1,29E-04	3,99E-02	1,41E-02
keijzer-7	1,63E-04	4,08E-02	1,49E-02
keijzer-8	0,00E+00	0,00E+00	0,00E+00
keijzer-9	7,93E-04	1,55E-01	1,11E-01
keijzer-10	9,84E-04	1,67E-02	1,15E-04
keijzer-11	3,50E-02	5,32E-01	4,69E-01
keijzer-12	1,01E-02	1,29E+01	1,04E+03
keijzer-13	2,86E-01	3,73E+00	5,69E+00
keijzer-14	4,21E-02	4,29E-01	8,53E-02
keijzer-15	2,52E-01	2,61E+00	4,10E+00
vladislavleva-1	9,23E-04	6,48E-03	1,96E-05
vladislavleva-2	9,45E-04	2,11E-02	4,60E-04
vladislavleva-3	3,51E-01	8,65E-01	2,91E-02
vladislavleva-4	2,16E-02	3,35E-02	2,22E-05
vladislavleva-5	4,78E-03	1,34E-01	9,50E-03
vladislavleva-6	1,23E+00	4,36E+00	3,49E+00
vladislavleva-7	1,05E+00	4,19E+00	4,08E+00
vladislavleva-8	1,53E-01	8,99E-01	3,63E-01

Table C.3: Best Fitness, MBF and sample Standard Deviation obtained by the CMP-GP Approach with mutation on the second chromosome on 50 runs tackling each of the 51 Symbolic Regression instances (First part).

	Mutation 2		
	Best	MBF	StDev
koza-1	0,00E+00	5,77E-03	1,27E-03
koza-2	0,00E+00	7,04E-05	2,44E-08
koza-3	0,00E+00	4,45E-04	2,49E-06
nguyen-1	0,00E+00	7,82E-03	1,32E-03
nguyen-2	0,00E+00	1,10E-03	2,55E-05
nguyen-3	0,00E+00	9,98E-04	1,34E-05
nguyen-4	0,00E+00	5,56E-04	1,60E-06
nguyen-5	0,00E+00	4,52E-04	7,99E-07
nguyen-6	0,00E+00	1,88E-02	1,04E-03
nguyen-7	0,00E+00	1,39E-02	1,74E-03
nguyen-8	3,16E-11	4,56E-03	6,73E-05
nguyen-9	0,00E+00	5,43E-03	4,30E-05
nguyen-10	0,00E+00	7,00E-03	8,96E-05
pagie-1	2,57E-04	5,41E-02	2,65E-03
pagie-2	1,39E-02	1,74E-01	3,43E-03
korns-1	8,98E-02	4,61E+04	1,88E+10
korns-2	1,34E+02	2,10E+08	2,15E+18
korns-3	3,95E+03	9,66E+11	1,98E+25
korns-4	3,01E-05	4,98E-02	5,83E-02
korns-5	4,84E+29	4,99E+29	2,90E+55
korns-6	4,90E+29	5,01E+29	1,71E+55
korns-7	2,66E+25	1,47E+26	7,12E+51
korns-8	4,89E+29	5,00E+29	2,93E+55
korns-9	7,70E+29	7,76E+29	1,47E+55
korns-10	1,58E+04	1,17E+13	6,80E+27
korns-11	5,94E+01	6,08E+01	3,34E-01
korns-12	1,08E+00	1,11E+00	1,20E-04
korns-13	5,09E+07	7,99E+10	1,01E+23
korns-14	5,50E+05	1,30E+09	4,89E+19
korns-15	5,85E+29	5,95E+29	2,57E+55

Table C.4: Best Fitness, MBF and sample Standard Deviation obtained by the CMP-GP Approach with mutation on the second chromosome on 50 runs tackling each of the 51 Symbolic Regression instances (Second part).

	Mutation 2		
	Best	MBF	StDev
keijzer-1	4,08E-04	7,03E-03	1,63E-05
keijzer-2	8,71E-03	4,51E-02	1,15E-04
keijzer-3	6,26E-02	1,18E-01	2,69E-04
keijzer-4	2,76E-02	7,47E-02	6,51E-04
keijzer-5	8,88E-07	6,12E-02	5,19E-03
keijzer-6	4,79E-05	1,96E-01	9,21E-02
keijzer-7	1,38E-04	3,61E-01	1,77E-01
keijzer-8	0,00E+00	0,00E+00	0,00E+00
keijzer-9	5,32E-03	6,64E-01	2,48E-01
keijzer-10	5,51E-03	2,53E-02	3,99E-05
keijzer-11	1,15E-01	1,22E+00	4,95E+00
keijzer-12	3,56E-01	4,51E+01	6,56E+03
keijzer-13	3,71E-01	4,74E+00	8,98E+00
keijzer-14	3,68E-02	5,66E-01	6,06E-02
keijzer-15	2,16E-01	3,61E+00	2,83E+00
vladislavleva-1	2,44E-03	1,47E-02	8,09E-05
vladislavleva-2	1,24E-04	2,89E-02	7,77E-04
vladislavleva-3	1,32E-01	8,94E-01	5,66E-02
vladislavleva-4	2,52E-02	3,73E-02	4,36E-04
vladislavleva-5	3,08E-02	1,71E-01	1,15E-02
vladislavleva-6	1,78E+00	4,63E+00	2,94E+00
vladislavleva-7	1,33E+00	4,54E+00	5,27E+00
vladislavleva-8	1,36E-01	1,12E+00	7,15E-01

Table C.5: Best Fitness, MBF and sample Standard Deviation obtained by the CMP-GP Approach with mutation on both chromosomes on 50 runs tackling each of the 51 Symbolic Regression instances (First part).

	Mutation Both		
	Best	MBF	StDev
koza-1	0,00E+00	2,02E-04	2,69E-07
koza-2	0,00E+00	5,78E-05	6,42E-09
koza-3	0,00E+00	7,70E-05	3,74E-08
nguyen-1	0,00E+00	1,03E-03	3,17E-05
nguyen-2	0,00E+00	7,43E-04	1,03E-05
nguyen-3	0,00E+00	1,15E-03	1,42E-05
nguyen-4	0,00E+00	4,45E-04	1,15E-06
nguyen-5	0,00E+00	1,95E-04	1,18E-07
nguyen-6	0,00E+00	1,16E-03	1,78E-05
nguyen-7	0,00E+00	2,43E-04	2,88E-07
nguyen-8	1,12E-07	1,82E-03	1,29E-05
nguyen-9	0,00E+00	1,90E-03	5,48E-06
nguyen-10	0,00E+00	6,18E-04	1,74E-06
pagie-1	1,11E-03	3,23E-02	1,20E-03
pagie-2	5,40E-03	1,25E-01	2,86E-03
korns-1	4,90E-03	3,93E+03	7,63E+08
korns-2	3,24E+01	5,83E+06	9,72E+14
korns-3	2,91E+03	1,40E+10	4,48E+21
korns-4	3,46E-05	7,05E-03	4,02E-05
korns-5	4,89E+29	5,01E+29	2,18E+55
korns-6	4,88E+29	5,01E+29	2,57E+55
korns-7	2,33E+21	1,18E+26	6,61E+51
korns-8	4,90E+29	5,00E+29	2,97E+55
korns-9	7,67E+29	7,75E+29	1,46E+55
korns-10	1,74E+04	5,02E+08	8,75E+18
korns-11	5,95E+01	6,05E+01	2,38E-01
korns-12	1,08E+00	1,11E+00	1,72E-04
korns-13	4,29E+07	1,36E+11	2,95E+23
korns-14	5,97E+05	6,53E+07	3,39E+16
korns-15	5,83E+29	5,94E+29	2,39E+55

Table C.6: Best Fitness, MBF and sample Standard Deviation obtained by the CMP-GP Approach with mutation on both chromosomes on 50 runs tackling each of the 51 Symbolic Regression instances (Second part).

	Mutation Both		
	Best	MBF	StDev
keijzer-1	2,44E-05	3,72E-03	1,01E-05
keijzer-2	1,64E-02	3,54E-02	8,11E-05
keijzer-3	5,37E-02	1,02E-01	2,35E-04
keijzer-4	5,50E-03	4,85E-02	6,36E-04
keijzer-5	5,63E-06	2,88E-02	2,28E-03
keijzer-6	1,66E-04	3,38E-02	1,77E-02
keijzer-7	1,84E-04	1,79E-02	4,51E-04
keijzer-8	0,00E+00	0,00E+00	0,00E+00
keijzer-9	6,29E-04	6,98E-02	4,61E-02
keijzer-10	7,39E-04	1,72E-02	1,14E-04
keijzer-11	9,53E-02	3,91E-01	3,21E-02
keijzer-12	1,66E-05	8,21E+00	1,36E+02
keijzer-13	3,70E-01	3,35E+00	4,39E+00
keijzer-14	1,80E-02	4,00E-01	6,93E-02
keijzer-15	1,32E-01	2,05E+00	2,83E+00
vladislavleva-1	6,94E-04	6,34E-03	2,10E-05
vladislavleva-2	3,51E-04	2,26E-02	4,44E-04
vladislavleva-3	3,11E-01	8,68E-01	3,76E-02
vladislavleva-4	1,60E-02	3,24E-02	3,05E-05
vladislavleva-5	3,75E-04	1,07E-01	7,15E-03
vladislavleva-6	1,61E+00	4,54E+00	3,14E+00
vladislavleva-7	1,32E+00	4,59E+00	4,93E+00
vladislavleva-8	9,23E-02	6,80E-01	2,12E-01

Table C.7: Full 5 number quartile information for CMP-GP with mutation on the first chromosome on each of the 51 Symbolic Regression test instances (First part).

			Mutation 1		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0,00E+00	0,00E+00	2,20E-05	2,04E-04	4,09E-03
koza-2	0,00E+00	1,29E-06	1,20E-05	7,72E-05	3,40E-04
koza-3	0,00E+00	1,91E-06	8,09E-06	4,58E-05	4,86E-03
nguyen-1	0,00E+00	0,00E+00	0,00E+00	3,02E-05	2,35E-03
nguyen-2	0,00E+00	0,00E+00	3,23E-05	2,27E-04	6,44E-03
nguyen-3	0,00E+00	0,00E+00	1,02E-04	3,70E-04	1,29E-02
nguyen-4	0,00E+00	2,83E-07	5,80E-05	4,43E-04	2,42E-02
nguyen-5	6,16E-08	1,36E-05	7,16E-05	2,36E-04	1,65E-03
nguyen-6	0,00E+00	0,00E+00	0,00E+00	3,12E-05	4,47E-03
nguyen-7	0,00E+00	1,51E-05	6,66E-05	2,09E-04	2,17E-02
nguyen-8	0,00E+00	4,57E-05	3,12E-04	2,56E-03	3,20E-02
nguyen-9	0,00E+00	1,37E-06	9,58E-04	2,01E-03	6,92E-03
nguyen-10	0,00E+00	8,11E-06	2,27E-04	5,61E-04	2,83E-03
pagie-1	2,12E-03	1,44E-02	3,54E-02	7,80E-02	1,36E-01
pagie-2	9,13E-03	1,24E-01	1,62E-01	1,82E-01	2,49E-01
korns-1	4,03E-02	8,82E+00	1,16E+01	3,96E+01	9,48E+04
korns-2	5,80E+01	1,59E+04	4,31E+04	1,60E+05	2,94E+06
korns-3	2,72E+03	1,53E+06	1,00E+08	1,56E+09	4,12E+13
korns-4	1,07E-05	8,43E-03	8,47E-03	8,54E-03	3,46E-02
korns-5	4,87E+29	4,97E+29	4,99E+29	5,03E+29	5,10E+29
korns-6	4,85E+29	4,97E+29	4,99E+29	5,01E+29	5,08E+29
korns-7	1,53E+25	6,55E+25	1,31E+26	2,30E+26	2,74E+26
korns-8	4,91E+29	4,96E+29	5,00E+29	5,02E+29	5,08E+29
korns-9	7,64E+29	7,71E+29	7,75E+29	7,78E+29	7,88E+29
korns-10	1,48E+04	5,53E+05	5,30E+06	9,75E+07	1,11E+14
korns-11	5,96E+01	6,01E+01	6,05E+01	6,09E+01	6,19E+01
korns-12	1,07E+00	1,10E+00	1,11E+00	1,12E+00	1,15E+00
korns-13	2,20E+07	3,11E+08	1,11E+09	2,10E+10	2,22E+12
korns-14	3,41E+05	1,45E+06	6,28E+06	2,34E+07	9,10E+08
korns-15	5,87E+29	5,92E+29	5,95E+29	5,98E+29	6,04E+29

Table C.8: Full 5 number quartile information for CMP-GP with mutation on the first chromosome on each of the 51 Symbolic Regression test instances (Second part).

			Mutation 1		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	4,65E-04	1,95E-03	2,86E-03	4,73E-03	1,37E-02
keijzer-2	2,05E-02	3,42E-02	3,87E-02	4,46E-02	5,60E-02
keijzer-3	7,94E-02	9,71E-02	1,05E-01	1,12E-01	1,32E-01
keijzer-4	2,01E-02	5,07E-02	5,99E-02	7,34E-02	1,01E-01
keijzer-5	4,05E-05	1,21E-03	5,29E-03	4,17E-02	2,59E-01
keijzer-6	1,29E-04	9,67E-04	4,13E-03	1,10E-02	6,77E-01
keijzer-7	1,63E-04	5,68E-03	1,35E-02	3,06E-02	8,61E-01
keijzer-8	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
keijzer-9	7,93E-04	7,16E-03	1,74E-02	4,70E-02	1,01E+00
keijzer-10	9,84E-04	4,44E-03	1,89E-02	2,52E-02	3,73E-02
keijzer-11	3,50E-02	3,24E-01	4,21E-01	5,17E-01	4,17E+00
keijzer-12	1,01E-02	1,69E+00	3,49E+00	9,62E+00	2,04E+02
keijzer-13	2,86E-01	1,65E+00	3,70E+00	4,95E+00	9,12E+00
keijzer-14	4,21E-02	1,88E-01	3,71E-01	5,97E-01	1,16E+00
keijzer-15	2,52E-01	8,65E-01	2,17E+00	4,14E+00	9,04E+00
vladislavleva-1	9,23E-04	3,43E-03	5,10E-03	8,33E-03	1,96E-02
vladislavleva-2	9,45E-04	4,97E-03	1,10E-02	3,87E-02	8,87E-02
vladislavleva-3	3,51E-01	7,52E-01	9,20E-01	9,69E-01	1,18E+00
vladislavleva-4	2,16E-02	3,11E-02	3,35E-02	3,68E-02	4,21E-02
vladislavleva-5	4,78E-03	6,48E-02	1,09E-01	1,98E-01	4,17E-01
vladislavleva-6	1,23E+00	3,11E+00	3,95E+00	5,46E+00	8,86E+00
vladislavleva-7	1,05E+00	2,48E+00	3,94E+00	5,71E+00	8,87E+00
vladislavleva-8	1,53E-01	4,07E-01	7,77E-01	1,29E+00	2,52E+00

Table C.9: Full 5 number quartile information for CMP-GP with mutation on the second chromosome on each of the 51 Symbolic Regression test instances (First part).

	Mutation 2				
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0,00E+00	0,00E+00	1,96E-05	2,21E-04	2,52E-01
koza-2	0,00E+00	1,39E-06	1,53E-05	7,36E-05	1,04E-03
koza-3	0,00E+00	1,79E-06	9,94E-06	2,62E-05	8,28E-03
nguyen-1	0,00E+00	0,00E+00	5,13E-06	4,02E-04	2,53E-01
nguyen-2	0,00E+00	0,00E+00	7,00E-06	1,32E-04	3,49E-02
nguyen-3	0,00E+00	0,00E+00	1,02E-05	1,45E-04	2,08E-02
nguyen-4	0,00E+00	1,64E-07	8,06E-05	4,68E-04	5,80E-03
nguyen-5	0,00E+00	3,22E-06	5,63E-05	4,92E-04	4,67E-03
nguyen-6	0,00E+00	6,97E-06	2,24E-04	3,47E-02	1,20E-01
nguyen-7	0,00E+00	1,88E-05	8,30E-05	5,52E-04	2,01E-01
nguyen-8	3,16E-11	2,50E-04	6,97E-04	5,60E-03	4,54E-02
nguyen-9	0,00E+00	2,79E-04	1,92E-03	1,20E-02	1,99E-02
nguyen-10	0,00E+00	1,02E-04	5,56E-04	1,50E-02	2,57E-02
pagie-1	2,57E-04	5,45E-03	3,47E-02	1,15E-01	1,36E-01
pagie-2	1,39E-02	1,43E-01	1,59E-01	2,32E-01	3,10E-01
korns-1	8,98E-02	1,45E+01	7,68E+01	3,57E+02	4,62E+05
korns-2	1,34E+02	2,44E+04	6,01E+04	2,53E+05	1,04E+10
korns-3	3,95E+03	9,09E+06	1,22E+08	3,88E+09	2,90E+13
korns-4	3,01E-05	8,44E-03	8,48E-03	8,52E-03	1,70E+00
korns-5	4,84E+29	4,96E+29	4,99E+29	5,03E+29	5,12E+29
korns-6	4,90E+29	4,99E+29	5,01E+29	5,04E+29	5,09E+29
korns-7	2,66E+25	6,90E+25	1,37E+26	2,32E+26	2,88E+26
korns-8	4,89E+29	4,97E+29	5,00E+29	5,04E+29	5,09E+29
korns-9	7,70E+29	7,73E+29	7,75E+29	7,78E+29	7,87E+29
korns-10	1,58E+04	8,48E+05	6,23E+06	5,69E+07	5,83E+14
korns-11	5,94E+01	6,05E+01	6,07E+01	6,11E+01	6,26E+01
korns-12	1,08E+00	1,10E+00	1,11E+00	1,11E+00	1,13E+00
korns-13	5,09E+07	2,12E+08	1,12E+09	5,81E+09	2,13E+12
korns-14	5,50E+05	2,36E+06	8,33E+06	5,08E+07	4,86E+10
korns-15	5,85E+29	5,91E+29	5,94E+29	5,98E+29	6,09E+29

Table C.10: Full 5 number quartile information for CMP-GP with mutation on the second chromosome on each of the 51 Symbolic Regression test instances (Second part).

			Mutation 2		
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	4,08E-04	2,87E-03	8,04E-03	1,18E-02	1,50E-02
keijzer-2	8,71E-03	3,78E-02	4,64E-02	5,59E-02	5,64E-02
keijzer-3	6,26E-02	1,05E-01	1,30E-01	1,30E-01	1,32E-01
keijzer-4	2,76E-02	5,41E-02	7,09E-02	1,01E-01	1,16E-01
keijzer-5	8,88E-07	1,30E-02	4,50E-02	7,36E-02	3,07E-01
keijzer-6	4,79E-05	1,38E-03	1,01E-02	6,77E-01	8,40E-01
keijzer-7	1,38E-04	1,58E-02	3,06E-02	8,54E-01	1,09E+00
keijzer-8	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
keijzer-9	5,32E-03	2,18E-02	1,01E+00	1,02E+00	1,34E+00
keijzer-10	5,51E-03	2,13E-02	2,48E-02	2,83E-02	4,53E-02
keijzer-11	1,15E-01	4,13E-01	4,73E-01	5,67E-01	9,07E+00
keijzer-12	3,56E-01	4,56E+00	1,02E+01	6,91E+01	4,04E+02
keijzer-13	3,71E-01	2,18E+00	4,29E+00	6,93E+00	1,15E+01
keijzer-14	3,68E-02	4,45E-01	5,53E-01	7,44E-01	1,08E+00
keijzer-15	2,16E-01	2,88E+00	3,57E+00	4,70E+00	6,43E+00
vladislavleva-1	2,44E-03	8,44E-03	1,29E-02	1,76E-02	3,73E-02
vladislavleva-2	1,24E-04	6,98E-03	1,64E-02	5,30E-02	1,01E-01
vladislavleva-3	1,32E-01	7,51E-01	9,30E-01	1,05E+00	1,18E+00
vladislavleva-4	2,52E-02	3,09E-02	3,42E-02	3,79E-02	1,77E-01
vladislavleva-5	3,08E-02	8,34E-02	1,48E-01	2,18E-01	4,60E-01
vladislavleva-6	1,78E+00	3,34E+00	4,52E+00	5,61E+00	8,85E+00
vladislavleva-7	1,33E+00	2,46E+00	4,43E+00	6,23E+00	9,33E+00
vladislavleva-8	1,36E-01	5,00E-01	8,15E-01	1,85E+00	4,01E+00

Table C.11: Full 5 number quartile information for CMP-GP with mutation on both chromosomes on each of the 51 Symbolic Regression test instances (First part).

	Mutation Both				
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0,00E+00	0,00E+00	5,98E-06	1,64E-04	3,05E-03
koza-2	0,00E+00	2,89E-06	1,81E-05	8,95E-05	3,38E-04
koza-3	0,00E+00	2,42E-06	1,12E-05	4,31E-05	1,04E-03
nguyen-1	0,00E+00	0,00E+00	0,00E+00	1,87E-05	3,90E-02
nguyen-2	0,00E+00	0,00E+00	1,40E-05	8,08E-05	2,24E-02
nguyen-3	0,00E+00	0,00E+00	4,08E-05	4,61E-04	2,35E-02
nguyen-4	0,00E+00	1,42E-05	1,19E-04	3,90E-04	5,46E-03
nguyen-5	0,00E+00	2,04E-06	3,22E-05	2,23E-04	1,37E-03
nguyen-6	0,00E+00	0,00E+00	1,47E-05	1,52E-04	2,16E-02
nguyen-7	0,00E+00	7,64E-06	5,20E-05	1,95E-04	2,74E-03
nguyen-8	1,12E-07	5,92E-05	3,20E-04	1,33E-03	1,63E-02
nguyen-9	0,00E+00	0,00E+00	5,86E-04	3,57E-03	7,18E-03
nguyen-10	0,00E+00	6,01E-06	2,38E-04	5,69E-04	8,05E-03
pagie-1	1,11E-03	8,28E-03	2,45E-02	4,02E-02	1,63E-01
pagie-2	5,40E-03	8,69E-02	1,36E-01	1,59E-01	2,65E-01
korns-1	4,90E-03	7,10E+00	9,51E+00	1,78E+01	1,95E+05
korns-2	3,24E+01	1,34E+04	3,42E+04	7,88E+04	2,19E+08
korns-3	2,91E+03	6,42E+05	1,38E+07	6,01E+08	4,53E+11
korns-4	3,46E-05	2,53E-04	8,42E-03	8,51E-03	3,63E-02
korns-5	4,89E+29	4,98E+29	5,01E+29	5,03E+29	5,11E+29
korns-6	4,88E+29	4,98E+29	5,02E+29	5,03E+29	5,12E+29
korns-7	2,33E+21	6,09E+25	7,76E+25	2,10E+26	2,63E+26
korns-8	4,90E+29	4,96E+29	4,99E+29	5,04E+29	5,12E+29
korns-9	7,67E+29	7,73E+29	7,76E+29	7,78E+29	7,84E+29
korns-10	1,74E+04	1,06E+06	5,25E+06	2,47E+07	2,10E+10
korns-11	5,95E+01	6,01E+01	6,05E+01	6,09E+01	6,14E+01
korns-12	1,08E+00	1,10E+00	1,11E+00	1,12E+00	1,14E+00
korns-13	4,29E+07	3,04E+08	1,48E+09	1,20E+10	3,50E+12
korns-14	5,97E+05	2,08E+06	7,81E+06	1,74E+07	1,13E+09
korns-15	5,83E+29	5,92E+29	5,94E+29	5,97E+29	6,04E+29

Table C.12: Full 5 number quartile information for CMP-GP with mutation on both chromosomes on each of the 51 Symbolic Regression test instances (Second part).

	Mutation Both				
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	2,44E-05	1,59E-03	2,58E-03	5,15E-03	1,37E-02
keijzer-2	1,64E-02	2,78E-02	3,64E-02	4,25E-02	5,59E-02
keijzer-3	5,37E-02	9,44E-02	1,04E-01	1,14E-01	1,30E-01
keijzer-4	5,50E-03	2,69E-02	5,35E-02	6,25E-02	9,85E-02
keijzer-5	5,63E-06	1,35E-03	1,10E-02	4,37E-02	2,90E-01
keijzer-6	1,66E-04	9,91E-04	4,36E-03	1,01E-02	6,77E-01
keijzer-7	1,84E-04	2,38E-03	1,05E-02	3,06E-02	1,18E-01
keijzer-8	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
keijzer-9	6,29E-04	1,02E-02	1,74E-02	1,78E-02	1,01E+00
keijzer-10	7,39E-04	6,69E-03	1,87E-02	2,49E-02	3,85E-02
keijzer-11	9,53E-02	2,98E-01	3,86E-01	4,86E-01	1,25E+00
keijzer-12	1,66E-05	1,26E+00	4,66E+00	1,02E+01	5,47E+01
keijzer-13	3,70E-01	1,85E+00	3,35E+00	4,38E+00	1,02E+01
keijzer-14	1,80E-02	1,68E-01	3,51E-01	5,71E-01	9,84E-01
keijzer-15	1,32E-01	5,83E-01	1,60E+00	3,15E+00	6,33E+00
vladislavleva-1	6,94E-04	2,90E-03	5,29E-03	7,27E-03	1,79E-02
vladislavleva-2	3,51E-04	7,00E-03	1,17E-02	4,96E-02	5,49E-02
vladislavleva-3	3,11E-01	7,57E-01	9,14E-01	9,87E-01	1,18E+00
vladislavleva-4	1,60E-02	2,83E-02	3,32E-02	3,57E-02	4,35E-02
vladislavleva-5	3,75E-04	4,45E-02	8,78E-02	1,48E-01	3,23E-01
vladislavleva-6	1,61E+00	3,06E+00	4,50E+00	6,10E+00	8,00E+00
vladislavleva-7	1,32E+00	2,76E+00	4,28E+00	6,05E+00	9,43E+00
vladislavleva-8	9,23E-02	3,27E-01	5,60E-01	9,20E-01	1,84E+00

Table C.13: Median and interquartile range information obtained by CMP-GP with mutation on the first chromosome on all 51 instances of Symbolic Regression problems (First part).

	Mutation 1	
	Median	IQR
koza-1	2,20E-05	2,04E-04
koza-2	1,20E-05	7,59E-05
koza-3	8,09E-06	4,39E-05
nguyen-1	0,00E+00	3,02E-05
nguyen-2	3,23E-05	2,27E-04
nguyen-3	1,02E-04	3,70E-04
nguyen-4	5,80E-05	4,43E-04
nguyen-5	7,16E-05	2,22E-04
nguyen-6	0,00E+00	3,12E-05
nguyen-7	6,66E-05	1,94E-04
nguyen-8	3,12E-04	2,51E-03
nguyen-9	9,58E-04	2,01E-03
nguyen-10	2,27E-04	5,53E-04
pagie-1	3,54E-02	6,36E-02
pagie-2	1,62E-01	5,80E-02
korns-1	1,16E+01	3,08E+01
korns-2	4,31E+04	1,44E+05
korns-3	1,00E+08	1,56E+09
korns-4	8,47E-03	1,11E-04
korns-5	4,99E+29	5,80E+27
korns-6	4,99E+29	4,60E+27
korns-7	1,31E+26	1,65E+26
korns-8	5,00E+29	5,90E+27
korns-9	7,75E+29	7,31E+27
korns-10	5,30E+06	9,69E+07
korns-11	6,05E+01	8,62E-01
korns-12	1,11E+00	1,72E-02
korns-13	1,11E+09	2,07E+10
korns-14	6,28E+06	2,20E+07
korns-15	5,95E+29	6,00E+27

Table C.14: Median and interquartile range information obtained by CMP-GP with mutation on the first chromosome on all 51 instances of Symbolic Regression problems (Second part).

	Mutation 1	
	Median	IQR
keijzer-1	2,86E-03	2,77E-03
keijzer-2	3,87E-02	1,04E-02
keijzer-3	1,05E-01	1,48E-02
keijzer-4	5,99E-02	2,27E-02
keijzer-5	5,29E-03	4,05E-02
keijzer-6	4,13E-03	1,00E-02
keijzer-7	1,35E-02	2,49E-02
keijzer-8	0,00E+00	0,00E+00
keijzer-9	1,74E-02	3,98E-02
keijzer-10	1,89E-02	2,07E-02
keijzer-11	4,21E-01	1,93E-01
keijzer-12	3,49E+00	7,93E+00
keijzer-13	3,70E+00	3,30E+00
keijzer-14	3,71E-01	4,09E-01
keijzer-15	2,17E+00	3,27E+00
vladislavleva-1	5,10E-03	4,90E-03
vladislavleva-2	1,10E-02	3,37E-02
vladislavleva-3	9,20E-01	2,17E-01
vladislavleva-4	3,35E-02	5,69E-03
vladislavleva-5	1,09E-01	1,33E-01
vladislavleva-6	3,95E+00	2,35E+00
vladislavleva-7	3,94E+00	3,23E+00
vladislavleva-8	7,77E-01	8,80E-01

Table C.15: Median and interquartile range information obtained by CMP-GP with mutation on the second chromosome on all 51 instances of Symbolic Regression problems (First part).

	Mutation 2	
	Median	IQR
koza-1	1,96E-05	2,21E-04
koza-2	1,53E-05	7,22E-05
koza-3	9,94E-06	2,44E-05
nguyen-1	5,13E-06	4,02E-04
nguyen-2	7,00E-06	1,32E-04
nguyen-3	1,02E-05	1,45E-04
nguyen-4	8,06E-05	4,68E-04
nguyen-5	5,63E-05	4,88E-04
nguyen-6	2,24E-04	3,47E-02
nguyen-7	8,30E-05	5,33E-04
nguyen-8	6,97E-04	5,35E-03
nguyen-9	1,92E-03	1,17E-02
nguyen-10	5,56E-04	1,49E-02
pagie-1	3,47E-02	1,10E-01
pagie-2	1,59E-01	8,83E-02
korns-1	7,68E+01	3,42E+02
korns-2	6,01E+04	2,29E+05
korns-3	1,22E+08	3,87E+09
korns-4	8,48E-03	8,08E-05
korns-5	4,99E+29	6,70E+27
korns-6	5,01E+29	5,40E+27
korns-7	1,37E+26	1,63E+26
korns-8	5,00E+29	7,90E+27
korns-9	7,75E+29	4,59E+27
korns-10	6,23E+06	5,61E+07
korns-11	6,07E+01	6,47E-01
korns-12	1,11E+00	1,51E-02
korns-13	1,12E+09	5,60E+09
korns-14	8,33E+06	4,85E+07
korns-15	5,94E+29	7,11E+27

Table C.16: Median and interquartile range information obtained by CMP-GP with mutation on the second chromosome on all 51 instances of Symbolic Regression problems (Second part).

	Mutation 2	
	Median	IQR
keijzer-1	8,04E-03	8,94E-03
keijzer-2	4,64E-02	1,81E-02
keijzer-3	1,30E-01	2,49E-02
keijzer-4	7,09E-02	4,66E-02
keijzer-5	4,50E-02	6,07E-02
keijzer-6	1,01E-02	6,76E-01
keijzer-7	3,06E-02	8,38E-01
keijzer-8	0,00E+00	0,00E+00
keijzer-9	1,01E+00	1,00E+00
keijzer-10	2,48E-02	7,01E-03
keijzer-11	4,73E-01	1,53E-01
keijzer-12	1,02E+01	6,45E+01
keijzer-13	4,29E+00	4,76E+00
keijzer-14	5,53E-01	2,99E-01
keijzer-15	3,57E+00	1,82E+00
vladislavleva-1	1,29E-02	9,17E-03
vladislavleva-2	1,64E-02	4,60E-02
vladislavleva-3	9,30E-01	2,94E-01
vladislavleva-4	3,42E-02	6,96E-03
vladislavleva-5	1,48E-01	1,34E-01
vladislavleva-6	4,52E+00	2,27E+00
vladislavleva-7	4,43E+00	3,77E+00
vladislavleva-8	8,15E-01	1,35E+00

Table C.17: Median and interquartile range information obtained by CMP-GP with mutation on both chromosome on all 51 instances of Symbolic Regression problems (First part).

	Mutation Both	
	Median	IQR
koza-1	5,98E-06	1,64E-04
koza-2	1,81E-05	8,66E-05
koza-3	1,12E-05	4,07E-05
nguyen-1	0,00E+00	1,87E-05
nguyen-2	1,40E-05	8,08E-05
nguyen-3	4,08E-05	4,61E-04
nguyen-4	1,19E-04	3,76E-04
nguyen-5	3,22E-05	2,21E-04
nguyen-6	1,47E-05	1,52E-04
nguyen-7	5,20E-05	1,87E-04
nguyen-8	3,20E-04	1,27E-03
nguyen-9	5,86E-04	3,57E-03
nguyen-10	2,38E-04	5,63E-04
pagie-1	2,45E-02	3,19E-02
pagie-2	1,36E-01	7,17E-02
korns-1	9,51E+00	1,07E+01
korns-2	3,42E+04	6,54E+04
korns-3	1,38E+07	6,00E+08
korns-4	8,42E-03	8,26E-03
korns-5	5,01E+29	5,00E+27
korns-6	5,02E+29	5,10E+27
korns-7	7,76E+25	1,49E+26
korns-8	4,99E+29	8,20E+27
korns-9	7,76E+29	5,12E+27
korns-10	5,25E+06	2,36E+07
korns-11	6,05E+01	7,48E-01
korns-12	1,11E+00	1,76E-02
korns-13	1,48E+09	1,17E+10
korns-14	7,81E+06	1,54E+07
korns-15	5,94E+29	5,12E+27

Table C.18: Median and interquartile range information obtained by CMP-GP with mutation on both chromosome on all 51 instances of Symbolic Regression problems (Second part).

	Mutation Both	
	Median	IQR
keijzer-1	2,58E-03	3,56E-03
keijzer-2	3,64E-02	1,47E-02
keijzer-3	1,04E-01	1,98E-02
keijzer-4	5,35E-02	3,56E-02
keijzer-5	1,10E-02	4,23E-02
keijzer-6	4,36E-03	9,12E-03
keijzer-7	1,05E-02	2,82E-02
keijzer-8	0,00E+00	0,00E+00
keijzer-9	1,74E-02	7,61E-03
keijzer-10	1,87E-02	1,83E-02
keijzer-11	3,86E-01	1,88E-01
keijzer-12	4,66E+00	8,90E+00
keijzer-13	3,35E+00	2,53E+00
keijzer-14	3,51E-01	4,03E-01
keijzer-15	1,60E+00	2,57E+00
vladislavleva-1	5,29E-03	4,36E-03
vladislavleva-2	1,17E-02	4,26E-02
vladislavleva-3	9,14E-01	2,30E-01
vladislavleva-4	3,32E-02	7,42E-03
vladislavleva-5	8,78E-02	1,04E-01
vladislavleva-6	4,50E+00	3,04E+00
vladislavleva-7	4,28E+00	3,28E+00
vladislavleva-8	5,60E-01	5,93E-01

Table C.19: Comparison between different Mutation setups for CMP-GP. Instances where the p-value obtained by the Wilcoxon Mann Whitney test was below the 0.05 alpha value are identified (First part).

	Base vs Mutation 1	Base vs Mutation 2	Base vs Mutation Both
nguyen-1			
nguyen-6	Mut 1		Mut B
nguyen-7	Mut 1		Mut B
nguyen-8			
nguyen-9			
nguyen-10	Mut 1		Mut B
pagie-1			
pagie-2			Mut B
korns-1	Mut 1		Mut B
korns-2	Mut 1	Mut 2	Mut B
korns-3			Mut B
korns-4	Mut 1		Mut B
korns-6			
korns-7			Mut B
korns-9	Mut 1		
korns-11	Mut 1		Mut B
keijzer-1	Mut 1		Mut B
keijzer-2	Mut 1		Mut B
keijzer-3	Mut 1		Mut B
keijzer-4			Mut B
keijzer-5	Mut 1		Mut B
keijzer-6	Mut 1		Mut B
keijzer-7	Mut 1		Mut B
keijzer-8			
keijzer-9	Mut 1		Mut B
keijzer-10	Mut 1		Mut B
keijzer-11			Mut B
keijzer-12	Mut 1		Mut B
keijzer-13			Mut B
keijzer-14	Mut 1		Mut B
keijzer-15	Mut 1		Mut B
vladislavleva-1	Mut 1		Mut B
vladislavleva-3	Mut 1		Mut B
vladislavleva-4	Mut 1		Mut B
vladislavleva-5	Mut 1		Mut B
vladislavleva-8			

Table C.20: Comparison between different Mutation setups for CMP-GP. Instances where the p-value obtained by the Wilcoxon Mann Whitney test was below the 0.05 alpha value are identified (Second part).

	Mutation 1 vs Mutation 2	Mutation 1 vs Mutation Both	Mutation 2 vs Mutation Both
nguyen-1	Mut 1		
nguyen-6	Mut 1		Mut B
nguyen-7			
nguyen-8			Mut B
nguyen-9	Mut 1		Mut B
nguyen-10	Mut 1		Mut B
pagie-1		Mut B	
pagie-2		Mut B	Mut B
korns-1	Mut 1		Mut B
korns-2			
korns-3			Mut B
korns-4		Mut B	Mut B
korns-6	Mut 1	Mut 1	
korns-7			
korns-9			
korns-11			Mut B
keijzer-1	Mut 1		Mut B
keijzer-2	Mut 1		Mut B
keijzer-3	Mut 1		Mut B
keijzer-4	Mut 1	Mut B	Mut B
keijzer-5	Mut 1		Mut B
keijzer-6	Mut 1		Mut B
keijzer-7	Mut 1		Mut B
keijzer-8			
keijzer-9	Mut 1		Mut B
keijzer-10	Mut 1		Mut B
keijzer-11	Mut 1		Mut B
keijzer-12	Mut 1		Mut B
keijzer-13			Mut B
keijzer-14	Mut 1		Mut B
keijzer-15	Mut 1		Mut B
vladislavleva-1	Mut 1		Mut B
vladislavleva-3			
vladislavleva-4			
vladislavleva-5			Mut B
vladislavleva-8			Mut B

Table C.21: Comparison between different Mutation setups for the CMP-GP approach. Number of runs where the error between the best individual and the optima was below $1E-4$.

	Base	Mutation 1	Mutation 2	Mutation Both
koza-1	39	33	31	35
koza-2	37	42	41	38
koza-3	42	42	40	43
nguyen-1	37	42	32	41
nguyen-2	33	33	37	39
nguyen-3	28	25	35	30
nguyen-4	25	31	27	23
nguyen-5	27	29	31	34
nguyen-6	25	42	20	35
nguyen-7	25	32	27	32
nguyen-8	12	16	9	17
nguyen-9	13	13	11	18
nguyen-10	16	19	12	17
korns-4	0	2	1	9
keijzer-1	1	0	0	2
keijzer-5	1	4	3	2
keijzer-6	1	0	1	0
keijzer-12	0	0	0	1

Table C.22: Comparison between different Mutation setups for CMP-GP. Instances where the p-value obtainded by Taillard's proportion's tests was below the 0.05 alpha value are identified.

	Base vs Mutation 1	Base vs Mutation 2	Base vs Mutation Both
koza-1		Mut B	
nguyen-1			
nguyen-3			
nguyen-4			
nguyen-6	Mut 1		Mut B
nguyen-8			
korns-4			Mut B

	Mutation 1 vs Mutation 2	Mutation 1 vs Mutation Both	Mutation 2 vs Mutation Both
koza-1			
nguyen-1	Mut 1		Mut B
nguyen-3	Mut 2		
nguyen-4		Mut 1	
nguyen-6	Mut 1	Mut 1	Mut B
nguyen-8	Mut 1		Mut B
korns-4		Mut B	Mut B

Appendix D

Comparison with Standard approach

Table D.1: Best Fitness, MBF and sample Standard Deviation obtained by Standard Approach with mutation. Results from 50 runs tackling each of the 51 Symbolic Regression instances (First part).

	Standard with Mutation		
	Best	MBF	MBF stdev
koza-1	0,00E+00	5,02E-04	2,04E-06
koza-2	8,82E-09	3,35E-04	1,44E-06
koza-3	0,00E+00	5,23E-04	1,70E-06
nguyen-1	0,00E+00	2,05E-03	5,63E-05
nguyen-2	0,00E+00	2,04E-03	1,14E-04
nguyen-3	0,00E+00	7,40E-03	1,94E-03
nguyen-4	0,00E+00	1,51E-03	1,10E-05
nguyen-5	1,25E-08	7,04E-04	2,29E-06
nguyen-6	0,00E+00	1,92E-02	8,52E-04
nguyen-7	1,36E-06	1,25E-02	1,12E-03
nguyen-8	0,00E+00	1,77E-02	2,69E-03
nguyen-9	0,00E+00	7,49E-03	7,11E-05
nguyen-10	0,00E+00	1,44E-02	5,82E-04
pagie-1	1,80E-03	5,96E-02	2,79E-03
pagie-2	2,61E-02	1,88E-01	3,18E-03
korns-1	2,92E+00	1,28E+05	4,27E+10
korns-2	6,73E+02	2,44E+06	1,49E+14
korns-3	1,07E+04	1,42E+17	6,23E+35
korns-4	2,47E-04	1,00E-01	1,66E-01
korns-5	4,88E+29	5,00E+29	2,99E+55
korns-6	4,88E+29	5,00E+29	2,39E+55
korns-7	2,92E+25	1,70E+26	5,58E+51
korns-8	4,86E+29	5,00E+29	2,88E+55
korns-9	7,65E+29	7,76E+29	1,91E+55
korns-10	2,04E+04	1,48E+17	1,09E+36
korns-11	5,86E+01	6,13E+01	6,64E+00
korns-12	1,08E+00	1,11E+00	1,62E-04
korns-13	5,35E+07	8,04E+11	2,23E+25
korns-14	1,11E+06	3,39E+08	2,25E+18
korns-15	5,83E+29	5,94E+29	2,53E+55

Table D.2: Best Fitness, MBF and sample Standard Deviation obtained by Standard Approach with mutation. Results from 50 runs tackling each of the 51 Symbolic Regression instances (Second part).

	Standard with Mutation		
	Best	MBF	MBF stdev
keijzer-1	1,04E-03	7,18E-03	1,63E-05
keijzer-2	1,61E-02	4,84E-02	1,60E-04
keijzer-3	5,82E-02	1,20E-01	3,12E-04
keijzer-4	6,92E-03	7,56E-02	7,68E-04
keijzer-5	1,99E-04	9,62E-02	7,44E-03
keijzer-6	2,36E-04	2,04E-01	8,98E-02
keijzer-7	5,03E-04	2,14E-01	1,16E-01
keijzer-8	0,00E+00	0,00E+00	0,00E+00
keijzer-9	4,88E-04	6,40E-01	2,45E-01
keijzer-10	7,51E-04	2,55E-02	8,19E-05
keijzer-11	2,13E-02	1,09E+00	5,94E+00
keijzer-12	5,36E-01	1,57E+02	6,85E+04
keijzer-13	3,87E-01	4,70E+00	8,58E+00
keijzer-14	1,15E-01	5,51E-01	5,43E-02
keijzer-15	3,00E-01	3,72E+00	3,82E+00
vladislavleva-1	7,04E-04	1,86E-02	8,50E-05
vladislavleva-2	6,11E-04	3,17E-02	9,08E-04
vladislavleva-3	6,66E-02	9,20E-01	7,10E-02
vladislavleva-4	2,30E-02	3,87E-02	2,00E-04
vladislavleva-5	1,59E-02	1,75E-01	9,41E-03
vladislavleva-6	6,58E-01	5,24E+00	3,68E+00
vladislavleva-7	1,10E+00	6,96E+00	7,66E+00
vladislavleva-8	3,46E-02	1,23E+00	7,65E-01

Table D.3: Full 5 number quartile information for Standard Approach with mutation. Results for the 51 Symbolic Regression test instances (First part).

	Standard with Mutation				
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
koza-1	0,00E+00	0,00E+00	1,70E-05	3,74E-04	9,06E-03
koza-2	8,82E-09	7,07E-06	2,26E-05	1,01E-04	8,13E-03
koza-3	0,00E+00	7,94E-06	1,98E-05	1,58E-04	5,56E-03
nguyen-1	0,00E+00	0,00E+00	0,00E+00	3,05E-04	4,15E-02
nguyen-2	0,00E+00	0,00E+00	2,81E-05	4,10E-04	7,53E-02
nguyen-3	0,00E+00	6,38E-07	2,24E-04	1,58E-03	3,12E-01
nguyen-4	0,00E+00	9,89E-05	3,06E-04	1,45E-03	1,70E-02
nguyen-5	1,25E-08	4,97E-06	2,98E-05	6,58E-04	8,22E-03
nguyen-6	0,00E+00	8,55E-05	1,09E-03	3,34E-02	1,03E-01
nguyen-7	1,36E-06	6,01E-05	2,59E-04	4,48E-03	1,96E-01
nguyen-8	0,00E+00	2,80E-04	8,62E-04	5,98E-03	2,48E-01
nguyen-9	0,00E+00	9,37E-04	4,14E-03	1,34E-02	3,12E-02
nguyen-10	0,00E+00	6,77E-04	5,27E-03	1,90E-02	1,16E-01
pagie-1	1,80E-03	1,07E-02	3,99E-02	1,16E-01	1,85E-01
pagie-2	2,61E-02	1,58E-01	1,94E-01	2,35E-01	2,90E-01
korns-1	2,92E+00	2,01E+01	7,77E+01	4,48E+05	4,92E+05
korns-2	6,73E+02	3,77E+04	8,08E+04	3,91E+05	8,55E+07
korns-3	1,07E+04	1,78E+07	2,54E+08	1,04E+10	5,34E+18
korns-4	2,47E-04	8,47E-03	8,52E-03	8,75E-03	2,38E+00
korns-5	4,88E+29	4,97E+29	4,99E+29	5,03E+29	5,11E+29
korns-6	4,88E+29	4,97E+29	5,00E+29	5,03E+29	5,11E+29
korns-7	2,92E+25	8,37E+25	1,85E+26	2,29E+26	2,70E+26
korns-8	4,86E+29	4,97E+29	5,01E+29	5,04E+29	5,13E+29
korns-9	7,65E+29	7,73E+29	7,76E+29	7,79E+29	7,84E+29
korns-10	2,04E+04	6,47E+05	9,85E+06	7,12E+07	7,39E+18
korns-11	5,86E+01	6,06E+01	6,09E+01	6,14E+01	7,85E+01
korns-12	1,08E+00	1,10E+00	1,11E+00	1,12E+00	1,14E+00
korns-13	5,35E+07	5,59E+08	3,38E+09	1,53E+10	3,34E+13
korns-14	1,11E+06	3,61E+06	1,24E+07	5,07E+07	1,01E+10
korns-15	5,83E+29	5,90E+29	5,95E+29	5,98E+29	6,07E+29

Table D.4: Full 5 number quartile information for Standard Approach with mutation. Results for the 51 Symbolic Regression test instances (Second part).

	Standard with Mutation				
	Minimum	1st Quartile	Median	3rd Quartile	Maximum
keijzer-1	1,04E-03	2,70E-03	8,05E-03	1,18E-02	1,30E-02
keijzer-2	1,61E-02	4,16E-02	5,59E-02	5,60E-02	7,16E-02
keijzer-3	5,82E-02	1,13E-01	1,30E-01	1,30E-01	1,34E-01
keijzer-4	6,92E-03	5,61E-02	8,37E-02	1,01E-01	1,16E-01
keijzer-5	1,99E-04	5,30E-02	7,07E-02	8,32E-02	3,31E-01
keijzer-6	2,36E-04	9,33E-03	2,29E-02	6,77E-01	8,35E-01
keijzer-7	5,03E-04	2,02E-02	3,49E-02	1,61E-01	1,01E+00
keijzer-8	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
keijzer-9	4,88E-04	1,75E-02	1,01E+00	1,01E+00	1,35E+00
keijzer-10	7,51E-04	2,05E-02	2,66E-02	3,14E-02	4,06E-02
keijzer-11	2,13E-02	3,78E-01	4,76E-01	5,46E-01	1,31E+01
keijzer-12	5,36E-01	6,93E+00	4,18E+01	1,59E+02	1,13E+03
keijzer-13	3,87E-01	2,41E+00	4,32E+00	7,74E+00	9,64E+00
keijzer-14	1,15E-01	4,01E-01	5,07E-01	7,50E-01	9,92E-01
keijzer-15	3,00E-01	2,43E+00	3,73E+00	4,84E+00	8,78E+00
vladislavleva-1	7,04E-04	1,29E-02	1,97E-02	2,54E-02	3,56E-02
vladislavleva-2	6,11E-04	6,80E-03	1,60E-02	5,42E-02	1,01E-01
vladislavleva-3	6,66E-02	8,54E-01	9,69E-01	1,16E+00	1,18E+00
vladislavleva-4	2,30E-02	3,40E-02	3,65E-02	4,04E-02	1,16E-01
vladislavleva-5	1,59E-02	8,66E-02	1,79E-01	2,61E-01	4,23E-01
vladislavleva-6	6,58E-01	3,48E+00	5,46E+00	6,76E+00	8,73E+00
vladislavleva-7	1,10E+00	5,29E+00	7,22E+00	8,88E+00	1,19E+01
vladislavleva-8	3,46E-02	6,36E-01	1,00E+00	1,65E+00	3,51E+00

Table D.5: Median and interquartile range information obtained by the Standard Approach with mutation. Results for the 51 instances of Symbolic Regression problems (First part).

	Standard with Mutation	
	Median	IQR
koza-1	1,70E-05	3,74E-04
koza-2	2,26E-05	9,40E-05
koza-3	1,98E-05	1,50E-04
nguyen-1	0,00E+00	3,05E-04
nguyen-2	2,81E-05	4,10E-04
nguyen-3	2,24E-04	1,58E-03
nguyen-4	3,06E-04	1,35E-03
nguyen-5	2,98E-05	6,53E-04
nguyen-6	1,09E-03	3,33E-02
nguyen-7	2,59E-04	4,42E-03
nguyen-8	8,62E-04	5,70E-03
nguyen-9	4,14E-03	1,24E-02
nguyen-10	5,27E-03	1,83E-02
pagie-1	3,99E-02	1,05E-01
pagie-2	1,94E-01	7,72E-02
korns-1	7,77E+01	4,48E+05
korns-2	8,08E+04	3,53E+05
korns-3	2,54E+08	1,04E+10
korns-4	8,52E-03	2,85E-04
korns-5	4,99E+29	6,90E+27
korns-6	5,00E+29	5,80E+27
korns-7	1,85E+26	1,45E+26
korns-8	5,01E+29	7,20E+27
korns-9	7,76E+29	5,65E+27
korns-10	9,85E+06	7,06E+07
korns-11	6,09E+01	7,80E-01
korns-12	1,11E+00	1,81E-02
korns-13	3,38E+09	1,47E+10
korns-14	1,24E+07	4,71E+07
korns-15	5,95E+29	7,35E+27

Table D.6: Median and interquartile range information obtained by the Standard Approach with mutation. Results for the 51 instances of Symbolic Regression problems (Second part).

	Standard with Mutation	
	Median	IQR
keijzer-1	8,05E-03	9,10E-03
keijzer-2	5,59E-02	1,43E-02
keijzer-3	1,30E-01	1,71E-02
keijzer-4	8,37E-02	4,47E-02
keijzer-5	7,07E-02	3,02E-02
keijzer-6	2,29E-02	6,68E-01
keijzer-7	3,49E-02	1,41E-01
keijzer-8	0,00E+00	0,00E+00
keijzer-9	1,01E+00	9,97E-01
keijzer-10	2,66E-02	1,09E-02
keijzer-11	4,76E-01	1,68E-01
keijzer-12	4,18E+01	1,53E+02
keijzer-13	4,32E+00	5,33E+00
keijzer-14	5,07E-01	3,49E-01
keijzer-15	3,73E+00	2,41E+00
vladislavleva-1	1,97E-02	1,24E-02
vladislavleva-2	1,60E-02	4,74E-02
vladislavleva-3	9,69E-01	3,08E-01
vladislavleva-4	3,65E-02	6,39E-03
vladislavleva-5	1,79E-01	1,74E-01
vladislavleva-6	5,46E+00	3,27E+00
vladislavleva-7	7,22E+00	3,59E+00
vladislavleva-8	1,00E+00	1,02E+00

Table D.7: Comparison between Standard with and without Mutation and each Mate Choice approach with Mutation on both chromosomes. Instances where the p-value obtained by the Wilcoxon Mann Whitney test was below the 0.05 alpha value are identified (First part).

	Standard vs Standard Mut	Standard vs PIMP Mut B	Standard vs CMP-GP Mut B
koza-1	Std Mut		CMP-GP
koza-2	Std Mut	PIMP	CMP-GP
koza-3		PIMP	
nguyen-1			CMP-GP
nguyen-2	Std Mut	PIMP	CMP-GP
nguyen-3			
nguyen-4		PIMP	CMP-GP
nguyen-5			CMP-GP
nguyen-6		PIMP	CMP-GP
nguyen-7		PIMP	CMP-GP
nguyen-8			
nguyen-9		PIMP	CMP-GP
nguyen-10		PIMP	CMP-GP
pagie-1		PIMP	CMP-GP
pagie-2		PIMP	CMP-GP
korns-1		PIMP	CMP-GP
korns-2	Std Mut	PIMP	CMP-GP
korns-3		PIMP	CMP-GP
korns-4		PIMP	CMP-GP
korns-5			
korns-7			CMP-GP
korns-10			
korns-11			
keijzer-1		PIMP	CMP-GP
keijzer-2		PIMP	CMP-GP
keijzer-3		PIMP	CMP-GP
keijzer-4		PIMP	CMP-GP
keijzer-5		PIMP	CMP-GP
keijzer-6		PIMP	CMP-GP
keijzer-7	Std Mut	PIMP	CMP-GP
keijzer-9		PIMP	CMP-GP
keijzer-10		PIMP	CMP-GP
keijzer-11			
keijzer-12		PIMP	CMP-GP
keijzer-13		PIMP	CMP-GP
keijzer-14		PIMP	CMP-GP
keijzer-15		PIMP	CMP-GP
vladislavleva-1		PIMP	CMP-GP
vladislavleva-2			CMP-GP
vladislavleva-3		PIMP	CMP-GP
vladislavleva-4			CMP-GP
vladislavleva-5		PIMP	CMP-GP
vladislavleva-6			
vladislavleva-7		PIMP	CMP-GP
vladislavleva-8		PIMP	CMP-GP

Table D.8: Comparison between Standard with and without Mutation and each Mate Choice approach with Mutation on both chromosomes. Instances where the p-value obtained by the Wilcoxon Mann Whitney test was below the 0.05 alpha value are identified (Second part).

	Standard Mut vs PIMP Mut B	Standard Mut vs CMP-GP Mut B	PIMP Mut B vs CMP-GP Mut B
koza-1			CMP-GP
koza-2	PIMP		
koza-3	PIMP		
nguyen-1			
nguyen-2			
nguyen-3	PIMP	CMP-GP	
nguyen-4	PIMP	CMP-GP	
nguyen-5			CMP-GP
nguyen-6	PIMP	CMP-GP	PIMP
nguyen-7	PIMP	CMP-GP	
nguyen-8	PIMP	CMP-GP	
nguyen-9	PIMP	CMP-GP	
nguyen-10	PIMP	CMP-GP	
pagie-1	PIMP	CMP-GP	
pagie-2	PIMP	CMP-GP	CMP-GP
korns-1	PIMP	CMP-GP	
korns-2	PIMP	CMP-GP	
korns-3	PIMP	CMP-GP	
korns-4	PIMP	CMP-GP	
korns-5			PIMP
korns-7	PIMP	CMP-GP	
korns-10	PIMP		PIMP
korns-11	PIMP	CMP-GP	
keijzer-1	PIMP	CMP-GP	
keijzer-2	PIMP	CMP-GP	CMP-GP
keijzer-3	PIMP	CMP-GP	
keijzer-4	PIMP	CMP-GP	CMP-GP
keijzer-5	PIMP	CMP-GP	
keijzer-6	PIMP	CMP-GP	
keijzer-7	PIMP	CMP-GP	
keijzer-9	PIMP	CMP-GP	
keijzer-10	PIMP	CMP-GP	
keijzer-11	PIMP	CMP-GP	
keijzer-12	PIMP	CMP-GP	
keijzer-13	PIMP	CMP-GP	
keijzer-14	PIMP	CMP-GP	
keijzer-15	PIMP	CMP-GP	
vladislavleva-1	PIMP	CMP-GP	
vladislavleva-2			CMP-GP
vladislavleva-3	PIMP	CMP-GP	
vladislavleva-4		CMP-GP	CMP-GP
vladislavleva-5		CMP-GP	CMP-GP
vladislavleva-6	PIMP	CMP-GP	
vladislavleva-7	PIMP	CMP-GP	
vladislavleva-8	PIMP	CMP-GP	

Table D.9: Comparison between Standard Approach with and without Mutation with each Mate Choice approach with Mutation on both chromosomes. Number of runs where the error between the best individual and the optima was below $1E-4$.

	Standard	Standard Mut	PIMP Mut B	CMP-GP Mut B
koza-1	18	35	24	35
koza-2	23	36	43	38
koza-3	35	35	44	43
nguyen-1	34	35	39	41
nguyen-2	18	30	32	39
nguyen-3	26	20	29	30
nguyen-4	14	13	24	23
nguyen-5	23	29	26	34
nguyen-6	15	13	43	35
nguyen-7	22	15	30	32
nguyen-8	19	8	15	17
nguyen-9	8	4	24	18
nguyen-10	12	7	33	17
korns-4	1	0	1	9
keijzer-1	1	0	0	2
keijzer-5	2	0	1	2
keijzer-6	1	0	1	0
keijzer-12	0	0	1	1

Table D.10: Comparison between Standard Approach with and without Mutation and each Mate Choice approach with Mutation on both chromosomes. Instances where the p-value obtainded by Taillard's proportion's tests was below the 0.05 alpha value are identified.

	Standard vs Standard Mut	Standard vs PIMP Mut B	Standard vs CMP-GP Mut B
koza-1	Std Mut		CMP-GP
koza-2	Std Mut	PIMP	CMP-GP
koza-3		PIMP	CMP-GP
nguyen-1			CMP-GP
nguyen-2	Std Mut	PIMP	CMP-GP
nguyen-3			
nguyen-4		PIMP	CMP-GP
nguyen-5			CMP-GP
nguyen-6		PIMP	CMP-GP
nguyen-7		PIMP	CMP-GP
nguyen-8	Std Mut		
nguyen-9		PIMP	CMP-GP
nguyen-10		PIMP	
korns-4			CMP-GP

	Standard Mut vs PIMP Mut B	Standard Mut vs CMP-GP Mut B	PIMP Mut B vs CMP-GP Mut B
koza-1	Std Mut		CMP-GP
koza-2	PIMP		
koza-3	PIMP	CMP-GP	
nguyen-1			
nguyen-2		CMP-GP	
nguyen-3	PIMP	CMP-GP	
nguyen-4	PIMP	CMP-GP	
nguyen-5			CMP-GP
nguyen-6	PIMP	CMP-GP	PIMP
nguyen-7	PIMP	CMP-GP	
nguyen-8	PIMP	CMP-GP	
nguyen-9	PIMP	CMP-GP	PIMP
nguyen-10	PIMP	CMP-GP	PIMP
korns-4		CMP-GP	CMP-GP

Appendix E

Experimental Function Set

Table E.1: Function Sets for studied functions. Terminals for variables (x, y, z, v, w) not shown. Vladislavleva's constants are functions with arguments, not terminals: ε is a uniform random value from $[-5,5]$. Koza's function set traditionally has optional $[-1,1)$ constants: but no constants are assumed by default. (Adapted from [193]).

	Functions	Constants (ERC)
Koza	$+$ $-$ $\times$ % sin cos e^n $\ln(\lvert n\rvert)$	None
Korns	$+$ $-$ $\times$ % sin cos e^n $\ln(\lvert n\rvert)$ n^2 n^3 $\sqrt{n}$ tan tanh	Random finite 64-bit IEEE double
Keijzer	$+$ $\times$ $\frac{1}{n}$ $-n$ $\sqrt{n}$	Random value from $N(\mu=0,\sigma=5)$
Vladisdalvela-A	$+$ $-$ $\times$ % n^2	n^ε $n+\varepsilon$ $n\varepsilon$
Vladisdalvela-B	$+$ $-$ $\times$ % n^2 e^n e^{-n}	n^ε $n+\varepsilon$ $n\varepsilon$
Vladisdalvela-C	$+$ $-$ $\times$ % n^2 e^n e^{-n} sin cos	n^ε $n+\varepsilon$ $n\varepsilon$

Table E.2: Symbolic Regression Functions. $U[a,b,c]$ is c uniform random samples drawn from a to b, inclusive, for the variable. $E[a,b,c]$ is a grid of points evenly spaced (for this variable) with an interval of c, from a to b inclusive (First Part, adapted from [193])

	Vars	Objective Function	Training Set
Koza-1, Nguyen-2	1	$x^4+x^3+x^2+x$	$U[-1,1,20]$
Koza-2	1	x^5-2x^3+x	$U[-1,1,20]$
Koza-3	1	x^6-2x^4+x	$U[-1,1,20]$
Nguyen-1	1	x^3+x^2+x	$U[-1,1,20]$
Nguyen-3	1	$x^5+x^4+x^3+x^2+x$	$U[-1,1,20]$
Nguyen-4	1	$x^6+x^5+x^4+x^3+x^2+x$	$U[-1,1,20]$
Nguyen-5	1	$\sin(x^2)\cos(x)-1$	$U[-1,1,20]$
Nguyen-6	1	$\sin(x)+\sin(x+x^2)$	$U[-1,1,20]$
Nguyen-7	1	$\ln(x+1)+\ln(x^2+1)$	$U[0,2,20]$
Nguyen-8	1	$\sqrt{x}$	$U[0,4,20]$
Nguyen-9	2	$\sin(x)+sin(y^2)$	$U[0,1,20]$
Nguyen-10	2	$2\sin(x)\cos(y)$	$U[0,1,20]$
Pagie-1	2	$\frac{1}{1+x^{-4}}+\frac{1}{1+y^{-4}}$	$E[-5,5,0.4]$
Korns-1	5	$1.57+24.3v$	$U[-50,50,10000]$
Korns-2	5	$0.23+14.2\frac{v+y}{3w}$	$U[-50,50,10000]$
Korns-3	5	$-5.41+4.9\frac{v-x+\frac{y}{w}}{3w}$	$U[-50,50,10000]$
Korns-4	5	$-2.3+0.13\sin(z)$	$U[-50,50,10000]$
Korns-5	5	$3+2.13\ln(w)$	$U[-50,50,10000]$
Korns-6	5	$1.3+0.13\sqrt{x}$	$U[-50,50,10000]$
Korns-7	5	$213.80940889(1-e^{-0.54723748542x})$	$U[-50,50,10000]$
Korns-8	5	$6.87+11\sqrt{7.23xvw}$	$U[-50,50,10000]$
Korns-9	5	$\frac{\sqrt{x}}{\ln y}\frac{e^x}{v^2}$	$U[-50,50,10000$
Korns-10	5	$0.81+24.3\frac{2y+3z^2}{4(v)^3+5(w)^4}$	$U[-50,50,10000]$
Korns-11	5	$6.87+11\cos(7.23x^3)$	$U[-50,50,10000]$
Korns-12	5	$2-2.1\cos(9.8x)\sin(1.3w)$	$U[-50,50,10000]$
Korns-13	5	$32-3\frac{\tan(x)}{\tan(y)}\frac{\tan(z)}{\tan(v)}$	$U[-50,50,10000]$
Korns-14	5	$22-4.2(\cos(x)-\tan(y))\frac{\tanh(z)}{\sin(v)}$	$U[-50,50,10000]$
Korns-15	5	$12-6\frac{\tan(x)}{e^y}(\ln(z)-\tan(v))$	$U[-50,50,10000]$

Table E.3: Symbolic Regression Functions. $U[a,b,c]$ is c uniform random samples drawn from a to b, inclusive, for the variable. $E[a,b,c]$ is a grid of points evenly spaced (for this variable) with an interval of c, from a to b inclusive (Second Part, adapted from [193])

	Vars	Objective Function	Training Set
Keijzer-1	1	$0.3x\sin(2\pi x)$	$E[-1,1,0.1]$
Keijzer-2	1	$0.3x\sin(2\pi x)$	$E[-2,2,0.1]$
Keijzer-3	1	$0.3x\sin(2\pi x)$	$E[-3,3,0.1]$
Keijzer-4	1	$x^3e^{-x}\cos(x)\sin(x)(\sin^2(x)\cos(x)-1)$	$E[0,10,0.05]$
Keijzer-5	3	$\frac{30xz}{(x-10)y^2}$	$x,z:U[-1,1,1000]$ $y:U[1,2,1000]$
Keijzer-6	1	$\sum_i^x \frac{1}{i}$	$E[1,50,1]$
Keijzer-7	1	$\ln x$	$E[1,100,1]$
Keijzer-8	1	$\sqrt{x}$	$E[0,100,1]$
Keijzer-9	1	$\operatorname{arcsinh}(x)$	$E[0,100,1]$
Keijzer-10	2	x^y	$U[0,1,100]$
Keijzer-11	2	$xy+sin((x-1)(y-1))$	$U[-3,3,20]$
Keijzer-12	2	$x^4-x^3+\frac{y^2}{2}-y$	$U[-3,3,20]$
Keijzer-13	2	$6\sin(x)\cos(y)$	$U[-3,3,20]$
Keijzer-14	2	$\frac{8}{2+x^2+y^2}$	$U[-3,3,20]$
Keijzer-15	2	$\frac{x^3}{5}+\frac{y^3}{2}-y-x$	$U[-3,3,20]$
Vladislavleva-1	2	$\frac{e^{-1(x-1)^2}}{1.2+(y-2.5)^2}$	$U[0.3,4,100]$
Vladislavleva-2	1	$e^{-x}x^3(\cos x\sin x)(\cos x\sin^2 x-1)$	$E[0.05,10,0.1]$
Vladislavleva-3	2	$e^{-x}x^3(\cos x\sin x)(\cos x\sin^2 x-1)(y-5)$	$x:E[0.05,10,0.1]$ $y:E[0.05,10.05,2]$
Vladislavleva-4	5	$\frac{10}{5+(x-3)^2+(y-3)^2+(z-3)^2+(v-3)^2+(w-3)^2}$	$U[0.05,6.05,1024]$
Vladislavleva-5	3	$30\frac{(x-1)(z-1)}{y^2(x-10)}$	$x:U[0.05,2,300]$ $y:U[1,2,300]$ $z:U[0.05,2,300]$
Vladislavleva-6	2	$6\sin(x)\cos(y)$	$U[0.1,5.9,30]$
Vladislavleva-7	2	$(x-3)(y-3)+2\sin((x-4)(y-4))$	$U[0.05,6.05,300]$
Vladislavleva-8	2	$\frac{(x-3)^4+(y-3)^3-(y-3)}{(y-2)^4+10}$	$U[0.05,6.05,50]$

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