

Exploring the Behavior of Building Blocks for Multi-Objective Variation Operator Design using Predator-Prey Dynamics

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ABSTRACT

In this paper, we utilize a predator-prey model in order to identify characteristics of single-objective variation operators in the multi-objective problem domain. In detail, we analyze exemplarily Gaussian mutation and simplex recombination to find explanations for the observed behaviors within this model. Then, both operators are combined to a new complex one for the multi-objective case in order to aggregate the identified properties. Finally, we show that (a) characteristic properties can still be observed in the combination and (b) the collaboration of those operators is beneficial for solving an exemplary multi-objective problem regarding convergence and diversity.

Categories and Subject Descriptors

F.2.2 [Analysis of Algorithms and Problem Complexity]: Nonnumerical Algorithms and Problems—*Computations on Discrete Structures*; G.3 [Mathematics of Computing]: Probability and Statistics—*Markov Processes*; I.2.8 [Artificial Intelligence]: Problem Solving, Control Methods, and Search—*Heuristic Methods*; I.6.4 [Simulation and Modeling]: Model Validation and Analysis

General Terms

Experimentation, Algorithm, Theory

Keywords

Multi-Objective Optimization, Predator-Prey Model, Population Dynamics, Variation Operator Design

1. INTRODUCTION

During the last years, various evolutionary algorithms for multi-objective optimization have been proposed [1] and im-

provements in this area have mostly been made by enhancing the performance of selection operators, introducing increasingly complex mechanisms [8]. That is in contrast to the single-objective case, where variation operators are considered more important and ubiquitously used. There, sophisticated methodologies for accelerating convergence are legion and employed in many contexts. Approved concepts like Rechenberg's *1/5th* rule [13], Schwefel's mutative self-adaptation [13] and more modern heuristics like Runarsson's adaption rule [12] are only examples for the manifold research in this area.

Against this background, it is surprising that almost no effort has been put into the design of adequate variation operators for the multi-objective case: To our knowledge the research is limited to the use of diploid representations for two objective test functions [6] and the problem of finding an appropriate controlling mechanism for the mutation strength in the multi-objective case [11, 4]. Only Schoenauer and Rudenko [10] addressed the problem of new variation operator design. Their approach can be seen as a combination of standard operators from the single-objective domain to a complex one for multi-objective problems.

Recently, a predator-prey model that was originally introduced by Laumanns et al. [7] has been adopted by Grimme and Lepping [2] to investigate the behavior of single-objective variation operators in the context of a multi-objective problem. This model features the idea of interaction between consuming (predators) and evolving (prey) populations of individuals classified by a set of species in a self-contained environment. The prey represent instances in a multi-objective solution space and have a fixed habitat in the environment. Predators roam across this environment randomly and consume prey. By using single-objective elitist selection, each predator favors a certain diet, represented by a destined objective within the solution space. After the consumption of a prey individual, it is replaced by a new offspring which is formed by the consuming predator's specific variation operator. On the long run, it is expected that the evolved population obeys the combined effects of the operators, thus gains a certain resistance against all hunting predators, and finally amounts to trade-off solutions in the search space. The use of spatial populations for multi-objective evolutionary algorithms is elementary for this algorithm and has been recently subject to investigation in works of Kirley et al. [5] and Nebro et al. [9].

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GECCO'07, July 7–11, 2007, London, England, United Kingdom.

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In this paper, we will take advantage of this model to analyze the interplay of two variation operators on a spatial distributed population in detail. To this end, we review a building block approach for operator design in Section 2 to found our studies. Section 3 features a formal description of the employed predator-prey model. Subsequently, in Section 4, a technique for visualizing a specific spatial population’s structure is proposed. With this at hand, we analyze the behavior of two exemplary variation operators in Section 5 and show afterward in Section 6 that identified properties can still be perceived in the combined application of both operators. Section 7 concludes this work with a discussion of our results.

2. A BUILDING BLOCK APPROACH FOR OPERATOR DESIGN

The lack of adequate variation operators for evolutionary multi-objective algorithms may arise from the difficulty to obtain both convergence and diversity at the same time which is in contrast to the single-objective case where the focus lies on converging as close as possible to one optimum solution. Grimme and Lepping [2] show empirically that their modified predator-prey model is suitable for the coupling of single-objective variation operators in order to design complex operators for multi-objective problems in a building block manner. Each predator is specifically sensitive for one objective and affects the population with one exclusive variation mechanism. Observing the variation operators’ single as well as aggregated effects on the population, one can apply the gained knowledge to the combination of multiple operators to possibly benefit from the identified effects or to cancel out adverse properties. Different predators may here trigger a variety of operators for the same objective, allowing flexible tuning and making the whole configuration scalable.

In order to come toward a general design concept for multi-objective variation operators that originate from single-objective ones this model may serve as base for our analysis. As such, our methodology can be described by the following steps:

1. Empirical observation of the relevant operators and their individual behavior within the population.
2. Detailed analysis of the relevant operators in the context of the predator-prey model to identify the impact of their different inherent characteristics on the population.
3. Selection and combination of operators with promising properties.
4. Identification of possible interference between the combined operators with special regard to their ratio.

While the focus of the aforementioned work was on steps 1 and partly on 3, in this paper we will tackle step 2 for an exemplarily test problem. The empirical studies already made reveal that a beneficial combination is possible. Here, we try to find models and explanations for the observed behavior. Finally, we will combine the examined operators and evaluate their collaboration. As a main result we want to show that the observed behavior for single operators can still be identified when applying their combination. This insight

may lead to step 4 of our general design concept, although this last step is beyond the scope of this paper.

In order to allow a thorough analysis, a formal foundation for our model is necessary, which will be given and instantiated in the next section, along with a technique for representing the population.

3. MODEL

For our studies, we base upon a tailored model loosely adopting Laumanns [7] ideas, but introducing substantial changes in order to support our modular approach. In the following, we will give an informal description of this model along with a corresponding formal definition.

3.1 General Definition

The interaction environment for our system is represented by a graph $G = (V, E)$, which is populated by both predator and prey individuals. The latter represent possible solutions of a multi-objective optimization problem and are immobile (each individual inhabits a single, fixed vertex). As such, there exist $\text{card}(V)$ prey individuals $b \in B$, building the population. Furthermore, all prey are of equal kind and can therefore be classified by a single species.

On the contrary, predator individuals can differ from each other regarding their properties, such as their consumption characteristics and reproduction model.

$$\begin{aligned} C &:= \{\triangleleft : B \times B \mapsto \{yes, no\}\} \\ O &:= \{oper : \mathcal{P}(B) \mapsto B\} \end{aligned} \quad (1)$$

The first property is the selection criterion $c \in C$, which defines a relationship between prey individuals with respect to a single objective. This may be for example realized as the elitist selection of the worst prey. The second property describes a variation operator $o \in O$, which specifies the creation model for the replacement of consumed prey individuals. For these variation operators mutation as well as different recombination schemes may be considered. The two sets are detailed in Equation (1).

Every predator consists of a pair of one selection criterion and one variation operator. This determines the kind of a predator, which will be further on referred to as the predator’s species. In detail, every predator belongs to one predator species τ , all being gathered in the set of species

$$\mathfrak{R} := C \times O = \{(c, o) | c \in C, o \in O\} \quad (2)$$

Now, each predator individual r_{ij} can be identified by two indices: while $0 \leq i \leq \text{card}(\mathfrak{R})$ denotes the species a predator belongs to, the j distinguishes one individual from others of the same species. Consequently, the set of all predators is given by

$$R := \{r_{ij} | \tau_i \in \mathfrak{R}, j \in \mathbb{N}\} \quad (3)$$

Other than prey, predators are allowed to move within the interaction environment. This roaming behavior can be characterized by a general movement function

$$walk : V \mapsto (V \mapsto [0, 1]) \quad (4)$$

where—from a given origin—other nodes can be visited with a certain probability. Furthermore, we define the consumption frequency δ , denoting the number of walks a predator does between two consumptions.

The beat within predators interact with (hunt) prey is restricted to a locally confined area, the neighborhood. Formally, a neighborhood is defined as a set of vertices N given by a neighborhood function

$$nbh : V \times V \mapsto [0, 1] \quad (5)$$

Contrary to Laumanns, we do not allow diverging neighborhoods for selection and reproduction. This is because such a setup may result in an offspring worse than the influencing parents in the case of reproduction: the participating parents are of uncertain nature regarding the prior selection [3]. The dynamic behavior of the system is described by its state and a corresponding transition function. The current state is specified by $S = (s_b, s_r)$ where $s_b : V \mapsto B$ denotes the current prey setup and $s_r : R \mapsto V$ the current predator position. The transition from one state into another is con-

Algorithm 1 Transition function for a single predator r_{ij} .

Input: $s = (s_b, s_r)$
Output: $s' = (s'_b, s'_r)$, initialized with s_b, s_r
1: **for** δ times **do**
2: $v_t := walk(s_r(r_{ij}))$
3: **end for**
4: $s'_r(r_{ij}) := v_t$
5: **for all** $v \in V$ **do**
6: $N := N \cup v$ with probability $nbh(v_t, v)$
7: **end for**
8: $B_w := \{v \in N | \forall v_k \in N, v_k \neq v : s_b(v_k) \triangleleft s_b(v)\}$
9: **if** $B_w = \emptyset$ **then**
10: $B_w := N$
11: **end if**
12: Choose v_c from B_w uniformly distributed
13: $s'_b(v_c) := oper_i(s_b(N))$
14: **return** $s' = (s'_b, s'_r)$

ducted by a transition function $evol : S \mapsto S$, the actual specification of which is shown in Algorithm 1. There, the predator moves δ times corresponding to the walking function $walk$ to a target vertex v_t (Line 2). Next, the worst prey B_w within the relative neighborhood N of v_t are selected regarding r 's selection criterion (Lines 6 and 8). In case that the selection process did not yield any individuals, the whole neighborhood is assumed. Now, one prey v_c is chosen uniformly distributed from B_c for consumption (Line 12) and replaced by a new individual bred using the predator's operator $oper_i$ (Line 13). This process is repeated for every $r_{ij} \in R$, either sequentially or in parallel.

Summarizing, a predator-prey model is represented by

$$PPM = (G, B, C, O, \mathfrak{A}, R, walk, \delta, nbh, S, evol) \quad (6)$$

3.2 Model Instantiation

For the aspired behavior analysis of operators, we need to substantiate the model for a specific case. Here, we will examine the multi-sphere problem $\mathcal{F}_m : \mathbb{R}^n \rightarrow \mathbb{R}^m$ with $\vec{x} \in \mathbb{R}^n$ and $n, m \in \mathbb{N}$, the function of which is defined in Equation (7).

$$\mathcal{F}_m(\vec{x}) = \begin{pmatrix} f_1(\vec{x}) \\ \vdots \\ f_m(\vec{x}) \end{pmatrix} = \begin{pmatrix} (\vec{x} - \vec{c}_1)^2 \\ \vdots \\ (\vec{x} - \vec{c}_m)^2 \end{pmatrix} \quad (7)$$

Here, n determines the dimension of the decision space, m

denotes the number of objectives, and the $\vec{c}_1, \dots, \vec{c}_m \in \mathbb{R}^n$ are constants. In the following, we will focus on the two-dimensional specialization $\mathcal{F}_2(\vec{x})$ from Equation (8) with constants $\vec{c}_1 = (0, 0)^T$ and $\vec{c}_2 = (2, 0)^T$. This problem is convex and has a corresponding Pareto-set described by a single line given as $0 \leq x_1 \leq 2$ and $x_2 = 0$.

$$\mathcal{F}_2(\vec{x}) = \begin{pmatrix} f_1(\vec{x}) \\ f_2(\vec{x}) \end{pmatrix} = \begin{pmatrix} x_1^2 + x_2^2 \\ (x_1 - 2)^2 + x_2^2 \end{pmatrix} \\ \text{with } \vec{x} \in [-10, 10]^2 \text{ and } n = m = 2 \quad (8)$$

As the spatial population structure, we assume a two-dimensional toroidal grid with a size of 40×40 vertices, which implies an equally probable accessibility of all grid points [7]. Also, due to the special structure, the neighborhood of a particular vertex v can be spanned by the number of steps taken from v , the so-called radius rad .

$$N(v, rad) = \bigcup_{(v, \nu) \in E} N(\nu, rad - 1) \quad (9)$$

More formally, a neighborhood $N(v, rad)$ can be generally described by Equation (9), with a starting point $N(v, rad = 0) = v$. The number of neighbors for a given radius can be then determined by $c_N = (rad + 1)^2 + rad^2$. For our experiments, we set $rad = 1$ and thus have a neighborhood function

$$nbh(v_t, v) = \begin{cases} 1 & \text{if } v \in N(v_t, 1), \\ 0 & \text{otherwise.} \end{cases} \quad (10)$$

The selection criteria for the different predator species can be directly derived from the aforementioned function $\mathcal{F}_2(\vec{x})$, using objective $f_1(\vec{x})$ for the first criterion and objective $f_2(\vec{x})$ for the second criterion, respectively. Moreover, we use two distinct operators for our analysis:

1. **Gaussian distributed mutation**, which creates an offspring $\vec{x}' \in \mathbb{R}^n$ from one selected parent individual $\vec{x} \in \mathbb{R}^n$. The variation is defined by $\vec{x}' = \vec{x} + \vec{z}$ with $\vec{z} \in \mathbb{R}^n, z_i \in \mathcal{N}(0, \sigma), 0 \leq i \leq n$, where σ denotes the mutation step size [13].
2. **Simplex recombination**, which provides a rotation-independent variation [3] of an offspring $\vec{x}' \in \mathbb{R}^n$ based on $n + 1$ parent individuals \vec{x}_i , with $1 \leq i \leq n + 1$. The calculation of the new individual \vec{x}' in the solution space is done using

$$\vec{x}' = \sum_{i=1}^{n+1} \left((1 - \lambda_i) \prod_{j=0}^{i-1} \lambda_j \right) \vec{x}_i \\ \text{with } \lambda_0 := 1 \text{ and } \lambda_{n+1} := 0 \quad (11)$$

The vectors \vec{x}_i span the actual simplex, while the λ_j values determine the position of \vec{x}' . In order to ensure a uniform distribution of selections of \vec{x}' , random numbers $z_j \sim \mathcal{U}(0, 1)$ are generated and applied in

$$\lambda_j = \sqrt[k]{z_j} \text{ with } k = (n + 1) - j \quad (12)$$

Herewith, the predator species and individuals will be constructed for the different behavior analysis below. The walking function used, see Equation (13), implies a uniform distribution on the set of directly connected nodes, introducing

a random walk policy for predators. By $d(v)$ the degree of vertex v is denoted.

$$\text{walk}(v)(v_t) = \begin{cases} \frac{1}{d(v)} & \text{if } (v, v_t) \in E \\ 0 & \text{otherwise.} \end{cases} \quad (13)$$

4. VISUALIZING THE SPATIAL POPULATION STRUCTURE

To explain the effects of the predator’s interaction with the prey, it is important to understand the dynamics of the evolutionary process. Here, we focus on very local processes that are involved with a single predator’s move. Therefore, a simple visualization concept is desired that is able to display the entire population in both positional mapping and objective value. Since the development of a general visualization technique is quite difficult for multi-objective optimization problems with multi-modal objective functions, we restrict ourselves to the afore defined test problem $\mathcal{F}_2(\vec{x})$ in Equation (8). As mentioned, the Pareto optimal set of this problem is given by a line between $(0, 0)$ and $(2, 0)$ in the decision space with the endpoints as optimal solutions for $f_1(\vec{x})$ and $f_2(\vec{x})$ respectively. Thus, a good solution for $f_1(\vec{x})$ is a bad solution for $f_2(\vec{x})$ simultaneously and vice versa. This yields the following construction rule for a two dimensional representation of the population:

Let $\mathcal{C} = (c_1, \dots, c_l, c_{l+1})$ be a discrete color scale containing $l + 1$ colors. We apply the following mapping: l intervals of objective function $f_1(\vec{x})$, $\vec{x} = (x_1, x_2)^T$ with $0 \leq x_1 \leq 2$ are mapped to l colors. One color $l + 1$ is assigned to all remaining values of the objective function in order to mark them as being outside the considered range. Further, let $\mathcal{Q} = \{q_{ij} | i, j \in \{1, \dots, k\}\}$ be a square divided in k^2 subsquares. Here, k is equal to the side length of the toroidal grid. Any subsquare $q_{ij} \in \mathcal{Q}$ denotes a prey’s position on the torus. Finally, coloring subsquares from \mathcal{Q} with colors from \mathcal{C} results in a depiction of the population concerning both objectives. The color of an optimal solution regarding objective $f_1(\vec{x})$ is given by c_1 while the optimum of objective $f_2(\vec{x})$ is represented by c_l . All other trade-off solutions are displayed by intermediate colors. An example of the introduced visualization method is shown in Figure 1 along with its corresponding color scale. Note that

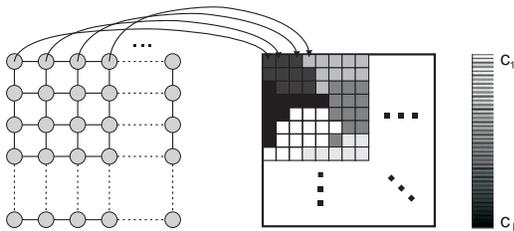


Figure 1: Schematic depiction of the population visualization. The color of each subsquare denotes the proximity of the represented individual to the respective objective.

this method only holds for a small set of multi-objective optimization problems which show similar characteristics as the assessed problem $\mathcal{F}_2(\vec{x})$. Furthermore, this visualization does not express anything about the convergence behavior to the Pareto-set and only yields a restricted statement on diversity due to the quadratic nature of both objectives.

5. BEHAVIOR OF OPERATORS

In this section we analyze the two operators Gaussian mutation and simplex recombination as defined in Section 3.2. In most investigations a model is provided first and observations only serve as a proof of concept. However, we start from the observations that can be made in the population behavior and try to find a simple model to explain the results.

5.1 Mutation Analysis and Evaluation

First, we focus on the Gaussian mutation as an exclusive operator and apply the previously introduced problem $\mathcal{F}_2(\vec{x})$ to our analysis. Both predators apply Gaussian mutation exclusively and we evaluate 100,000 predator walk steps with a consumption frequency of $\delta = 1$ within a randomly initialized population on the torus. The results of the optimization are shown in Figure 2. Obviously, the whole population crowds at the extremal points of both objectives within the Pareto-set, see Figure 2(a), while there are no intermediary solution found. The population structure is depicted in Figure 2(b) where it comes apparent that both extreme solutions are represented by a more or less large contiguous zones on the torus. They lead us to the assumption that

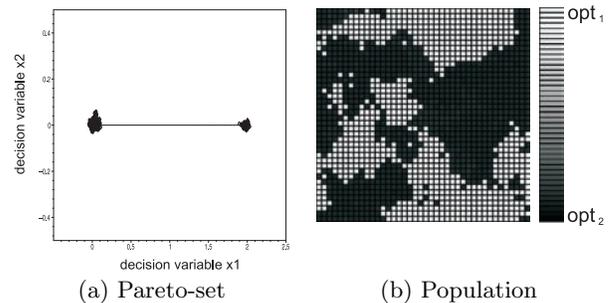


Figure 2: Population and Pareto-set after 100,000 evaluations of \mathcal{F}_2 with exclusive mutation.

only similar offspring are generated: on the long run only an interchange of individuals takes place and it is not possible to create innovations concerning intermediary solutions in the population. In those contiguous areas the evolutionary process is similar to the single-objective case.

Furthermore, there are squared edges between the different extreme solution representations while also no intermediary solutions are found at these borders. This is quite contrary to the original assumption that the development of a predator-prey model with exclusive mutation was founded on [7]. Laumanns et al. trusted in the automatic adaptation of prey to all objectives in analogy to the natural assimilation processes in predator-prey interplay. However, our results do not support this assumption. In the following, we try to find explanations for the made observations.

Remember that in the predator-prey model, while the predator is moving randomly, the worst prey is replaced by a potentially better one. Thus, whenever a predator visits the same selection neighborhood again, it becomes more likely that a prey is bred which is superior regarding the predator’s objective. Thus, there is a strong tendency to move all prey within the selection neighborhood toward the predator’s objective. This, however, comes along with a loss of

diversity: once a prey has reached the almost optimum for the objective, it will not be consumed by the predator anymore and, respectively, the replacement of this individual is becoming very unlikely.

In order to explain this phenomenon, we use a simple Markov chain that describes the transition probabilities of possible neighborhood states, see Table 1. We assume a single predator that has a static position within the torus and is not affected by any other predator. Furthermore, we consider a neighborhood with $rad = 1$ which results in five prey. Now, let us assume a representation where one extreme solution is displayed as black prey and the other as white ones. For simplicity reason, we assume that the whole torus is already occupied by white prey and our predator selects regarding the black objective. If the neighborhood consists of five

System State	s_0	s_1	s_2	s_3	s_4	s_5
# Black Prey	0	1	2	3	4	5
# White Prey	5	4	3	2	1	0

Table 1: Possible configuration of black and white prey within mutation neighborhood.

white prey we can always expect a white new mutated individual on the free position if the mutation step size σ is not too large. Therefore, the probability of starting from state s_0 and end up in s_0 is equal to 1. The same holds for the opposite in this case. This means that once the whole neighborhood is covered with kindred individuals, it is not possible to leave this state anymore if σ is small. To be more precise, there is a probability of $\bar{\epsilon} = (1 - \epsilon)$ that a black prey is the descendant of a mutated white parent. We can compute all possible transition probabilities between the states and formulate the transition matrix \mathbf{T} of the Markov chain:

$$\mathbf{T} = \begin{bmatrix} \bar{\epsilon} & \epsilon & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.75 - 0.5\epsilon & 0.25 + 0.5\epsilon & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.5 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.25 + 0.5\epsilon & 0.75 - 0.5\epsilon & 0 & 0 \\ 0 & 0 & 0 & 0 & \epsilon & \bar{\epsilon} & \bar{\epsilon} \\ 0 & 0 & 0 & 0 & \epsilon & \bar{\epsilon} & \bar{\epsilon} \end{bmatrix}$$

Within this matrix, transition probabilities are arranged in ascending order of states for rows and columns respectively. Using this model, we can compute the final transition probabilities after many steps of selections and mutations by computing the resulting transition matrix $\mathbf{T}^\infty = \lim_{t \rightarrow \infty} \mathbf{T}^t$ for a fixed mutation step size. Note that we refer to problem $\mathcal{F}_2(\vec{x})$ where the maximum distance of the Pareto-set has the length 2, see Equation (8) and Figure 2(a). Thus, we compute ϵ as the Gaussian distributed probability to perform a jump within the search space of length 2 which would result in a direct change of a black prey into a white prey, see Equation 14.

$$\epsilon = \frac{1}{\sigma\sqrt{2\pi}} \int_2^\infty \exp\left\{-\frac{x^2}{2\sigma^2}\right\} dx \quad (14)$$

The resulting matrices \mathbf{T}_σ^∞ for $\sigma_1 = 0.5$ and $\sigma_2 = 1$ are shown in Equation (15).

$$\mathbf{T}_{\sigma_1}^\infty = \begin{bmatrix} 0 & \dots & 1 \\ \vdots & \ddots & 1 \\ \vdots & \ddots & 1 \\ 1 & & 1 \\ 1 & & 1 \\ 1 & & 1 \end{bmatrix}, \mathbf{T}_{\sigma_2}^\infty = \begin{bmatrix} 0 & \dots & 0.023 & 0.977 \\ \vdots & \ddots & 0.023 & 0.977 \end{bmatrix} \quad (15)$$

The convergence of \mathbf{T} is pretty fast as for $t > 5$ the matrix \mathbf{T} only slightly differs from the final matrix \mathbf{T}^∞ . Yet after few mutations within the same neighborhood, all individuals will be black regardless of the starting state. If we exemplarily set the mutation step size to $\sigma_1 = 0.5$, we can expect that—on the long run—the neighborhood will consist of only similar prey not depending on the initial representation. However, if the mutation is quite strong it becomes more likely that a white prey is created from only black prey in states s_4 and s_5 , see $\mathbf{T}_{\sigma_2}^\infty$.

If we also consider the walk of the predator, the observed structures in the population can be explained as follows. As δ is notably small in this experiment it is likely that the same area is considered for mutation several times. Therefore, once the neighborhood only consists of nearly optimal prey, the predator tends to conserve or even expand this area. If both predators act in this fashion nothing but an interchange of solutions takes place. Furthermore, an increment of σ is expected to only delay but never prevent the crowding of the population at extreme points. Note that this process can already be observed within the initial population where it contributes to the formation of stable areas. However, those areas do not yet represent a single objective's extremal solution but agglomerate around the neighborhood's best individual. On the long run, the areas touch and the one containing the worse individuals with respect to the predator's objective is extinct. This again is due to the aforementioned principle.

However, if we increase δ significantly, the interaction with the same local neighborhood cannot be guaranteed. In Figure 3 the results for $\delta = 40$, which is equal to the torus size are shown. Now, the mutation is performed with ap-

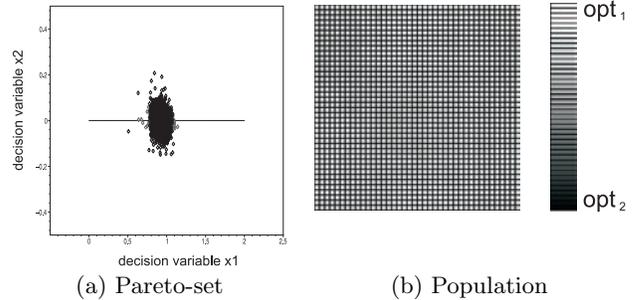


Figure 3: Population and Pareto-set after 100,000 evaluations of \mathcal{F}_2 with exclusive mutation and consumption frequency δ equal to the torus size.

proximately equal distribution over the whole torus and no local contiguity or connectivity is observable. The interaction of the two predators however comes more into play and the population consequently tends towards the center of the Pareto-set. As expected, the whole population consists of similar prey, see Figure 2(b), that are resistant against both predator species. Therefore, the mutation operator is closely connected to δ . As such, the consumption frequency favors the interaction between predator species and the intermediary solutions while a small δ guarantees a strong convergence to the solutions' extrema and favors the conservation of those points in contiguous areas within the population structure. A similar effect was observed in the original

predator prey model, see Laumanns [7], when increasing the number of predators. Both are ways to increase the predator changing frequency.

5.2 Recombination Analysis and Evaluation

In contrast to preliminary assumptions for the predator prey model [7], the importance of recombination has recently been shown empirically [3, 2]. Thus, this section takes a closer look to the population’s dynamics under the influence of a special kind of intermediate recombination, namely simplex recombination. To this end, we apply the afore introduced methodology of representing a population, see Section 4, and exclude mutation predators from the evolutionary process. Instead, for each objective one predator triggering simplex recombination is used.

In previous studies, the simplex recombination was considered to support convergence to the Pareto-set as well as diversity preservation. These interpretations are based on observing global characteristics of the mechanism. In the following, both global and local properties of simplex recombination on a spacial population will be reviewed.

Global properties

An obvious property of simplex recombination is to collapse an initial population in its convex hull. If there is no selection pressure at all, the individuals urge to the center of gravity. Otherwise, the center of gravity is dislocated depending on the objectives. As a consequence, the final position of a collapsed population strongly correlates to the area the initial population covers and the objectives obeyed. Hence, an initial population with a convex hull surrounding the set of Pareto optimal solutions will collapse near by this set while a population initially located in a distance from the Pareto-set will collapse close to the border of the initial convex hull. Because of the lack of mutation and thus innovation, these bounds cannot be crossed. Figure 4(a) exemplarily shows those two cases of initial populations where a multi-objective problem’s Pareto optimal set covered and not covered respectively. The objectives’ global influence on

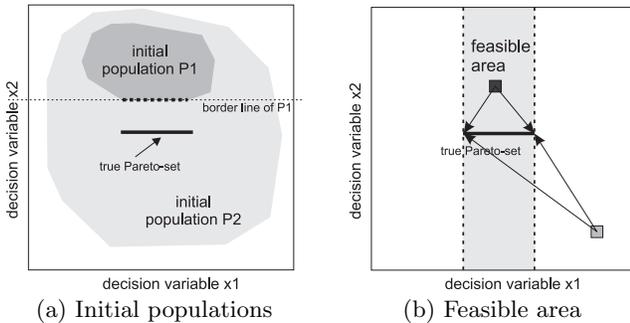


Figure 4: Exemplary depiction of an initial population not covering the optimal set of solutions (a) and the feasible area (b) in which predators objective do not collaborate.

convergence only differs in its rate. Replacing the elitist selection in Algorithm 1 by a uniform random selection mechanism would result in a slower but still ongoing contraction of the population. Until now, this effect of simplex recombination seems to somehow foster convergence. In combination with elitist selection mechanisms it probably even leads to

best possible closeness to the Pareto optimal solution. This however depends on the bounds of the initial population given by the convex hull.

Local Properties

Apparently, predators with different objectives collaborate as long as prey solutions are outside the *feasible area*. Exemplary, the feasible area for a test problem similar to ours is depicted in Figure 4(b). In general, we consider this area to be given by a subset of the decision space above and below the Pareto-set, bounded by normal lines through the extremal points. Outside the feasible area, an advancement toward one objective is most probably an advancement toward the other objectives if the angle between the respective gradients is small. Inside the feasible area, predators favoring

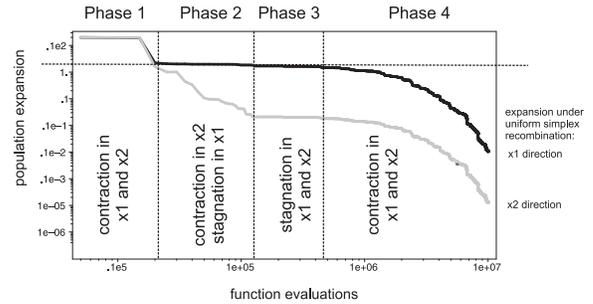


Figure 5: Maximum expansion of the population’s convex hull considering decision space components for simplex recombination.

objective $f_1(\vec{x})$ judge prey individuals which are good concerning objective $f_2(\vec{x})$ as being bad concerning their own objective. This, however, results in a significant slowdown referring to the contraction of the population in the direction of the objectives’ connection line. This effect is displayed in Figure 5 which shows the contraction of population referring the coordinate directions of decision space over time. The contraction process can obviously be subdivided in four phases of different behavior. First, the global effect resulting from the collaboration of both predator species yields to an equal contraction in x_1 and x_2 direction (phase 1). In phase 2, the population is inside the feasible area. Here, the population keeps on collapsing regarding x_2 , as both predators favor this direction the same, while the predators’ conflicting objectives seem to lead to a stagnation concerning the collapse of x_1 . Thereafter, phase 3 is characterized by total stagnation in both directions. However, in this phase the objectives become less important for the selection process as the individuals begin to collapse to the center of the population. This effect becomes apparent with the beginning of phase 4, where individuals in the barycenter of the population are more frequently produced than those at the boundaries of the convex hull. Thus, they increasingly often participate in the reproduction process which leads to more intermediary solutions in the evolving population. Finally, this increased participation rate results in a contraction of equal strength for both coordinate directions. Regarding phases 2 and 3, we focus on different processes inside the population when predators work against each other with respect to objective $f_1(\vec{x})$. Generally, there are two cases of neighborhood constellations in which the predators may re-

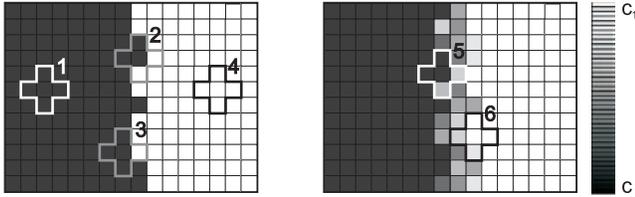


Figure 6: Simplified neighborhood constellation on the spatial structure and its development under recombination.

side. This is shown in Figure 6, where the black colored prey is preserved by predator r_1 while r_2 spares white prey. Following, these cases are detailed:

1. All prey in the spanned neighborhood are black for r_1 or all white for r_2 (Figure 6, cases 1 and 4). In this case the recombination has rather no effect as the predator can only create an offspring in the convex hull of quite similar prey. This effect is for some time similar to the replacement during mutation, see Section 5.1.
2. The predator resides on the border between areas with white and black prey individuals (Figure 6, cases 2 and 3). If more than one prey is bad concerning the predators objective, the recombination mixes the parental prey to a intermediary solution. This leads to an increasing number of intermediary solutions over time, while two boundary regions emerge (Figure 6, cases 5 and 6). In one region black prey exist next to gray ones and in the analogue region white prey border gray ones. If the gray population has an appropriate size, it becomes more stable against both predators than the remaining black and white prey. This finally leads to a faster contraction to the barycenter of the population.

The before described behavior results in the slowdown of contraction in the feasible area. As individuals representing a inter-mixture of both objectives are generated only on the border of two conflicting regions, compromises arise just in a friction of the reproduction processes. Nevertheless, as Figure 7 shows, even this initially slow process leads to contraction after of a lot of steps. The pictures of the population development where taken after 100,000 function evaluations (phase 2), 500,000 function evaluation (phase 3), and $2 \cdot 10^6$ function evaluations (phase 4).



Figure 7: Population development under simplex recombination, taken after 100,000 and 500,000 as well as $2 \cdot 10^6$ function evaluations (from the left to the right).

6. COMBINED APPLICATION OF REVIEWED OPERATORS

Until now, we analyzed the behavior of the two operators independently and were able to identify several properties for each. Regarding Gaussian mutation, we identified a tendency for spatial populations to loom contiguous areas of similar prey with respect to a single objective. Accompanying to this, there is a strong convergence towards extremal solutions, while no intermediary solutions are being created. Thus, the mutation operator's behavior degenerates to a plain replacement strategy. This holds independently from the variation of mutation step size σ , since an increase of this parameter only delays the crowding at extremal solutions as the final status. However, the consumption frequency δ directly influences the aforementioned behavior, as this parameter softens the spatial structure. With an increase of δ , this leads to an aggregated selection mechanism on a panmictic population.

The simplex recombination—as already shown empirically—supports global convergence and has a strong notion towards an emergence of intermediary solutions on the long run. The former, however, highly depends on the initial solution distribution in decision space as the collapsing behavior is only convergent to the true Pareto-set if it is enclosed by the convex hull of the population. Generally, this operator has mainly blending character which can be divided into four phases: global contraction (phase 1), mutual exchange (phase 2), accumulation of intermediary solutions (phase 3), and mixture dominance (phase 4).

In order to show these properties for the combined application of both operators, we analyzed the test problem \mathcal{F}_2 with a total of four predators, covering all possible permutations of selection criteria and operators. Here, we set $\delta = 1$, $\sigma = 0.1$, and made 10^7 function evaluations. As depicted in

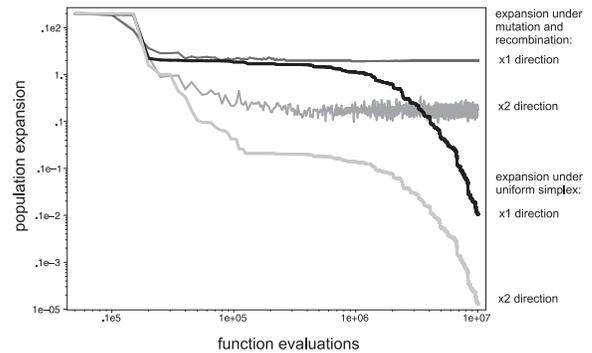


Figure 8: Maximum expansion of the population's convex hull considering decision space components for both operators. For comparison, the development of simplex recombination is also depicted.

Figure 8, the combination of mutation and recombination operators reveals several characteristics that have been already identified for the non-combined operators. Although the behavior of the combined operators is different to the one shown for its building blocks, it is still explainable by the single operators' properties. At the beginning of the evolutionary process, the collapsing of the initial population towards the Pareto-set visualizes the strong influence of the recombination. Thereafter, the mutation operator

dominates further development by preserving the extent of the population at both extremal solutions: apparently, the population keeps maximum expansion for the x_1 component while simultaneously oscillating on the x_2 component within the scale of the constant mutation step size σ . Due to the

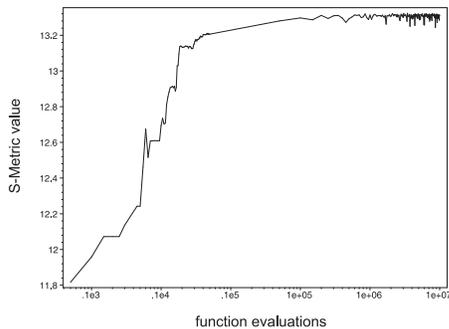


Figure 9: \mathcal{S} -Metric development over 10^7 function evaluations for the two combined operators. The maximum value is at $13.\bar{3}$ for test problem \mathcal{F}_2 .

influence of the recombination operator we would expect that besides the extremal points intermediary solutions are also found which would result in an increased diversity of individuals in the solution space. To quantify this effect, we computed the \mathcal{S} -Metric [14] value of our approximated solution set for every function evaluation during the evolutionary process. Clearly, the diversity of the population increases strongly and, after approximately 100,000 function evaluations, nearly reaches the maximum value of $13.\bar{3}$, see Figure 9. Finally, in Figure 10 the solution sets in the de-

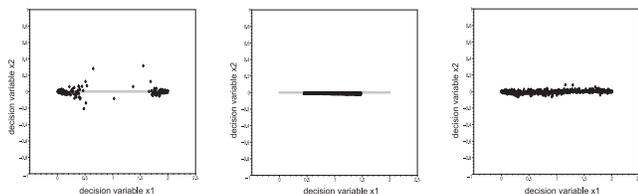


Figure 10: Approximated Pareto-sets for the two-dimensional multisphere test problem, see Equation (8). From left to right we applied only mutation, only simplex recombination and both operators in combination.

cision space for both non-combined operators as well as the cooperating variant are shown. This impressively demonstrates that the proposed use of a building block approach yields better results due to the preservation of beneficial properties of the single-objective evolutionary operators.

7. CONCLUSION AND FUTURE WORK

In the presented work, we analyzed two single-objective variation operators within the multi-objective problem domain using a modified predator-prey model. We reviewed the independent influence of each on the dynamics in a spatially structured population and identified different properties. Then, we applied both in combination and were able

to show that the advantageous properties of both can still be perceived. From this we conclude that a structured design of complex variation operators for evolutionary multi-objective optimization can be based on an adroit combination of single-objective operator characteristics in a building block manner.

Finding an appropriate combination ratio is, however, an open research problem. Further on, additional single-objective operators should be analyzed in the here proposed fashion in order to augment the repertoire of basic building blocks.

Acknowledgement

Joachim Lepping is member of the Collaborative Research Center 531, "Computational Intelligence", at Dortmund University with financial support of the Deutsche Forschungsgemeinschaft (DFG).

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