A Self-adaptive Mate Choice Model for Symbolic Regression

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Abstract—**Sexual Selection through Mate Choice has for the past few decades attracted the attention of many researchers from different fields. Numerous contributions and supporting evidence for the role and impact of Sexual Selection through Mate Choice in Evolution have emerged since then. Just like Evolutionary Theory has had to adapt its models to account for Sexual Selection through Mate Choice and its effects, it is relevant to study and analyse the impact that Mate Choice may have on Evolutionary Algorithms.**

In this study we describe a nature inspired self-adaptive Mate Choice approach designed to tackle Symbolic Regression problems. Results on a set of test functions are presented and compared to a standard approach, showing that Mate Choice is able to contribute to enhanced results on complex instances of Symbolic Regression. Also, the resulting behaviours are contrasted and discussed, suggesting that Mate Choice is able to evolve Mating evaluation functions that are able to select partners in meaningful and valuable ways.

I. INTRODUCTION

Darwin's theory of Natural Selection has for long been widely accepted by the scientific community. Described by Darwin as the result of competition within or between species affecting their individuals relative rates of survival [1], Natural Selection has found its way into many research fields and is utterly relevant in Evolutionary Computation (EC). Given a population where genetic variance occurs, individuals with favorable characteristics have a higher rate of survival and are more likely to spread their genes through future generations by means of heritability while unfavored characteristics and corresponding genes are gradually discarded.

In the years after his masterpiece on Natural Selection, Darwin put much effort on developing his theory of Sexual Selection, a force capable of shaping complex traits and behaviours across the species. He described it as the result of competition within species affecting its individuals relative rate of reproduction [2], but unlike Natural Selection, this theory found little acceptance at the time. Interest rose however in the 1970s mostly due to Zahavis works [3] and previous contributions by Fisher [4], [5]. With the emergence of new fields of research such as Evolutionary Anthropology [6] and Evolutionary Psychology [7], aided by modern knowledge and technology, new ideas and supporting evidence have contributed to a much wider acceptance of Sexual Selection as playing a major role in evolution.

Darwin has proposed two main processes composing Sexual Selection: Male Competition and Female Mate Choice. The latter is the psychological process by which individuals choose their mating partners based on their perception of others and mating preferences and is the scope of this study. Just like Evolutionary Theory, EC is an ongoing research field, where new ideas are constantly introduced and experimented with. The same way that Evolutionary Theory has had to adapt its evolutionary models to account for Sexual Selection through Mate choice, it is relevant to study the impact and inherent effects that it may have on Evolutionary Algorithms (EA).

Studying Sexual Selection through Mate Choice in EC presents a number of challenges, the most prominent being the difficulty of modeling nature-inspired Mate Choice mechanisms as well as analysing its effects on EAs. The process depends on individuals' ornamentation, perception of others and mating preferences that evolve similarly to physical traits [4], which is not straightforward to model. Also, unlike Natural Selection based models, individuals adapt not only to an environment but also in relation to each other through the intrinsic relation between mating preferences and displayed ornaments or characteristics [5]. This presents a new paradigm that is challenging to analyse.

In this research we propose a self-adaptive [8] Mate Choice approach to Symbolic Regression. The study aims at analysing the ability of the nature-inspired model to evolve mating evaluation functions that help choose mating partners in meaningful and beneficial ways. The performance of the proposed strategy is discussed and the impact on the algorithm's behaviour is addressed with a particular interest on destructive crossover.

The following section introduces Sexual Selection through Mate Choice, including a review of the theory's background and of related work and implementations on Evolutionary Algorithms. A Mate Choice approach for symbolic regression is then introduced and implementation details addressed. Section III describes the experimental setup and results are analysed and discussed. Conclusions are drawn in Sec. IV and future work presented.

II. SEXUAL SELECTION THROUGH MATE CHOICE

The subject of Sexual Selection through Mate Choice is introduced on the following subsections. Firstly, sec. II-A covers theoretical background on Sexual Selection through Mate Choice. Secondly, previous research on Mate Choice in EC is presented in sec. II-B. Finally, sec. II-C discusses our approach to symbolic regression.

A. Background

Ever since publishing his theory of Natural Selection, Darwin was interested in the origin of animal ornamentation and courtship behaviours, briefly addressing the subject in his masterpiece *On the Origin of Species* [1] and later extensively discussing the subject in *The Descent of Man, and Selection in Relation to Sex* [2]. Darwin's intrigue was that Natural Selection could not explain the emergence of these costly and complex traits that don't seem to contribute to the individuals survival ability. To some extent they seemed counterproductive to Natural Selection. Nonetheless, Darwin knew that in order for ornaments and courtship behaviours to emerge and spread they needed to bring some kind of evolutionary advantage to individuals. In order to account for such traits, Darwin envisioned the theory of Sexual Selection, a trait-shaping selection feature capable of evolving complex traits that bring reproductive rather than survival advantages.

While Natural Selection adapts species to their environment [1], Sexual Selection adapts individuals in relation to others in a struggle of individuals of one sex for access to individuals of the other [2]. In this scenario, failure means that the individuals will produce few or no offspring. While such individuals may have strong survival abilities, from an evolutionary perspective, individuals that have a small reproductive success are akin to individuals with weak survival abilities as their genes are less likely to spread through future generations. Darwin's ideas on Sexual Selection showed that adaption occurs not only due to differences in survival rates but also from differences in reproductive success. They also show how psychological traits can shape physical traits through Mate Choice.

The theory of Sexual Selection imposes that individual's reproductive success is determined by how attractive they are to others. Such a paradigm includes cases where individuals with poor survival abilities may attain a high reproductive success because they display phenotypic characteristics that are favored by mating preferences and the other way around. The role of mating preferences is therefore of great relevance. Fisher [4], [5] has made important contributions to better understand the relation between mating preferences and evolved traits. He suggested that ornaments have evolved as indicators of fitness and that individual whose mating preferences favour ornaments associated to highly fit individuals will have an evolutionary advantage as they will select fitter mating partners, helping produce fitter offspring and contributing to the spread of their genetic material [4]. Fisher also proposed, among other contributions, that mating preferences are heritable as part of the genotype and are therefore subject to evolution in a similar way as physical traits [5].

The aforementioned characteristics suggest an intrinsic and deep dependence between both mating preferences and evolved physical traits. Fisher described the relation as a positive-feedback loop [5], an arms race where both mating preferences evolve in relation to exhibited ornaments and ornaments adapt according to existing mating preferences. In a nutshell, features that result on a higher survival rate will bring evolutionary advantage to individuals whose mating preferences favour them, which results on the reinforcement and spreading of both ornaments and mating preferences. The opposite may also occur, with ornaments adapting to popular mating preferences in order to bring reproductive success to individuals, resulting on the reinforcement of both ornaments and mating preferences [5].

The feedback loop described above makes Sexual Selection through Mate Choice an extremely difficult subject to analyse. Moreover, Zahavi introduced the *handicap principle* [3] which suggests that not all ornaments act as honest indicators of fitness. Examples such as the peacock's tail or the Irish elk's antlers show that ornaments may work as handicaps. Only individuals with a high fitness are able to maintain such costly ornaments, indicating good genes. A variety of behaviours can result from Sexual Selection through Mate Choice, with sometimes unexpected results that are challenging to analyse and interpret.

B. Related Work

The increasing interest of researchers on Sexual Selection through Mate Choice has spread its impact to various research fields. While on EC the number of publications on the subject is still reduced, there are a number of contributions regarding the design and implementation of Sexual Selection through Mate Choice that are worth reviewing. We are especially interested in models that follow three nature-inspired rules:

1) individuals must choose who they mate with based on their perception of others and on their own mating preferences;
2) mating preferences are heritable the same way as physical traits;
3) mate selection introduces its own selection pressure but is subject to selection pressure itself [9];

Several publications fall into this scope but others have given important contributions as well. The remainder of this section covers relevant contributions to the present work.

Eshelman et al. [10] applied an approach that relies on a Hamming distance threshold, below which recombination is inhibited. An alternative approach has been proposed by Craighurst et al. [11] where similarity between individuals is measured by their genealogical trees. Individuals sharing ancestors to a certain degree are prevented from mating with each other. Fernandes and Rosa [12] have studied the two aforementioned strategies on a Genetic Algorithms (GA) model applied to the royal road function. Results show an increase in performance on both approaches, specially if coupled with populations with varying sizes. It is also discussed that approaches showing a greater diversity along the evolutionary process don't necessarily result in a better performance despite that being the goal of both the non-random mating strategies.

Burke et al. [13] have proposed a different approach where individuals are grouped according to their lineage. During selection, two groups are randomly selected and one individual is also randomly selected from each group. This approach entirely removes the influence of fitness from the selection process and focuses on lineage alone. Lineage selection, as labeled by the authors, reportedly changes the dynamics of evolution on various domains, aiming at the promotion of diversity. On regression of Binomial-3 problems, improving diversity resulted on worst results when compared to a standard approach. The authors discuss that combining parts of dissimilar solutions doesn't always result in solutions that make sense due to nodes losing their context. They argue that converged populations have an easier task when combining genetic material from different individuals without them losing context, suggesting that there should be a balance between selection pressure and diversity handling.

Vrajitoru [14] proposed a scheme where individuals are grouped into four genders: self-fertilizing, hermaphrodite, female or male. Each gender is associated with its own mating preferences, i.e. what groups they may mate with. Two approaches are compared, either with or without fitness-proportionate selection. It is discussed that natural selection plays a role on determining each individual's reproduction mode as dominant individuals will promote their gender through future generations.

Gustafson et al. [15] experimented with mating between dissimilar individuals on regression of binomial-3 instances. In the discussed work, measuring the similarity between individuals relies on the edit-distance [13], [16]. Results suggest that the search process is equally influenced by unfit solutions and solutions that are both fit and dissimilar. Ultimately, the experimented approach resulted on improved solution quality.

Fernandes and Rosa [17] applied both negative and positive assortative mating to a Vector Quantization problem using a similarity measure that accounts for phenotype information regarding individuals. The approach selects both a parent and a set of mating candidates through a roulette wheel operator and the parent mates with the most similar or dissimilar candidate. Results show an enhanced performance on negative assortative mating and it is argued that diversity handling is a key factor.

Ratford et al. [18] proposed a seduction function that combines the fitness of the mating candidates with the Hamming distance to the first parent. The measure benefits mating between individuals that are neither too similar nor too dissimilar. They also propose dynamically adapting the bias of the function at each generation so that mating between dissimilar individuals is favoured at the beginning of each run but gradually gives space to mating between similar individuals through the evolution process. The ability of the approach on finding multiple solutions on multimodal problems was assessed and results show that the proposed strategy may be an important asset. The same research group has proposed a seduction function that doesn't rely on fitness but rather on either Hamming distance, Euclidean distance or common building block between the first parent and mating candidates [19]. They study the approach on a set of test problems and for the most of it, results are reported to be significantly better. It is also discussed that either similarity measure performed robustly without the need to rely on the fitness of the individuals for mating purposes.

Booker [20], [21] proposed an approach where classifier systems are allowed to mate only if they match the same message. If no full matches are possible, partial matching individuals are allowed to crossover. The approach was labeled *Restricted Mating*. Booker [20] and Goldberg [22] have also explored models where a tag is added to each individual's chromosome and mating occurs when a number of bit-positions between a tag and other individuals are matched. Variations such as one-way, two-way and partial matching have been proposed as well as matching tags with templates rather than individuals. Tags and templates are allowed to evolve as part of the genotype.

Fry et al. [9] experimented in GP with a negative assortative mating scheme that self-adapts along the run. They propose that individuals choose their partners based on a function combining fitness and dissimilarity so that mating between dissimilar pairs is promoted. Similarity is assessed based either on relative or absolute edit distance between individuals. Finally, they propose applying this operator, as an alternative to tournament selection, with a given probability. This value adapts along the run either on a population or on an individual level according to how successful crossover is. Results show that self-adapting the probability of choosing between the most fit or the most dissimilar mating partners provides a valuable balance between exploration and exploitation that enhances performance.

Hinterding and Michalewicz [23] tackle the constrained optimization of a nonlinear programming problem. They propose using a Mate Choice approach that promotes the feasibility of individuals rather than using traditional methods for constrained optimization. On their study, a individual is first selected using a tournament that favors feasible individuals which will then select a mating partner from a set of candidates. By preferring mates that, in conjunction with itself, violate the least number of constraints they aim at producing more feasible offspring. The approach was compared with standard constraint optimization methods achieving comparable results.

Smorokdina and Tauritz have proposed a self-adaptive approach where each individual encodes its own Mate selection function in addition to a candidate solution for the working problem [24]. The Mate selection function is represented using Genetic Programming (GP). The terminal nodes of the trees are, exclusively, the remaining individuals in the population. The non-terminals are a set of selection operators such as *tournament selection*, *biggest hamming distance*, etc. Constraints are enforced to make sure the operators are applied correctly. Mate selection functions are inherited from parents to offspring following one of two proposed rules: given that the new offspring show improvements they inherit the function that was actively used; otherwise, the function attributed to new offspring is the result of the recombination of those from both parents. Results on a set of test problems were slightly worse than a traditional approach.

Guntly and Tauritz [25] propose two variants to a Learning Individual Mating Preferences (LIMP) approach, either using a centralized (C-LIMP) or a decentralized approach (D-LIMP). LIMP has been designed for binary representations, using a real-valued preferences vector that encodes how desirable it is that each gene in the genotype is set to one. The D-LIMP approach attributes a preferences vector to each individual that is used to select mating partners. Offspring inherit the vectors from their parents so that preferences match the genes inherited from each one. Also, the vectors are adapted according to the success of the offspring. The C-LIMP approach relies on two centralized preferences vectors, one relative to genes set to 0 and the other relative to genes set to 1. These vectors are accessed by individuals when evaluating others and adapt to match the success of the offspring in the same fashion as in D-LIMP. Both approaches were compared with a traditional GA and a variable dissortative mating GA, achieving better results in part of the test set.

Machado and Leitão [26] describe a model with self-adapting mate evaluation functions for the Circle Packing in Squares (CPS) problem. They rely on the fact that candidate solutions to this problem also encode candidate solutions to smaller instances, which when assessed can be used as indicators of good genetic quality. Apart from a candidate solution to the problem, each individual also encodes an extra chromosome that represents its own mating preferences. Two approaches were tested either relying on GA or GP representations. The GA mate evaluation function was designed as a weighted sum matching the weights on the first individual with the fitness values obtained by each candidate on smaller instances of the problem. In this case only the weights are evolved. The GP approach evolves whole evaluation functions that are built using the fitness values from each candidate on smaller instances as the terminal set and a set of arithmetic operators as the function set. Results achieved by the GA approach were poor when compared to a standard approach. On the other hand, the GP approach was able to improve upon the results obtained with a classical approach. The same authors have studied a Mate Choice approach to the optimization of Morse Clusters [27]. The approach achieved a slightly more robust behaviour on a global level than a standard selection scheme. The Mate Choice mechanism is coupled with a steady state model and it is discussed that by adapting to the replacement strategy, it is able to produce a higher rate of valuable offspring which have a smaller yet longer impact on the population's structural diversity.

C. A Self-adaptive Mate Choice Approach to Symbolic Regression

The approach implemented for this study encodes in each individual its own mating preferences, which it uses to assess other individuals for mating purposes. In order to do so, each individual includes two chromosomes, the first representing a candidate solution to the target problem, as in a standard approach, and the second representing the mating preferences. Therefore, the approach follows the first rule set in sec. II-B since each individual will rely on its own preferences to assess and evaluate potential partners. The second rule is enforced by the heritability inherent in the evolution process. The application of genetic operators on each chromosome, independently, ensures that genetic material is passed both regarding candidate solutions and mating preferences. Finally, the spectrum of available mating preferences impacts the reproductive success of individuals by favoring certain characteristics over others. The selection pressure caused by mating preferences will ultimately impact both chromosomes by causing the adaption of individuals to each other, therefore adhering to the third rule.

Both chromosomes rely on a GP representation. The first tree is mapped to a candidate solution to the target function, once mapped this is the phenotype of the individual and hence visible to potential mating partners. The second chromosome encodes a tree that is mapped to a function representing the ideal mating partner according to the preferences of the individual. When assessing potential mating partners, each individual compares the function that represents its ideal mate with the phenotypes of each mating partner choosing the most similar one. In a nutshell, evaluation of mating candidates relies on the same mechanisms as when evaluating the first chromosome to determine its fitness. However, instead of comparing the function represented by the first chromosome to the target one, it is compared to the function representing the ideal mating partner. The differences between the ideal mating partner and each of the candidates are measured in a similar way as in a standard approach and the one that most resembles the ideal mating partner is selected for mating. The similarity measure therefore accounts for differences between phenotypes. Traditional choices such as edit distance rely on genotype characteristics, however, we feel that assessing others based on their phenotypes shows a closer resemblance to natural processes.

Algorithm 1 Parent selection using Sexual Selection through Mate Choice

```
mate selection {
    parent1 = parent_selection(Pop)
    candidates = mating_candidates_selection(Pop)
    evaluate_mating_candidates(parent1,candidates)
    parent2 = select_best(candidates)
}
```

Algorithm 1 succinctly describes the selection process applied. Firstly, *Parent1* is selected by means of Tournament Selection and a number of mating candidates is randomly sampled from the population. Secondly, *Parent1* assesses the displayed functions and chooses for mating the individual that

TABLE I
SYMBOLIC REGRESSION FUNCTIONS. $U[a, b, c]$ REPRESENTS c UNIFORM RANDOM SAMPLES DRAWN FROM THE INTERVAL $[a, b]$. $E[a, b, c]$ IS A SET OF POINTS EQUALLY SPACED WITH AN INTERVAL OF c, IN THE INTERVAL $[a, b]$.

Name	Objective Function	Set
Keijzer-1 [29]	$0.3xsin(2\pi x)$	E[-1,1,0.1]
Keijzer-2 [29]	$0.3xsin(2\pi x)$	E[-2,2,0.1]
Keijzer-3 [29]	$0.3xsin(2\pi x)$	E[-3,3,0.1]
Keijzer-4 [29]	$x^3e^{-x}cos(x)sin(x)(sin^2(x)cos(x) - 1)$	E[0,10,0.1]
Koza-1 [30]	$x^4 + x^3 + x^2 + x$	U[-1,1,20]
Nguyen-5 [31]	$sin(x^2)cos(x) - 1$	U[-1,1,20]

TABLE II
MEAN BEST FITNESS OBTAINED BY THE STANDARD, MATE CHOICE AND RANDOM APPROACHES ON EACH FUNCTION OVER 50 RUNS.

Function	Standard	Mate Choice	Random
Keijzer-1	0.008005462	**0.0059473756**	0.0072442644
Keijzer-2	0.0063776454	**0.0052139161**	0.0062104645
Keijzer-3	0.0071500245	**0.0056003145**	0.0067438776
Keijzer-4	0.0890397335	**0.0833904122**	0.0840754187
Koza-1	**0.0006384168**	0.0014386396	0.0006481816
Nguyen-5	0.0014892713	**0.0004783439**	0.0025763115

best matches its ideal partner. Afterwards, the pair generate offspring by means of GP operators applied independently to each chromosome and the new individuals are introduced into the population of the new generation. The process is repeated until the new population is complete.

This process illustrates how the attractiveness of each individual influences its reproductive success. Genes that are coupled with good mating preferences have a better chance of being mixed with good quality genes during reproduction, therefore increasing their chance of spreading through future generations. On the other hand, mating preferences coupled with attractive genetic material are also more prone to successfully spread. The resulting feedback-loop causes individuals in the population to not only adapt to the environment but also to each other in a struggle for reproduction. The success of the approach therefore relies on its ability to evolve mating preferences that help choose partners in ways that benefit the evolution process.

III. RESULTS

The following subsection details the experimental setup applied to study the effects of Sexual Selection through Mate Choice and the proposed approach on Symbolic Regression. The results are then analysed and discussed.

A. Experimental Setup

Experiments were conducted on symbolic regression targeting a set of functions mixing the six functions displayed in Table I. The decision to tackle this particular subset relies mostly on their inclusion and discussion on the publication regarding GP benchmarking by McDermott et al. [28].

Three approaches were considered: Standard approach where both individuals are selected using tournament selection and mating preferences take no part; a Random approach where the first parent is selected by means of tournament selection but its pair is selected randomly; the proposed approach where the first parent is selected through tournament selection and chooses from a pool a candidates the one that best resembles its ideal mating partner.

At each run, the Keijzer functions evolve a population of 100 individuals while for both the Koza and the Nguyen functions, populations of 500 individuals are evolved. The populations evolve for 100 generations. Tournament size has been set to 5 individuals and the number of mating candidates has also been set to 5. Crossover is applied on the selected parents, independently on the first and the second chromosomes, with a probability of 90% and is 90% biased to function nodes and 10% biased to terminal nodes as crossover points [30]. Elitism is also imposed so that the best individual of each generation is included in the next one. Information regarding the terminal and non-terminal sets can be found in McDermott's publication [28] and implementation details can be found in each of the articles describing the functions [29]–[31].

A total of 50 runs are executed for each approach and data regarding the fitness and the number of individuals resulting from destructive crossover are recorded for analysis. In this study, an individual is considered to be the result of destructive crossover if its fitness is worst than the fitness of the parent that actively chose a mate. An individual is considered the result of a neutral crossover if its fitness is equivalent to the fitness of the parent that actively chose a mate.

B. Analysis and Discussion

Table II shows a comparison of the Mean Best Fitness (MBF) obtained by each studied approach on each function along 50 runs. A Wilcoxon Mann Whitney test with a significance level of 0.01 was conducted, comparing each approach with the remaining two. The instances where the proposed approach performed significantly better than the Standard approach or the other way around are presented in bold in Table II. Regarding the Random approach, it performed significantly better than the Mate Choice approach on the Koza-1 instance but worst on Keijzer-1, Keijzer-2 and Keijzer-3 as well as on the Nguyen-5.

The Koza-1 instance is regarded as a particularly easy instance for symbolic regression [28] which may explain the results obtained, specially if the large size of the population is considered. The results suggest that the overhead created by the Mate Choice model does not payoff. The extra effort put on the evolution process to adapt mating preferences, as seen in Figure 1, slows down convergence, giving the Standard approach the observed advantage. Regarding the Nguyen-5 function, the three approaches performed considerably better than on the Keijzer instances. While the instance is not regarded as particularly simple for symbolic regression, the use of a population with 500 individuals may explain why the approaches were able to achieve better MBFs. In this case, the Standard approach seems able to benefit from a larger, and likely more diverse, population and achieve a lower MBF than the Random approach. Still, Mate Choice was able to

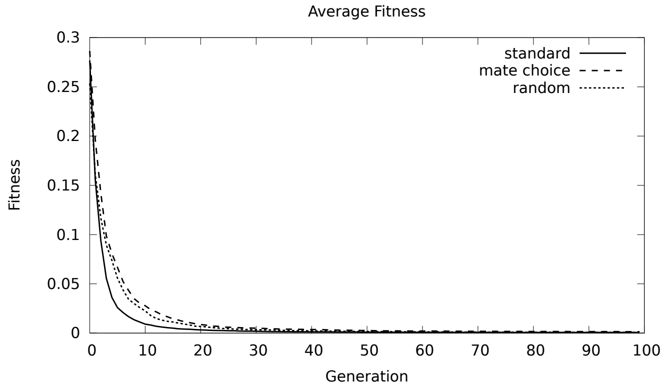

Fig. 1. Mean Best Fitness obtained along 50 runs for the Koza-1 function

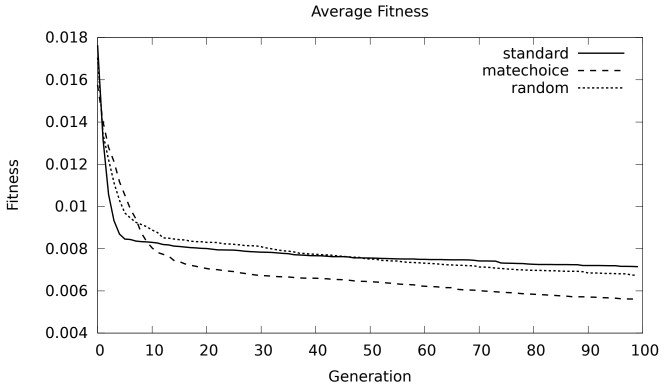

Fig. 2. Mean Best Fitness obtained along 50 runs for the Keijzer-3 function

TABLE III
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	**7198.2**	6808.86
Keijzer-4	5968.18	**7239.4**	6805.04
Koza-1	34889.32	**36399.72**	36797.82
Nguyen-5	27597.62	**34656.84**	30013.76

TABLE IV
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	3124.6	**1760.94**	2524.54
Keijzer-2	3278.84	**1708.12**	2060.58
Keijzer-3	2852.96	**1741.4**	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

outperform the Standard approach with a significant MBF difference.

The Mate Choice approach achieved a significantly better MBF value than the Standard approach on the Keijzer instances as well, suggesting that the proposed strategy is able to contribute to enhancing results. Despite the generated overhead on the evolution process, the approach seems capable of evolving mating preferences that favour mating partners in a way that is beneficial to the evolution process. Overall, the differences in MBFs between the proposed approach and the Random approach are quite noticeable, emphasizing that the behaviour produced by the Mate Choice strategy is not similar to randomly selecting mating partners, but a behaviour that produces larger benefits, therefore backing up our assumption that Mate Choice evolves mating preferences that help selecting mating partners in meaningful ways. It's also noticeable that while no significant differences were found between the Standard and the Random approaches, the later performs slightly but consistently better on the harder instances (Keijzer-1 to Keijzer-4), suggesting that the reduced selection pressure inherent may be beneficial, allowing for a better exploration rather than exploitation of the fittest individuals. Different studies explore selection pressure, one where different schemes are coupled with the ideas of Sexual Selection and compared has been conducted by Wagner and Affenzeller [32].

Tables III and IV further highlight behavioural differences between the studied approaches. Table III shows the mean cumulative number of destructive crossovers (MCDC) obtained along the 50 runs by each approach while Table IV shows the mean cumulative number of neutral crossovers (MCNC). A Wilcoxon Mann Whitney test with a significance level of 0.01 was conducted, comparing each pair of approaches. Instances where the Mate Choice approach achieved a significantly higher MCDC or a significantly smaller MCNC than the Standard approach are depicted in bold.

A brief perusal of Tables III and IV reveals that Mate choice consistently results in a higher MCDC than the standard approach. Conversely, it attains lower MCNC on all instances where it outperformed the other approaches. On the Koza-1 instance, probably due to its simplicity, the approach that performed the smallest MCDC was able to outperform the others as candidate solutions are likely to evolve faster and further towards the target function by means of successful crossovers. Although correlation does no imply causality, these results suggest that the explanation for the success of the Mate Choice approach may rest on the reduction of neutral crossover. Individuals that result from neutral crossovers make no contribution to fitness enhancements and may ultimately stall evolution and decrease diversity. The higher MCDC obtained by Mate Choice may be explained by the stochasticity it introduces in the mate selection process. Additionally, Mate Choice is outperforming other approaches and, as such, the results are inherently more difficult to improve.

Due to lack of space, further analysis will focus on a single function. However, the discussed behaviours generalize to the other instances with the exception of the Koza-1, where the Standard approach performs better. We have chosen to focus on the Keijzer-3 function. Figure 2 shows how the MBF evolves along the 100 generations while Figures 3 and 4 show

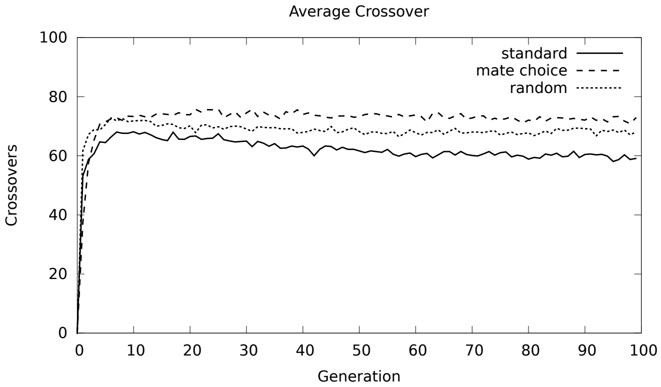

Fig. 3. Mean of Destructive Crossovers obtained along 50 runs for the Keijzer-3 function

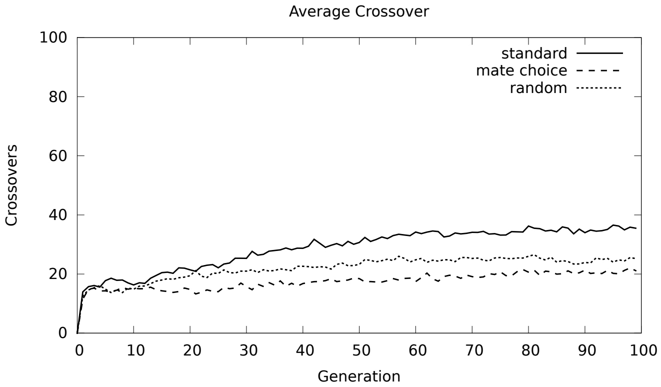

Fig. 4. Mean of Neutral Crossovers obtained along 50 runs for the Keijzer-3 function

the mean of destructive crossovers and the mean of neutral crossovers at each generation and how they evolve along the runs.

Figure 2 shows that the MBF rapidly evolves for the Standard approach for the first 5 or so generations, probably taking advantage of the initial population diversity. Figure 3 shows that for this period, the mean of destructive crossovers also raises rapidly, stabilizes and then gradually descends for the remaining of the generations. The behaviour suggests that, from this point on, the Standard approach promotes crossover between fit solutions. Individuals have a greater chance of promoting their genetic material by mating with fit partners, those who are unable to do so are gradually discarded and no longer contribute to evolution. This behaviour is supported by Figure 4 which shows that the Standard approach produces a gradually higher mean of neutral crossovers. This is consistent with a decreasingly diverse population where a small number of individuals takes over. As a result, while fitter individuals gradually mate with other fit individuals, their impact on the evolution process is reduced and advances are made slowly as individuals exploit a smaller set of genes.

The Mate Choice approach, as shown by Figure 2, has a slower MBF evolution on the first generations, surpassing however the Standard approach at around the 10th generation. Figure 3 shows that by generation 10, the Mate Choice approach is producing more destructive crossovers than the Standard approach. While mating between fit and similar solutions is less likely to cause destructive crossovers, mating with unfit or dissimilar individuals is more likely to produce destructive crossovers as genes mix either with worst genes or with genes from different contexts. The Mate Choice approach seems to promote this behaviour along the runs, causing the mean of destructive crossovers to remain steady for the remainder of the generations. However, as seen by Figure 2 and by Table II, such a behaviour has a positive impact on the MBF, likely the result of a better exploration through the contribution of genes from less fit or dissimilar individuals. Figure 4 supports this behaviour as a smaller mean of neutral crossovers is observed on the Mate Choice approach throughout the entire run. Thus, in the considered experimental settings, the Mate Choice strategy promotes risk-taking resulting in higher MCDC and lower MCNC and taking risks is beneficial in the most complex problem instances.

When comparing the Mate Choice approach with the Random one, both regarding the mean of destructive crossovers and the mean of neutral crossovers, it is noticeable that the produced behaviours happen with a different frequency, indicating that the evolution of mate preferences has an impact on the behaviour of the algorithm. The results reported in Table II and the analysis of Figure 2 show that such an impact is positive for the performance of the evolutionary process.

IV. CONCLUSIONS

Evolutionary Computation is an ongoing research field where, just like in Evolutionary Theory, new ideas are constantly introduced and experimented. While many research fields have come to study and embrace the theory of Sexual Selection, its impact on Evolutionary Computation and inherent effects are yet not fully understood. During this study we explore a nature-inspired Mate choice mechanism and analyse its effects on Evolutionary Algorithms. A comprehensive review of the background of Sexual Selection and more specifically Mate Choice is included as well as an extended review of related work and applications on Evolutionary Computation.

A self-adaptive Mate Choice approach to Symbolic Regression is proposed, following three nature inspired rules: individuals must choose who they mate with based on their perception of others and their own mating preferences; mating preferences are inherited the same way as physical traits; mate selection introduces its own selection pressure but is subject to selection pressure itself.

A representation of mating preferences as an extra chromosome on each individual is introduced and the means by which they are used to assess mating candidates and select the most desirable mating partners are presented. The mechanisms and operators by which mating preferences are inherited and undergo evolution are also discussed. A test suite is introduced and implementation details are presented. Three approaches are experimented and compared: Standard, Mate Choice, and Random.

The obtained results show that the Mate Choice approach is able to significantly outperform the other two on complex instances of Symbolic Regression. The behaviour of the approach is discussed and contrasted with the behaviour obtained by the Random and the Standard approaches, showing that the Mate Choice approach is able to evolve mating preferences that choose mating partners in meaningful ways, actively contributing to an enhanced performance by the Evolutionary Algorithm on the target problem.

Future work may include applying the presented model on a larger function set as well as studying the genealogical trees of the individuals, how mating preferences evolve and affect the evolution of candidate solutions.

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