# Inside a Predator-Prey Model for Multi-Objective Optimization: A Second Study 

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#### Abstract

In this article, new variation operators for evolutionary multiobjective algorithms (EMOA) are proposed. On the basis of a predator-prey model theoretical considerations as well as empirical results lead to the development of a new recombination operator, which improves the approximation of the set of efficient solutions significantly. Furtheron, it is shown that applying speciation to the analysed model makes it possible to handle even more complex problems.


## Categories and Subject Descriptors

F.2.2 [Theory of Computation]: Analysis of Algorithms and Problem Complexity-Nonnumerical Algorithms and Problems

## General Terms

Experimentation, Algorithm, Theory

## Keywords

predator-prey, variation operators, simplex-recombination, multi-objective optimization

## 1. INTRODUCTION

The design and analysis of representations and their corresponding genetic operators is the normal course of life in the field of evolutionary computation [2]. Often an adept combination of all components determines the system's success or failure. This insight is ubiquitous in the case of single-objective optimization. Today, it is difficult, even for an interested reader, to keep an overview of existing representations and their belonging genetic operators [1]. The advantages and the necessity of investigation and the design

[^0]of both components for a given heuristic-problem instance, are almost undisputed [22].

It is, therefore, even more amazing that regarding multiobjective optimization (MOO), the conceptual approaches are still mainly concerned with the selection operator. However, research focusing on the field of variation operators or representations remain rare, so only a few approaches can be found in literature: Kursawe examined for example the use of diploid representations for two-objective test-functions [9] while Rudolph [15] and Hanne [7] are concerned with the problem of finding an appropriate controlling mechanism for the mutation strength in the multi-objective case.

At the same time, as Büche et al. could show [3] for some state-of-the-art evolutionary multi-objective algorithms (EMOA), the interaction between selection and search operators is not co-ordinated well enough. They show that the approximation of the set of efficient solutions cannot be done with an arbitrary precision. The distance between the true Pareto-front and the approximated set can be reduced only by a noticeable rise of the size of the archives - nevertheless stagnation occurs. Also existing non-Pareto approaches seem to be unsuitable for the multi-objective case. Here the process of adaptation is taken from the single-objective algorithms (ESOA), which is more counter productive than helpful (see section 2). The consequence is that, depending on the used strategy, the EMOA approximate either the middle of the Pareto-front or its extrema, this, however, with nearly arbitrary precision. Furtheron there is the dilemma of stagnation with good diversity of the solution set on the one hand, or arbitrarily exact approximation of few points with bad diversity on the other hand. We conjecture that these trade offs can be attributed to the fact that interaction between the genetic operators cannot be taken over from the single-objective case and the exclusive change of the selection operator is not sufficient to meet the requirements of MOO.

Instead of adapting all genetic operators, like in the singleobjective algorithms, external or internal archives [23], metrics as new selection criteria [12] or other even more complicated and time consuming procedures are developed.

If, however, so many additional aids are obviously needed in order to reach the multi-criterion objectives, the assumptions of the standard search operators seem to be insufficient. We have to put back the tasks of adaptation of the Pareto-front and the diversity-preserving forces into the hands of the variation operators.

Topic of this article is the analysis and development of variation operators for multi-objective optimization.

For this we will not develop a new EMO-algorithm from scratch, but start from the predator-prey model of Laumanns et al. [10]. We deliberatly decided on this non-Pareto approach in order to:

- eliminate the influence of the Pareto-based selection and
- be able to examine the employment of the different search operators in a much better mode.

In section 2, Laumanns' predator-prey model is briefly presented, existing problems are sketched and some extensions are discussed. Subsequently, in section 3 some restrictions and modifications are made to the system's dynamics. Furthermore, the test suite used is presented and experimental techniques are described in the following section 4. Having these foundations, we proceed, in section 5, with some experiments and considerations about the model that guides us to the necessity of developing a new type of recombination in section 6 . Thereafter, section 7 displays the collaboration of the evolution factors and finally leads, in section 8 , to a major, but tantatively simple modification of Laumanns' model.

## 2. BACKGROUND

This section provides a relatively detailed, but necessary introduction into the predator-prey model of Laumanns et al. [10] as well as a brief overview of existing extensions. Some essential problems of this model are outlined which are the starting point of our investigations.

### 2.1 Laumanns' Model

At the beginning we should correct an alleged misunderstanding. None of the models, which are presented here, can be considered as co-evolutive. Co-evolution means, the evolution of two or more interdependent species, each adapting to changes in the other [5]. Since the predators are not subject to any changes, the definition does not apply. But the basic idea that individuals interact in time and space within their own species as well as with other species forms the basis of Laumanns' asynchronous spatial structured predator-prey model (PPM).

On the basis of Figure 1, the principle of the model is to be described. The "prey" are the usual individuals of the EMOA representing the possible solutions of the MOO problem. These prey are placed at vertices of a two-dimensional toroidal grid as the spatial population structure. The advantages of spatial structured populations are broadly discussed in [20] and will be omitted here. Due to this population structure the neighbourhood of a particular grid point is defined in terms of the number of steps taken from that grid point. All neighbourhoods are of identical size and shape so that the neighbourhood of every grid point overlaps with the neighbourhood of the grid points nearby. The upper picture of Figure 1 illustrates the selection process, which is done by the predators. The predators move across the spatial structure according to a random walk. The random walk function of the predators is realized as a uniformly distributed random movement in the direct neighbourhood of the position of a predator. The predator chases the prey only within its current neighbourhood and according to one


Figure 1: Schematic representation of the predatorprey model (selection process and recombination).
of the optimization criteria. Here a linear shape neighbourhood with a step size of 1 is depicted. The worst prey within this neighbourhood is "eaten". As soon as the grid point for the prey becomes free, it is refilled by a prey created by discrete or intermediate recombination of those prey which are elements of the recombination neighbourhood (see lower figure). It is important to annotate that the recombination neighbourhood ( $R N$ ) and the selection neighbourhood $(S N)$ do not contain inevitably the same set of prey since the neighbourhoods are constructed from the predator grid point or the freed grid point, respectively.

Because there are several predators with different selection criteria, those prey, which perform good with respect to all objectives are able to survive and represent the approximated Pareto-set after a while. So far on the philosophy of this approach, which convinces by its simplicity.

### 2.2 Problems and Extensions

In the original study two major problems were observed: Loss of diversity (in Figure 2 (a) a concentration of solutions around both extrema can be observed for problem $\mathcal{F}_{1}^{*}$ from equation 3) and stagnation of the process of convergence to the true Pareto-front (b). Thus, in principle this PPM combines the problems of Pareto- and non-Pareto approaches [8]. But it is essential that the results of the preliminary study could show that only suitable search operators were missing to develop a simple EMOA.

Nevertheless, only few extensions exist. Deb [4], for example, softens the strict one predator to one objective assignment with an individual weighted vector in each predator. From now on each predator selects the worst prey with respect to the weighted sum of all objectives. This individual selection allows each predator to steer prey to a specific region on the Pareto-front. Based on both approaches, Li proposed a real-coded predator-prey (RCPPGA) [11] model. In his approach he uses a genetic algorithm as the underlying search heuristic and investigates the two described fitness assignment methods from Laumanns and Deb. In addition he uses a dynamic population, where predators as well as prey are able to move within the structured environment.


Figure 2: Two problems of PPM: Loss of diversity (a) and stagnation of convergence to the Paretofront (b).

In contrast to the previous two models, recombination takes place only if two prey individuals are in the same neighbourhood. If a prey has no neighbours, no duplication is allowed. As concequence Li defines a special migration for both species to keep the prey population on a predefined level and prevent extermination. Another model was developed by Schmitt [17]. Here the steady-state approach of the PPM was replaced by the well-known controlling mechanism of the self-adapting ES [18]. In addition, the weighted intermediate recombination operator proposed by Schwefel and Rudolph [19] was used. These results show that an essential improvement in convergence is possible without any loss of good diversity. However, the problem is that many fitness function evaluations are necessary.

## 3. MODIFICATIONS: PART I

In the previous section we have shown that the PPM lacks on a useful controlling mechanism for the mutation strengths of the model. The problem of self-adaptive control of mutation strength in non-generational models like this is addressed by [16]. In his article Runarsson proposed a kind of adaptation mechanism for mutation strength for singleobjective optimization. We will investigate this adaptation rule for our model.

This heuristic may be seen as a combination of Rechenberg's 1/5-rule [14] and Schwefel's self-adaptation [18]. Since
it was proposed to realize adaptation of mutation strength in $(1+1)$-ES it is able to deal with the lack of birth surplus. For parallel implementation is based on threads and works with the available (unblocked) best and worst individual of the population and blocks them. A variation (depending on the strategy parameters) of the best individual replaces the worst one. Furthermore, a reproduction counter ( $\zeta$ ) indicates how often each individual has passed its own genetic information to a descendent, i.e. how often it was the best individual and no better descendent has been produced. If $\zeta$ for the best individual becomes greater than a fixed number of trials, the strategy parameters of the best are mutated themselves by a weighted average of the mutation strength of its grandparent. Good step sizes in the near past cannot be completely wrong in the present.

By using Runarsson's heuristic some problems occur immediately: because Laumanns' reproduction works with two different neighbourhoods the heuristic may fail due to the often rather different sets of individuals in these neighbourhoods. The prey removed by the predator is chosen from the selection neighbourhood $S N$ while the new prey is composed from individuals out of the reproduction neighbourhood $R N$. Runarssons heuristic replaces the worst individual of a given surrounding by a variation of the best individual out of the same surrounding. If $S N \neq R N$ those individuals from $R \backslash S$ must be looked upon as being of uncertain nature and are possibly worse than the removed individual. A second problem is caused by the fact that Runarsson's mechanism is intended to be implemented in a $(1+1)$-ES which works without recombination. The loss of recombination as evolution factor, however, is not desirable.

To handle the above problems two modifications are carried out to the model.

1. The selection neighbourhood is regarded as being equal to the reproduction neighbourhood: $S N=R N$. By doing this, there is no more uncertainty about the quality of the surviving prey from which the new individual is created.
2. Additionally, the search operators which are strongly bound to the selection mechanism of the predators are divided in two autonomous processes. By introducing a second group of predators we achieve the independent execution of mutation and recombination.

The recombination operators are chosen as in Laumanns' model. In addition to discrete and intermediate recombination the weighted intermediate recombination - originally proposed for ES by Schwefel and Rudolph [19] and adopted lately by Schmitt et al. [17] with some good results - is made use of. Hence two parental individuals $P_{1}$ and $P_{2}$ are given with decision vectors in $\mathbb{R}^{n}$. Furthermore $u_{i} \sim \mathcal{U}(0,1)$ with $i \in\{1, \ldots, n\}$ denotes a uniform distributed random number. Then the child $C$ of $P_{1}$ and $P_{2}$ is formed by

$$
\begin{equation*}
x_{C, i}=u_{i} \cdot x_{P_{1}, i}+\left(1-u_{i}\right) \cdot x_{P_{2}, i} \tag{1}
\end{equation*}
$$

The advantage of this weighted recombination can be illustrated on Figure 3. Two parents ( $P_{1}$ and $P_{2}$ ), who are to be recombined, span a rectangle in the search space. In the case of discrete recombination only the free corners can be occupied by the offsprings $\left(C_{1}\right.$ or $\left.C_{2}\right)$. By intermediate recombination only the point $C_{3}$ can be used. Due to the uniform distributed random numbers $u_{i}$ all positions in the
rectangle are possible. This increases the diversity of the offsprings considerably.


Figure 3: Schematic representation of the used recombination operators.

## 4. EXPERIMENTAL SETUP

We will restrict our examination on those test problems Laumanns et al. used in his work [10]. In addition we will instantiate a second special version of the multi-sphere problem $\mathcal{F}_{1}$. The problems $\mathcal{F}_{2}$ and $\mathcal{F}_{3}$ are used to verify proposed techniques which were developed using $\mathcal{F}_{1}$. All test problems are defined below:

$$
\begin{gather*}
\mathcal{F}_{1}: \mathbb{R}^{n} \rightarrow \mathbb{R}^{m} \text { with } x \in \mathbb{R}^{n}, n, m \in \mathbb{N} \\
\mathcal{F}_{1}(x)=\left(\begin{array}{c}
f_{1}(x) \\
\vdots \\
f_{m}(x)
\end{array}\right)=\left(\begin{array}{c}
\left(x-c_{1}\right)^{2} \\
\vdots \\
\left(x-c_{m}\right)^{2}
\end{array}\right)  \tag{2}\\
\mathcal{F}_{1}^{*}(x)=\binom{x_{1}^{2}+x_{2}^{2}}{\left(x_{1}-2\right)^{2}+x_{2}^{2}}  \tag{3}\\
\mathcal{F}_{1}^{\swarrow}(x)=\binom{x_{1}^{2}+\left(x_{2}-3\right)^{2}}{\left(x_{1}-2\right)^{2}+x_{2}^{2}} \tag{4}
\end{gather*}
$$

The $c_{1}, \ldots, c_{m} \in \mathbb{R}^{n}$ are constants with $c_{i} \neq c_{j}$ for $i \neq j$. The special problem $\mathcal{F}_{1}^{*}$ has constants $c_{1}=0$ and $c_{2}=2$ while $\mathcal{F}_{1}^{\zeta}$ has constants $c_{1}=3$ and $c_{2}=2$. The Paretofront of problem $\mathcal{F}_{1}$ is convex. For the special problems $\mathcal{F}_{1}^{*}$ and $\mathcal{F}_{1}^{K}$ the Pareto-set as well as the Pareto-front can be analytically determinedand the Pareto-set of both problems is represented by a line in search space. The solutions of $\mathcal{F}_{1}^{*}$ cover the interval $x_{1} \in[0,2]$ with $x_{2}=0$. Optimal solutions for $\mathcal{F}_{1}^{\Lambda}$ are given for $0 \leq t \leq 2$ by $x_{1}=t$ and $x_{2}=3-\frac{3}{2} t$.

In addition, two further test problems are included here to ensure comparability to Laumanns works and to validate results with more complex problems later on. Every component of problem $\mathcal{F}_{2}$ [13] has an infinite number of maxima and minima. The Pareto-front of this problem is concave and the Pareto-set is in contrast to the previous special problems not exactly determinable, even incoherent.

The Pareto-front of problem $\mathcal{F}_{3}$ proposed by Kursawe [9] has convex as well as concave parts. Like the previous problem it has a disconnected Pareto-set and is not exactly determinable.

### 4.1 Performance Metric

A number of performance metrics have been listed in [4] due to the fact, that a proper comparison of the results of MOO is a complex issue. In the following we use the hypervolume metric ( $\mathcal{S}$-metric) [23]. The $\mathcal{S}$-metric calculates a hyper-volume of a multi-dimensional region enclosed by the
non-dominated set to be assessed, the coordinate axes and a reference point to measure the diversity and the convergence of the obtained non-dominated set. Depending on the chosen reference point, two non-dominated sets can have different relative $\mathcal{S}$-metric values.

The volume of these regions can be compared to the volume of the region enclosed by the true Pareto-front, the coordinate axis and the reference point. Let $\mathcal{V}$ be the region of a cuboid then $\mathcal{S}(\mathcal{V})$ denotes the volume of this set. The ratio $\mathcal{S R}=\frac{\mathcal{S}(\mathcal{V})}{\mathcal{S}\left(\mathcal{V}_{P F}\right)}$ gives the propotionate coverage of the true Pareto-front by the approximated solutions. The volumes of the test problems' $\mathcal{F}_{1}^{*}$ and $\mathcal{F}_{1}^{\zeta}$ Pareto-fronts are easily calculated and listed in Table 1.

Table 1: Exact volumes of the regions enclosed by the Pareto-fronts of $\mathcal{F}_{1}^{*}$ and $\mathcal{F}_{1}^{K}$ with the given reference point respectively.

| test-problem | reference point | volume |
| :--- | :---: | :---: |
| $\mathcal{F}_{1}^{*}$ | $(4.0,4.0)$ | $13 . \overline{3}$ |
| $\mathcal{F}_{1}^{\swarrow}$ | $(13.0,13.0)$ | $140.8 \overline{3}$ |

Additionally the Euclidian distance is used to evaluate the median distance between the approximated solutions and the Pareto-set for problems $\mathcal{F}_{1}^{*}$ and $\mathcal{F}_{1}^{\swarrow}$.

## 5. EXPERIMENTS AND CONSIDERATION

First results from experiments with test problem $\mathcal{F}_{1}^{*}$ indicate that the step size adaption of Runarsson leads to a monotonous convergence to the optimal solutions in the cases of discrete and weighted intermediate recombination. These results are depicted in Figure 4.


Figure 4: Average distance to the Pareto-set of $\mathcal{F}_{1}^{*}$ with 2 predators per criteria where one predator triggers mutation, another recombination of one of the three types discrete, intermediate or weighted intermediate.

Intermediate recombination, however, leads to premature convergence. Looking at the results of the approximation, discrete recombination turns out to speed up the loss of diversity. At the end of the process the set of optimal solutions contains just the optima of the single criteria. Surprisingly the weighted intermediate recombination leads to both good convergence and a diverse set of solutions as shown in Figure
5. Additionally Table 2 displays the results of this experiment in detail.

Table 2: Results of the experiment with $\mathcal{F}_{1}^{*}$ and weighted intermediate recombination.

| distance to Pareto-set | $\sim 10^{-15}$ |
| :--- | ---: |
| volume $\mathcal{S}(\mathcal{V})$ | 13.263 |
| ratio $\mathcal{S} \mathcal{R}$ | 0.994725 |

Because of these results further investigation will be focused on weighted intermediate recombination.

Although, hitherto, the applied mechanisms worked well on a very simple test problem, but fail on a problem that does not possess a Pareto-set parallel to the axes of the coordinate system. Experiments with problem $\mathcal{F}_{1}^{\Lambda}$ demonstrate this behavior impressively. As visible in Figure 6, the approximation of the Pareto-set gets worse proportional to compromises becoming more balanced.



Figure 5: Approximation of Pareto-set (left) and front (right) for problem $\mathcal{F}_{1}^{*}$ with 2 predators per criteria where one triggers mutation another weighted intermediate recombination. Every predator carries out 80,000 fitness evaluations (FE).


Figure 6: Approximation of Pareto-set (left) and -front (right) for problem $\mathcal{F}_{1}^{〔}$ with 2 predators per criteria where one triggers mutation, another weighted intermediate recombination. Every predator carries out 80,000 FE.

A likely reason for the observed behavior seems to be the weighted intermediate recombination mechanism. A descendent of two parents is generated inside the subset of the search space that is restricted to the square spanned by the decision vectors of both parents as shown in Figure 7. Obviously, a descendent is not automatically better than at least
one parent ${ }^{1}$. Being created in area $A_{1}$ or $A_{2}$ it is worse than both parents regarding the distance towards the Pareto-set. Although this problem does not occur while working on the approximation of axis-parallel Pareto-sets, its effect seems to grow with increasing inclination of the Pareto-set and decreasing distance between the parents and the optimal set. To prove this observation we investigate the influence of those factors and distinguish two general cases. One case


Figure 7: The weighted intermediate recombination shown exemplary working on an inclined Pareto-set in search space.
is represented in Figure 7 and will be analyzed next while the second case with $x_{P_{1}, 1} \geq x_{P_{2}, 1}$ needs no more attention since no deterioration relative to the Pareto-set or the parents is possible. Furthermore, it may hold w.l.o.g that $x_{P_{1}, 2} \leq x_{P_{2}, 2}$ and $0 \leq \alpha \leq \pi / 2$. For different $\alpha$ similar considerations can be made, with $\pi \leq \alpha \leq 3 \pi / 2$ even the same holds.

For the depicted case $x_{P_{1}, 1} \leq x_{P_{2}, 1}$, however, the areas $A_{1}$ and $A_{2}$ must be estimated. Area $A_{1}$ can be easily calculated through

$$
\begin{equation*}
A_{1}=\frac{a b}{2}=\frac{\tan \alpha \cdot\left(x_{P_{2}, 1}-x_{P_{1}, 1}\right)^{2}}{2} \tag{5}
\end{equation*}
$$

while for calculation of $A_{2}$ the distance between the parents and the Pareto-set is needed. A deterioration relative to both parents is only possible, if the distance of a possible descendant to the Pareto-set is greater than the maximum of the parents distances to the optimal set.

$$
\begin{aligned}
d_{\max } & =\max \left\{d_{1}, d_{2}\right\} \\
d_{m} & =\left(x_{P_{2}, 2}-x_{P_{1}, 2}\right) \cdot \cos \alpha-d_{\max } \\
\delta & =d_{m}-d_{\max }
\end{aligned}
$$

With $\delta$ it is possible to decide whether $A_{2}$ exists. For now we assume $A_{2}$ may exist, then it is given by

$$
\begin{align*}
A_{2} & =\frac{1}{2} \cdot \frac{\delta}{\sin \alpha} \cdot \frac{\delta}{\cos \alpha} \\
& =\frac{\delta^{2}}{\sin 2 \alpha} \\
& =\frac{\left(\left(x_{P_{2}, 2}-x_{P_{1}, 2}\right) \cdot \cos \alpha-2 d_{\max }\right)^{2}}{\sin 2 \alpha} \tag{6}
\end{align*}
$$

[^1]Using the Heavyside function $\Theta(\delta)$ for case differentiation we get for the total area $A_{\text {neg }}$ of deterioration with respect to the Pareto-set

$$
\begin{align*}
A_{n e g} & =\frac{\tan \alpha \cdot\left(x_{P_{2}, 1}-x_{P_{1}, 1}\right)^{2}}{2} \\
& +\Theta(\delta)\left(\frac{\left(\left(x_{P_{2}, 2}-x_{P_{1}, 2}\right) \cdot \cos \alpha-2 d_{\max }\right)^{2}}{\sin 2 \alpha}\right) \tag{7}
\end{align*}
$$

To investigate the behavior with increasing convergence to the Pareto-set, we have to look at equation (7) with decreasing distance $d_{\text {max }}$.

$$
\begin{equation*}
d_{\max } \rightarrow 0 \Rightarrow A_{n e g} \rightarrow\left(x_{P_{2}, 1}-x_{P_{1}, 1}\right) \cdot\left(x_{P_{2}, 2}-x_{P_{1}, 2}\right) \tag{8}
\end{equation*}
$$

Obviously, the probability to generate a better descendant decreases dependent on $d_{\text {max }}$. Area $A_{\text {neg }}$ tends to reach the size of the square spanned by the parents. Near the Pareto-set a deterioration is almost certain. However, the size of $A_{\text {neg }}$ and with it the extend of deterioration also depends on the inclination of the Pareto-set given by $\alpha$. These results lead to the development of a recombination mechanism which is insensible to rotation of the Pareto-set inside the search space appropriately.

## 6. MODIFICATIONS PART II: A ROTATION-INDEPENDENT RECOMBINATION

One way to adapt the recombination mechanism to the position of the Pareto-set in search space may be to learn about the afore unknown angle $\alpha$ and use it to rotate the recombination respectively ${ }^{2}$. However, this approach leads to at least one more strategy parameter for each individual and may furthermore fail to approximate Pareto-sets which are disjoint. In the latter case even more angles (at least one for every subset) need to be learned. To avoid such problems we want to focus on utilizing a geometric shape to restrict reproduction search space.

A most promising shape seems to be the triangle or in general a $n$-simplex ${ }^{3}$. It is easy to see that in a search space of this shape, spanned by $n+1$ parents, a deterioration relative to those parents is impossible. Though it is easy to chose a descendent uniformly distributed out of a rectangle, it is more difficult for simplizia. Based upon barycentric coordinates Turk [21] showed a method for picking a random point from a triangle or a tetrahedron. A general technique to generate a random point in a $n$-simplex is presented here. Equivalences and used theorems are proved in [6].

Definition 6.1 (Barycentric Coordinates). Hence there are $(n+1)$ vectors $p_{1}, \ldots, p_{n+1}$ in the $n$-dimensional space. If $p_{2}-p_{1} \ldots p_{n+1}-p_{1}$ are linearly independent every point $q$ may be represented as a $(n+1)$-tupel of barycentric coordinates $\left(\beta_{1}, \ldots, \beta_{n+1}\right)$ qualifying $q$ by

$$
q=\beta_{1} p_{1}+\cdots+\beta_{n+1} p_{n+1} \text { and } \beta_{1}+\cdots+\beta_{n+1}=1
$$

The representation of a point $P$ in a 1 -simplex, a line between two points $A$ and $B$, is essential for the understanding

[^2]

Figure 8: Schematic procedure to generate a random point in a simplex depicted for a $1-, 2-$, and 3 -simplex.
of the creation of a random point in a simplex. The set of points between A and B is given by

$$
[A, B]:=\left\{a A+b B \mid a, b \in \mathbb{R}_{+}, a+b=1\right\}
$$

If we chose $a=(1-\lambda)$ and $b=\lambda$ then $P \in[A, B]$ results from

$$
\begin{equation*}
P=(1-\lambda) A+\lambda B \tag{9}
\end{equation*}
$$

The tupel $((1-\lambda), \lambda)$ yields the barycentric coordinates of $P$. This construction procedure can be used in $n$-simpliza as well. As depicted in Figure 8 for a triangle, one creates, starting from a point $A$, two points $P^{\prime}$ and $P^{\prime \prime}$ with the same barycentric coordinates. Finally point $P$ is created on the line between these new points in an analogous way. For a tetrahedron a third point $P^{\prime \prime \prime}$ is created to form a triangle. Then $P$ is generated as described before.

The procedure from above can generally be formalized in an expression which is easy and rather efficient to implement. The point $P_{n S}$ in an $n$-simplex is yielded by:

$$
\begin{equation*}
P_{n S}=\sum_{i=1}^{n+1}\left(\left(1-\lambda_{i}\right) \prod_{j=0}^{i-1} \lambda_{j}\right) A_{i} \tag{10}
\end{equation*}
$$

$$
\text { with } \lambda_{0}:=1 \text { and } \lambda_{n+1}:=0
$$

The vectors $A_{i}$ with $i=\{1, \ldots, n+1\}$ span the simplex. To chose $P_{n S}$ uniformly distributed for every $\lambda_{j} \in$ $\left\{\lambda_{1}, \ldots, \lambda_{n}\right\}$ a random number $z_{j} \sim \mathcal{U}(0,1)$ is generated and applied in:

$$
\begin{equation*}
\lambda_{j}=\left(z_{j}\right)^{\frac{1}{(n+1)-j}} . \tag{11}
\end{equation*}
$$

The square root until $n$-th root is taken to weight all portions of the simplex equally.



Figure 9: Approximation of Pareto-set (left) and front (right) for problem $\mathcal{F}_{1}^{\swarrow}$ with 2 predators per criteria where one triggers mutation another the proposed simplex-recombination. Every predator carries out 80,000 FE.

To finally prove the operability of the proposed recombination mechanism empirically, we rerun the experiment
from Figure 6. As shown in Figure 9 the result is much better than with weighted intermediate recombination. Table 3 depicts the evaluation of the shown experiment.

Table 3: Results of the experiment with $\mathcal{F}_{1}^{\swarrow}$ and simplex recombination.

| distance to Pareto-set | $\sim 10^{-12}$ |
| :--- | ---: |
| volume $\mathcal{S}(\mathcal{V})$ | 140.507 |
| ratio $\mathcal{S R}$ | 0.997685 |

## 7. ANALYSING THE INFLUENCE OF EVOLUTION FACTORS

The changes based on the previous investigations yield significantly better results than the original model proposed by Laumanns [10]. However the impact of mutation and recombination has not been examined, yet. Taking advantage of the detachment of these factors during the inital modifications we are able to explore the isolated factors' impact. By switching off mutation we concentrate on recombination directly as well as mutation indirectly and their share on generating a optimal set.

### 7.1 Influence of recombination

Based on the geometric shape of the recombination mechanism the descendent of $n+1$ parents is created inside the convex hull of the parents' location. Therefore, it may be considered as an intermediate crossover in the centre of gravity with differently weighted parents. Keeping in mind that the selection mechanism is strongly bound to the recombination and that the selection alternately favours only one criterion and discards those individuals complying to other criteria, we must assume that in the long term averaged individuals do better than individuals optimized for one criterion. Additionally, the recombination favours convergence towards the Pareto-set.

Thus, a long running time creates centred individuals (depending on the ratio of the criteria) as well as solutions which are near the optimal set as shown in Figure 10 (left). The real Pareto-set is depicted to illustrate the contraction of the approximated set.

### 7.2 Influence of mutation

The main influence of mutation is the gain of new information. By adding mutation to the model the position of an initial population in search space does not determine further convergence behaviour.

Figure 10 (right) shows the relevance of mutation indirectly by omitting it from the evolutionary process while at the same time initializing the population 'above' the Paretoset in search space. It is obvious that without mutation the convergence is limited to the bounds of the area of search space covered by the initial population. The same behaviour is found for populations uniformly initialized around the Pareto-set due to contraction during runtime.

Another effect of the mutation based on Runarssons heuristic [16] and strongly bound to the selection mechanism of a predator is the tendency to drive the population's individuals towards an, at least, local optimum regarding the criterium which is represented by that predator.

decision variable x 1

decision variable x

Figure 10: Approximated Pareto-set of $\mathcal{F}_{1}^{\swarrow}$ with only simplex-recombination initialized uniformly around the true Pareto-set, with 2 predators per criterium after 320,000 FE per predator (left) and Pareto-set of $\mathcal{F}_{1}^{*}$ with only weighted intermediate recombination initialized in $[-10,10] \times[0.5,10]$ with 2 predators per criterium and 40,000 FE per predator (right).

### 7.3 Interaction of both factors

Since mutation works strongly in opposition to the averaging mechanism of recombination we may consider the combination of both factors (mutation and recombination) as a new multi-objective optimization problem. Chosing a number of recombinating and a number of mutating predators we obtain a compromise of both diversity and convergence. Finally, the evaluation of an adequate compromise is left to the decision maker.

However, if we look at the interaction of those factors we find that these processes can be executed sequentially. Mutation may start to determine local optima whereupon recombination creates a diverse set of compromises from the results.

Although this might work with simple problems like $\mathcal{F}_{1}^{*}$ and $\mathcal{F}_{1}^{\zeta}$ which possess a Pareto-set on a line between the global optima of two criteria the method will fail on problems with disjoint subsets of the Pareto-set as $\mathcal{F}_{2}$ and $\mathcal{F}_{3}$. For those problems, finally, some local optima are yielded and connected by individuals which do not necessarily represent valid compromises for the problem.

## 8. CONCLUSION

Up to now we analyzed Laumanns' model in detail which resulted in several changes to it. To achieve convergence to the optimal solution we introduced a heuristic from Runarsson that suited perfectly for integration into a parallel system with steady state replacement. However, it was intended to work on a ( $1+1$ )-ES and, therefore, gave reason to modify Laumanns' selection and recombination neighborhood as well as to the division of the variation operators to autonomous processes bound to the predators. Furthermore, a weighted intermediate recombination was introduced to the model and yielded best results on simple problems having a Pareto-set parallel to the coordinate axes. Yet on an oblique Pareto-set the method failed due to the recombination's dependency on coordinate axes. Consequently, a recombination indifferent against the position of the Paretoset and based on the geometric form of a $n$-simplex was developed and proved to be well applicable. Subsequent to these modifications the analysis of the influence of variation operators revealed that the weighted intermediate recombination as well as the simplex-recombination tend to collapse
the population for a balanced compromise. At the same time the mutation was proved to be essential for introducing new information to the population and to drive the individuals towards the optima of the objective functions represented by the predators. The problem to find a sufficient solution concerning convergence and diversity was reduced to finding an adequate proportion of predators initiating mutation and recombination. Although these mechanisms worked perfectly on simple problems, the last section showed the difficulties to approximate complete solutions for problems with disjoint Pareto-sets.

To motivate further research concerning the variation operators even more and to demonstrate its potentialities we close this paper with a preliminary simple change of Laumanns' model to solve some of the addressed difficulties. To preserve local optima which may be part of the Pareto-set we change the mutation mechanism in such a way that the seperation of the variation operators is unmade while the recombination becomes the dominant factor. New information emerges inside the population by allowing the creation of a descendent outside the convex hull of a simplex. This is achieved by replacing the uniformly distributed choice of a random number for equation (11) with a positive normal distributed choice.

In addition to this, the population is divided into several species, each getting its own initial realm in decision space to start from. Although individuals of different species are not able to recombinate, they may leave their initial realm to approach a part of the Pareto-set.

First experiments with this modified model show (see Figure 11) that most parts of the Pareto-set can be computed. Indeed, some solutions are not Pareto-optimal, however, most solutions are covered by the results so that a dominance filter is able to extract them.



Figure 11: Approximated Pareto-sets of $\mathcal{F}_{2}$ (left) after $10,000 \mathrm{FE}$ and $\mathcal{F}_{3}$ after $20,000 \mathrm{FE}$ (right) per predator with the modified model. The search space $[0,3] \times[-5,5]$ of $\mathcal{F}_{2}$ was divided for 6 species positioned along the $x_{2}$ axis evenly. For $\mathcal{F}_{3} 2$ species initialize in $[-1,0] \times[-5,5]$ and $[0,1] \times[-5,5]$.

Thus, we may conclude, that variation operators for MOO are essential to yield sufficiently exact and diverse solutions. However, in addition, macro-evolutionary mechanisms or other assisting techniques seem to be necessary to fulfill the requirements of MOO.

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[^1]:    ${ }^{1}$ The denomination 'better' is used here by the meaning of the quasiordered relation $\leq$.

[^2]:     to be learned.
    ${ }^{3}$ A simplex is a $n$-dimensional polytope with $n+1$ points.

