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A Predator-Prey Approach for Pareto-Optimization

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A Predator-Prey Approach for Pareto-Optimization

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Abstract. This article presents a predator-prey approach for multi-objective optimization. Based on the underlying search heuristic – the evolution strategy – a consequent further development with respect to the manyfold requirements of multi-criterion optimization is done. Particular, the well proved self-adaptation mechanism in the single objective case is adopted for the multi-objective one. Six well-known test functions are used to demonstrate the practicability of the model.

1 Introduction

During the last decades, numerous heuristic-based search methods for solving multi-objective optimization (MO) problems have been developed. Evolutionary algorithms (EA) as well as recent developments like particle swarm algorithms (PSO) have proved very efficient in approximating the set of Pareto-optimal solutions. In [1–3], surveys of the existing variants for EA are provided. In many, if not most cases, these approaches are able to ensure convergence to an approximative good set of Pareto-optimal solutions. Differences between the search heuristics arise in the distribution of the obtained results and the computational effort [4–6].

Most of these multi-objective evolutionary algorithms (MOEA) developed in the past using techniques of genetic algorithms (GA) [4, 15, 16] or evolution strategies (ES) [8, 11, 9]. Modifications of these original single objective search heuristics are mainly concerned on the selection operators and additional methods to maintain diversity or to speed up the search (elitism), but in most cases the variation operators remain unchanged.

In modern synthesis of evolutionary theory their is a broad agree upon the hypothesis that species evolve by increasing their adaptation to the environment where they live. Theses adaptation process takes place by variation at the genotype level and by developing new strategies of competition with other species.

While the particular attention is payed on the genotype level in single objective optimization as well as in the multi-objective case, research focusing on the level of species interaction remained rare. In the last years, only a few approaches have been developed [29, 14, 3, 17, 18]. These studies have show that a predator-prey model is effective in the field of MOP. Their crucial advantages can be summarized into two main arguments:

- Scalability between single-objective and multi-objective optimization, and
- the consequential conduction of the inherent parallel alignment of each population based approach.

Scalability between single-objective optimization and multi-objective optimization is achieved by adding further predator species into the selection process only. Modifications of other components from the underlying heuristics are not necessary. The hope and the aim of these approaches is the design of a heuristic for single- and multi-objective problems at last. In the second, Laumanns et al. has designed his model in an asynchronous and parallel manner. Most models from ecology show that individuals interact in time and space within their own specie as well as with other species. Laumanns was the first, who has mimiced successfully both decisive factors from ecology in order to preserve diversity in the current population.

This article takes up the inspiration of the predator-prey models. Starting from the idea of using an evolution strategy (ES) as the basic underlying search heuristic the question that has to be answered is: "How an evolution strategy has to be modified or parameterized to solve multi-objective optimization problems".

In evolution strategies, as well as in every other search heuristic, too, the parameter settings for the given heuristic-problem combination decide on success or failure of the search. In case of single objective optimization, various so called standard parameterization can be found in literature [22, 23], but in most cases experiences show that the simple adaptation of the parameter settings yields to lower solution qualities. For example, in ES an effective control mechanism is developed to steer up the mutation strength. These self-adaptation mechanism is a powerful mechanism, but it can fail. The causes for the risk of failure might be found in various reasons. Starting from a disadvantageous parameterization of the exogenous parameters so the mechanism is not able to work and ending up to an actually failure of the mechanism themselve. But if the optimal parameterization decide on sucess or failure of the controlling mechanism in the single objective case, is it possible to adopt these well proved mechanism to the multi objective case through a simple new parameterization or it is neccesarry to develop a new controlling mechanism?

The rest of this paper is organized as follows: in Section 2 an overview of the basic principles of the underlying search heuristic is given. In particular the precondition for a fully operative controlling mechanism for the mutation strength is briefly discussed. In Section 3 existing predator-prey approaches are presented. In Section 4 the implementation details are briefly described while in Section 5 the experimental environment and the used statistical methods to set up the experiments are sketched. In Section 6 preliminary results are reported, and finally Section 7 conclude this article with a summary of the insights and with directions for further research.

2 Evolution Strategy

This section presents the main aspects of a multimembered evolution strategy (ES), which was needed for further discussion. For a comprehensive introduction the reader is referred to [19, 20].

In principle, existing parameters in evolution strategies can be distinguished between exogenous and endogenous parameters. Exogenous parameters such as μ (parent population size) or
lambda (size of descendants) which are kept constant during the optimization run, are a characteristic of most of the modern search heuristics. Endogenous parameters sich as σ (the used standard deviations) are a pecularity of ES: they are used to control the ability of self-adaptation in ES during the run.

The adaptation of the endogenous parameters – the so called strategy parameters – depends on various adjustments. First of all, the strategy parameters are closely coupled with the object parameters [19]. Each individual has its own set of strategy parameters. Like the object parameters, the strategy parameters undergo recombination (together with the object parameters) and mutation and are used to control the mutation of the object parameters. Due to this mechanism, the optimizer can hope – and only hope – the an individual is able to learn the approximately optimal strategy parameters for the specific problem.

The realization of the described self-adaptation mechanism depends further on the kind and the number of strategy parameters to be adapted. In most cases only 1 or N standard deviations are used, where N denote the dimension of the problem. In the sphere function, i.e. only one standard deviation [20] will do the work, in multimodal fitness landscapes it is favourable to use more then one standard deviation. The question, how many standard deviations are necessary for a specific algorithm-problem combination or how many are necessary in the moment of evolution, is still open.

Correlated mutations finalize the current self-adaptation mechanism in ES. For a deeper insight of correlated mutations the reader is referred to [21]. The use of correlated mutation introduces $N(N-1)/2$ additional strategy parameters which have to be controlled too. This may be the reason why correlated mutation is commonly not used. In many real-world applications, where the computational cost of optimization problems is mainly determined by the time-comsuming function evaluations, the computational effort of computing the correlations is relative small.

In order to obtain the best possible self-adaptation for the given problem the specification of the exogeneous parameters is required. Table 1 shows the main exogenous parameters used in ES and their common default parameterization.

Some of these default values originates from investigations in the sixties [24, 25] of the last century about only two artificial test functions (sphere and corridor model). Other values – such as the progress coefficient c_{τ_0} – are theoretically analyzed [26] very well, but also only for a specific test function. Experimental investigations from [23, 22] have yielded to principle recommendations for the parameter settings i.e. for the type of recombination that must be choosen if the test function is unimodal or multimodal or for the initial standard deviation.

Table 1. Exogenous parameters of an ES. Column 1 shows the usual symbols for the parameters. Column 3 holds their most used default values [22, 23].

Symbol	Description	Default Values
μ	number of parent individuals	15
λ	number of offspring individuals	100
$\sigma_i^{(0)}$	initial standard deviation	1.0
n_σ	number of standard deviations	problem-dimension
c_{τ_0}	progress coefficient	1
κ	Maximum age of an individual	$\{1; \infty\}$
β	correlation variablity	0.0873
ρ	Mixing number	2
R_x	Recombination type for the object variables	$r_{(d)}$ local discrete
R_σ	Recombination type for the standard deviations	$r_{(i)}$ local intermediate
R_α	Recombination type for the rotation angles	$r_{(-)}$ no recombination

Nevertheless, after a first specification of these parameters, an evolution strategy is performed as follows: The initial parental population of size μ will be generated. A new offspring population is produced then by the rule of the $(\mu/\rho\,\kappa\,\lambda)$ - notation. From the parent population of size μ, ρ individuals are randomly chosen as parents for one child. Depending of the specified types of recombination, the recombination of the endogenous and exogenous parameters takes place. With respect to the recombination step, the mutation of the strategy parameters is done. The learning parameters $\tau_{0/i}$ determines the rate and precision of the self-adaptation of the standard deviations and β determines the adaptation of the rotation angles. After having a new offspring population of size λ, the selection operator is used to select the new parental population for the next iteration. In the choice of usual values for μ and λ it is only neccessary that λ exceeds μ by a sufficient margin that on average at least one child can be better than its parents. The famous 1/5-success rule, originally developed for a $(1+1)$-ES, is based on these assumption that maximum progress can only be achieved through step sizes leading to a success probability of approximately 20%. $\kappa = 1$ referres to the well-known comma-selection scheme of an ES, and $\kappa = +\infty$ to the plus-selection scheme.

2.1 Some Implementation Details

In the following two implementation details of the multimembered ES are discussed that are also nessessary for the controlling mechanism of the mutation strengh. In the originally algorithm of a multimembered ES listed in [20], lower bounds ($\epsilon_{absolute/relative}$) for the standard deviations are defined. The reason for the definition of these lower bounds is to ensure that the standard deviation is able to variate each objective variable at least at the last place behind the comma. Therefore, the step lengths of each individual has to satisfy the constraints:

$$\left.\begin{aligned} \sigma_i^{(g)} &\geq \epsilon_{absolute} \\ \text{and}\,\sigma_i^{(g)} &\geq \epsilon_{relative}|x_i^{(g)}| \end{aligned}\right\}\forall i = 1(1)n \tag{1}$$

where

$$\begin{aligned} \epsilon_{absolute} &> 0 \\ \text{and}\ 1 + \epsilon_{relative} &> 1 \end{aligned} \tag{2}$$

according to the computational accuracy. Experiences gained during the last years determines the second endogenous and fix parameter: the upper bound of the step length of each standard deviation (max_ϵ). In practice this parameter setting is recommended to $max_\epsilon = \tau_0 * log(2.0)$. Values above this limit would lead to chaos.

While the lower bound is direct motivated by the necessity of variation in each iteration, the existence of an upper bound is solely well-founded through experiences in the single objective case.

3 Related Works

It may be discussed controversially, whether a predator-prey model is a kind of coevolution or not. Certainly it is a kind of arms race on the level of macroevolution. Individuals interact, in this case in a competetive way with each other. These interaction takes place in many ways in ecology, so that a construction of an exact model of these interactions is impossible. Most models from ecology or growth theory show that indivuduals interact in time and space within their own species as well as with other species [28].

Poloni [35] has been the first one to use structured populations to maintain diversity in multi-objective optimization problems (MOP). In his approach individuals are mapped onto the vertices of a two-dimensional torus. Recombination is performed by a predefined neighborhood-relation according to the dominance relation. A non-pareto approach proposed in [14], the Predator-Prey-ES (PPES) consists of a spatially distributed population, too. Selection is performed in a local spatial depended manner from predators, which move randomly across the population. Each predator select the preys in its neighborhood by a specific single objective. The worst prey is cought by the predator. The free vertex is replaced then by recombination of the parents selected from the neighborhood. Due to this $(\mu+1)$ approach, the controlling mechanism of the mutation strength must fail. Two conditions for a full operative controlling mechanism are not carefully implemented: their is no surplus of offsprings, so that the underlying ES has a low probability to produce a better offspring according to his parents. Due to the absent of a "comma strategy", there is no possibiliy to delete bad adapted individuals in local optima. More extensive investigation about the controlling mechanism of this model [36] takes these problems into consideration. First results show that an improvement in convergence and diversity in the case of a multi-sphere model is possible. The results on difficult test functions like Kursawe (see below) are as unsufficient as in the original approach. While the convergence to few small regions of the Pareto-front is possible the ability of maintaining a diverse set of non-dominated soluations is still poor. This loss of diversity will become increasingly impotant the more iterations are performed. A further development of PPES can be found in [3]. Deb mascerate the strikt one predator to one objective assignment with an individual weighted vector in each predator. From now on each predator select 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) [17] model. In his approach he uses a genetic algorithm as the underlying search heuristic and investigates the two discribed fitness assigment methods from Laumanns and Deb. In addition he uses a dynamic population, where predators as well as prey are able to move on the structured environment. In opposite to the previous two models, recombination takes place only if two prey individuals are in the same neighborhood. If a prey has no neighbours, no duplication is allowed. In the model of Li, it is possible that predators exterminate the entire prey population. In order to prevent this situation, Li defined a special migration for both species to keep the prey population on a predefined level. Another approach using a dynamic interaction between predators and preys can be found in [37]. In his asynchronous parallel evolution strategy (APES) that is developed to solve singleobjective multimodal problems, a Lotka-Volterra model is defined. Unfortunately, this model has great difficulties to hold a stabil state in order to prevent the extinction of a specie.

4 The Predator-Prey Model

In the following a predator-prey model for multi-objective optimization is presented. Based on the underlying search heuristc, which was described in Section 2, the necessary modifications to solve MOP are sketched.

4.1 Choice of Population Structure

In the last section it has been shown that the use of spatial population structures is favourable to achieve a diverse set of non-dominated solutions. In general the exchange from panmictic operating variation and selection operators through local ones are the main feature of the spatial structures. This will be modeled in this approach by dividing of the global population into subpopulations: the so called demes. The number of demes is a new exogenous parameter (N_{deme}). Starting from a global definition of a ($50 \;\kappa\; 200$)-ES the 50 parent individuals are divided into N_{deme} uniform demes, which have constant size during the evolutionary run.

Recombination: Recombination takes place within these demes only. No migration between demes is allowed. The number of offsprings is defined in the same manner as the number of parents. For example, in the case of $N_{deme} = 2$ the global population is devided into two uniform demes. Within each deme a ($25 \;\kappa\; 100$)-ES is performed.

Selection: The number of predators, which are used in the evolution is defined by a maximum number of predators per objective (N_{pred1}, and N_{pred2} for two objectives). Selection is performed by an uniformly distributed selection from the amount of predators. That defines how many predators perform in the specific deme the selection. In this way for every deme the composition of the pack of predators for the actual deme is defined anew. As long as the number of individuals in the specific deme is greater than the predefined number of parents, selection take place.

Mutation and Step Size Control: The self-adaptive mutation mechanism, described in section 2 is used. The only change is concerned to the upper and the lower bounds of the mutation strength. From now on the upper bound for this parameter is defined in every iteration by the formula:

$$max_{\epsilon} = \tau_0 * (\sigma_{bestObj-1} + \sigma_{bestObj-2}) \tag{3}$$

which defines the arithmetic mean of the global best standard deviation for the first objective ($\sigma_{bestObj-1}$) and the corresponding standard deviation for the second objective.

The lower bound of the mutation strength is defined for each individual by the formula:

$$\epsilon_{relative} = \epsilon_{absolute} * (\tau_0/(\sigma bestObj - 1 + \sigma_{bestObj-2}) + N(0, \tau_0) \tag{4}$$

In this way the controlling mechanism for the mutation strength is no longer restricted by an arbitrary fix upper or lower bound, but on bounds, which values are defined by the controlling mechanism themselve.

5 Experimental Set Up

5.1 Parameter Setting and Experimental Design

As mentioned in section 1, the problem of choosing optimal or nearly optimal parameter settings for a given heuristic-problem combination is essential for the success of a search process. Practitioners often use so-called standard parameters. For the ES the standard parameters are listed in table 1. Experiences from the last four decades show, that each heuristic-problem combination requires a specific parameterization. For this, [31, 30] proposed a statistical methodology to set up computer experiments in an efficient manner. Design of Experiments (DOE) as well as tree based methods (classification and regression trees CART) are used to find nearly optimal parameter settings for a specific combination. Following these proposals the resulting fractional factorial design is presented in table 2.

It shows a 2^{10-6}_{III} design, where the minus and the plus signs denote to the low and the high levels of the factors, respectively. For each parameter a low level and a high level has to be specified. Because of the lack of standard parameters for the multi-objective optimization with ES the low level and the high levels

Table 2. Fractional Factorial Design 2_{III}^{10-6} Design. The Design represents the starting design that is used for all test functions.

	A	B	C	D	$E = ABC$	$F = BCD$	$G = ACD$	$H = ABD$	$I = ABCD$	$J = AB$
1	−	−	−	−	−	+	+	+	−	+
2	+	−	−	−	+	+	−	−	+	−
3	−	+	−	−	+	−	+	−	+	−
4	+	+	−	−	−	−	−	+	−	+
5	−	−	+	−	+	−	−	+	+	+
6	+	−	+	−	−	−	+	−	−	−
7	−	+	+	−	−	+	−	−	−	−
8	+	+	+	−	+	+	+	+	+	+
9	−	−	−	+	−	+	+	+	−	+
10	+	−	−	+	+	+	−	−	+	−
11	−	+	−	+	+	−	+	+	+	−
12	+	+	−	+	−	−	−	−	−	+
13	−	−	+	+	+	−	−	−	+	+
14	+	−	+	+	−	−	+	+	−	−
15	−	+	+	+	−	+	−	−	−	−
16	+	+	+	+	+	+	+	+	+	+

are choosen under consideration of experiences in the single objective case. The resulting design matrix for the high and the low levels of the predator-prey evolution strategy is shown in Table 3.

All experiments, based on the experimental design in table 3, were performed to gather the data. Each experimental setting was repeated five times.

5.2 Test functions

In order to compare the predator-prey model with the results of Laumanns et al. and Deb, the same three test functions (F_2, F_4, and F_5) are chosen. In addition the ZDT_1 [33] (F_3) and the simple Schaffer [14] (F_1) test functions have also been analyzed. It is important to annotate that the first test function F_0 is single-objective. This function is added to the test suite, in order to show that within this model, changing between single-objective optimization and multi-objective optimization is possible (see section 6.1).

Test Function 0 (Sphere) [20]: This is an unimodal single-objective test function, with a single minimum at $\mathbf{x}^* = \mathbf{0}$

$$F_0(\mathbf{x}) = \sum_{i=1}^{n} x_i^2 \tag{5}$$

Test Function 1 (Schaffer) [34]: This test function is 1-dimensional, the optimal Pareto set is convex.

$$F_1(f_1(x), f_2(x)) = \begin{pmatrix} f_1(x) = x^2 \\ f_2(x) = (x-2)^2 \end{pmatrix} \tag{6}$$

Table 3. Corresponding fractional factorial design for the choosen model-problem combination: (d = discrete, i = intermediate recombination, and N = problem-dimension)

	μ	λ	σ_0^{init}	N_σ	κ	N_{demes}	N_{pred1}	N_{pred2}	R_x	R_σ
1	180	500	0.15	1	1	30	1	1	d	d
2	360	500	0.15	1	$+\infty$	30	10	10	i	i
3	160	700	0.15	1	$+\infty$	75	1	10	i	i
4	360	700	0.15	1	1	75	10	1	d	d
5	180	500	3	1	$+\infty$	75	10	1	i	d
6	360	500	3	1	1	75	1	10	d	i
7	180	700	3	1	1	30	10	10	d	i
8	360	700	3	1	$+\infty$	30	1	1	i	d
9	180	500	0.15	N	1	75	10	10	i	d
10	360	500	0.15	N	$+\infty$	75	1	1	d	i
11	180	700	0.15	N	$+\infty$	30	10	1	d	i
12	360	700	0.15	N	1	30	1	10	i	d
13	180	500	3	N	$+\infty$	30	1	10	d	d
14	360	500	3	N	1	30	10	1	i	i
15	180	700	3	N	1	75	1	1	i	i
16	360	700	3	N	$+\infty$	75	10	10	d	d

Test Function 2 (Multi-Sphere) [14]: This test fuction represents an extension of the well-known Sphere-function from the single objective case. In these experiments, the function ist restrictted on two dimensions.

$$F_2(f_1(\mathbf{x}), f_2(\mathbf{x})) = \begin{pmatrix} f_1(\mathbf{x}) = x_1^2 + x_2^2 \\ f_2(\mathbf{x}) = (x_1 + 2)^2 + x_2^2 \end{pmatrix} \tag{7}$$

Test Function 3 (ZDT-1) [32]: This test function is a composition of three functions f_1, g and h:

$$F_3(f_1(x), f_2(\mathbf{x})) \tag{8}$$

where

$$\begin{pmatrix} f_1(x) & = x_1 \\ f_2(\mathbf{x}) & = g(\mathbf{x}) * h(f_1, g) \\ g(\mathbf{x}) & = 1 + \sum_{i=2}^{30} (x_i - 0.5)^2 \\ h(f_1, g) & = 1 - \sqrt{f_1/g} \end{pmatrix}$$

Test Function 4 (Kursawe) [11]: In this test function, the Pareto optimal set is non–convex as well as discontinuous, and, thus, the values of the decision variables that correspond to the true Pareto optimal solutions are difficult to obtain:

$$F_4(f_1(\mathbf{x}), f_2(\mathbf{x})) = \begin{pmatrix} f_1(\mathbf{x}) = \sum_{i=1}^{n-1} -10 \exp(-0.2 \sqrt{x_1^2 + x_2^2}) \\ f_2(\mathbf{x}) = \sum_{i=1}^{n} (|x_i|^{0.8} + 5 * \sin^3(x_i)) \end{pmatrix} \tag{9}$$

Test Function 5 (Quagliarella) [14]: This function is a 16-dimensional uniform function. The corresponding Pareto-front is concav.

$$F_5(f_1(\mathbf{x}), f_2(\mathbf{x})) \tag{10}$$

where

$$\begin{pmatrix} f_1(\mathbf{x}) = \sqrt{\frac{A_1}{n}} \\ f_2(\mathbf{x}) = \sqrt{\frac{A_2}{n}} \end{pmatrix}$$

Restrictions:

$$\begin{pmatrix} A_1 = \sum_{i=1}^{n}[(x_i^2) - 10\cos[2 * \Pi(x_i)] + 10] \\ A_2 = \sum_{i=1}^{n}[(x_i - 1.5)^2 - 10\cos[2 * \Pi(x_i - 1.5)] + 10 \end{pmatrix}$$

6 Evaluation

The applicability of the predator-prey model is demonstrated in this section. In Section 1 one of the main advantages of predator-prey models is named by "scalability". This advantage has to be shown in an experimental manner at first. The well-known sphere model (F_0) is chosen for this task. Next the model is applied to the convex test functions F_1 to F_3. Two important questions are analyzed: the impact of the number of demes used in the model and the influence of a variable number of predators per objective. The results of the model for the test functions F_4 and F_5 finalize this section.

6.1 Scalability

The experiments in this section were set up in order to solve the single-objective function F_0. Therefore the number of predators are set to $N_{pred1} = 1$ and $N_{pred2} = 0$, respectively. The panmictic population, which is traditionally used in the evolution strategy is configured by $N_{deme} = 1$. No further modifications are necessary. The variation of three exogenous parameters will change the heuristic from multi-objective to single-objective optimization.

Due to comparability to the results found in [20], the type of initialization of each individal and the termination criterion are changed. Here, the number of iterations is measured that is needed "in going from the initial values

$$x_i^0 = x_i^* + \frac{(-1)^i}{\sqrt{(N)}}, \text{for } i = 1(1)n$$

to an approximation

$$|x_i^{(g)} - x_i^*| \leq \frac{1}{10}|x_i^{(0)} - x_i^*|, \text{for } i = 1(1)n.$$

" [20]. x_i^* denotes to the known optimal value for each objective variable, and $x_i^{(g)}$ to the actual value of the best individual in population (g). Table 4 shows the

Table 4. Comparison between the ES and the predator-prey model on test function F_0. The arithmetic mean of ten independent runs is presented. Results show that there is no significant difference between both heuristics. Particular, the predator-prey approach outperforms the ES in small dimensions.

problem-dimension	ES	predator-prey
3	4	4.2
6	10	8.8
10	20	12.9
20	37	28.7
30	55	58.8

obtained results for F_0. The arithmetic mean of ten independet runs is presented in column three. In the second column results taken from [20] are listed.

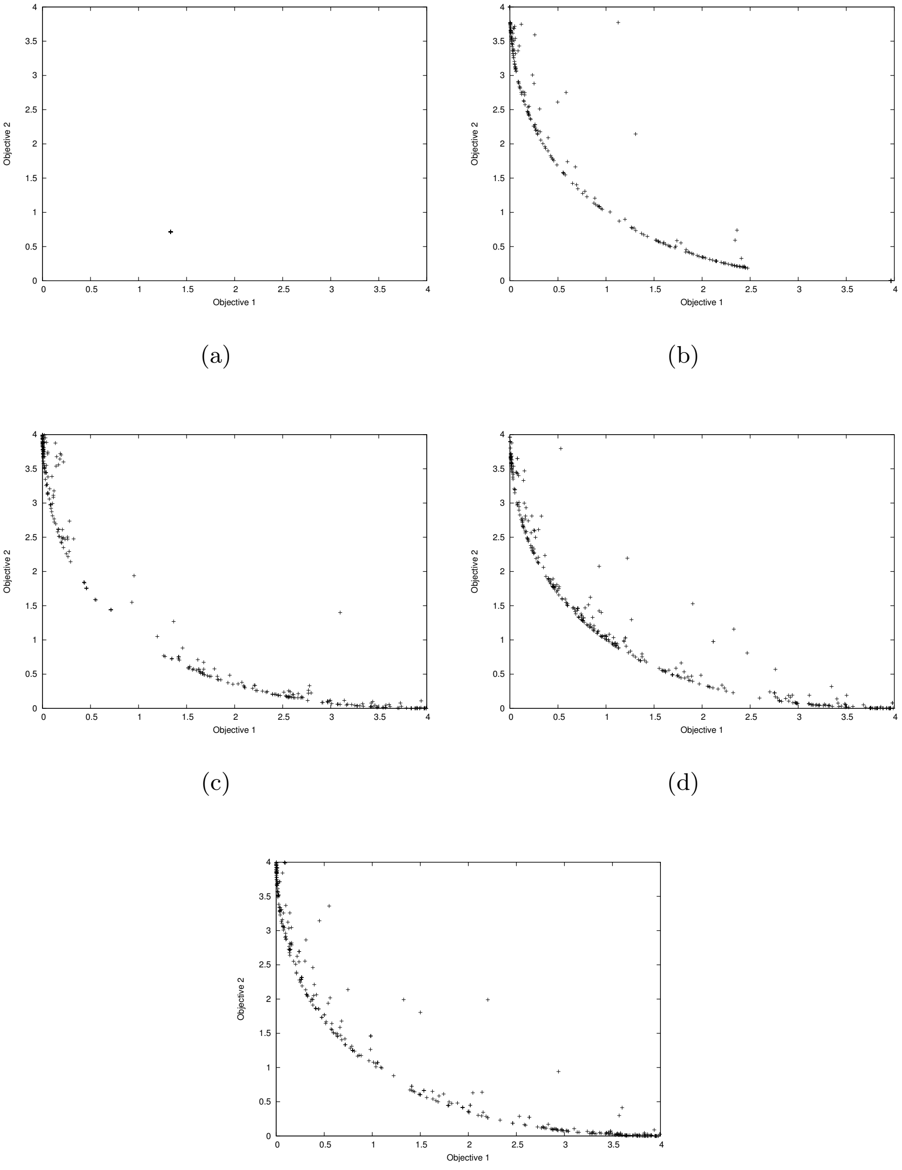
Results show that there is no significant difference between both heuristics. In particular, the predator-prey approach outperforms the ES in relative small dimensions ($N = \{6, 10, 20\}$). It can be conjectured that the modification of the controlling mechanism for the mutation strengths is also able to work in single objective cases.

6.2 Convex Pareto-Fronts

Starting from the initial parameterization listed in Table 3, first results from 90 experiments have shown that a good parameterization for this heuristic-problem combination reads: $\mu = 360$, $\lambda = 700$, $\sigma^0_{init} = 3.0$, $N_\sigma = 2$, $N_{demes} = 75$, $N_{pred1} = 10$, $N_{pred2} = 10$, $R_x = d$ (deterministic) and $R_\sigma = d$ by a predefined termination criterion of 100 iterations.

Figure 1 shows the approximation of the Pareto-front for the test function F_2. From (a) - (e) the number of demes is increased by $N_{demes} = 1, 2, 25, 50, 75$. All other parameters remain constant. Here it can be seen that the number of demes has a significant impact on the number of different solutions in the resulting population. Starting from a panmictic ($N_{deme} = 1$) model (a) only few solutions covering a very small region of the Pareto-front are obtained. Already the use of two seperated demes (b) allows to cover the whole region but with poor diversity. If the number of demes increased the final population gets more and more diverse (e). Similar results can be observed from test functions F_1 and F_3. In general, one can state that in this model, as well as in the models with a spatial population structure, the exchange from a panmictic population structure with panmictic variation and selection operators to local ones is favourable for a better diversity of the resulting population.

Next the number of predators per objective is analyzed. Figure 2 shows the approximation of the Pareto-front and its associated decision vectors for F_2. The top row represents the case of one predator per objective. The lower two rows show the state of the model with $N_{pred1/pred2} = 10, 100$ predators per objective, respectively. As a surprising result the number of predators for each objective



(a) (b)

(c) (d)

(e)

Fig. 1. Variable number of used demes for the test function F_2. From top to below, deme size is recommended to $N_{demes} = 1, 2, 25, 50, 75$. The greater the number of demes the better the diversity.

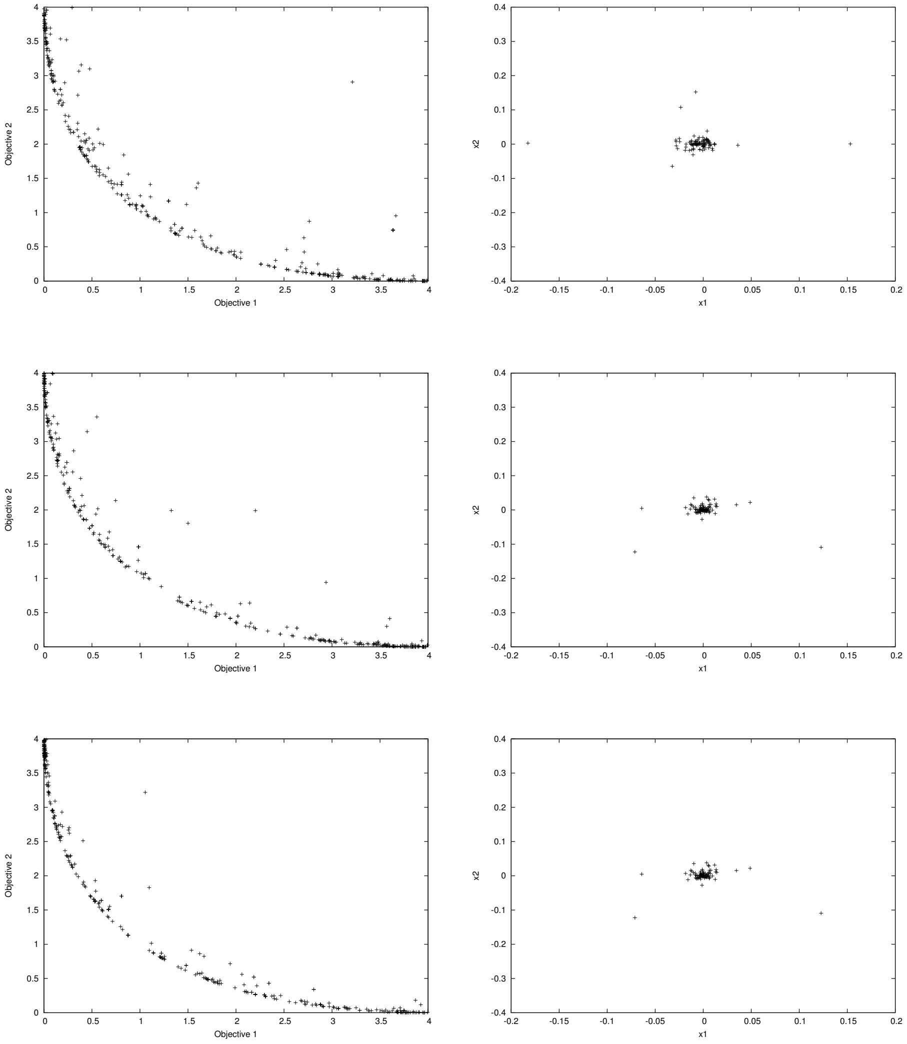


Fig. 2. Variable number of predators per objective for the test function F_2. From top to below, the number of predators is recommended to $N_{pred1/pred2} = 1, 10, 100$.

seems to have no significant impact for the distribution of the population. It could be conjectured that the decision if a deme is encountered by only one or both types of predators is sufficient to get a well distributed Pareto-front.

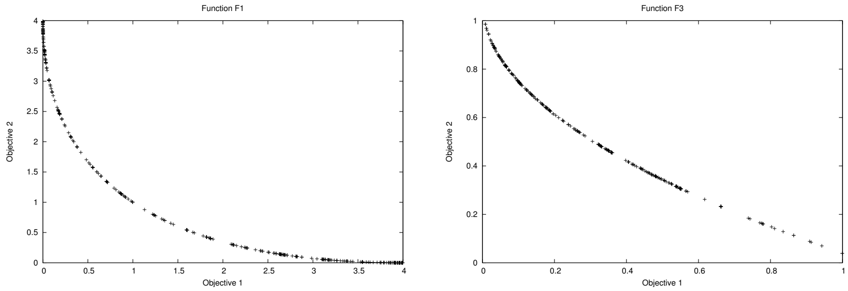


Fig. 3. Pareto-Fronts for the test functions F_1 and F_3. Both fronts are well approximated by the model.

The number of used predators is not relevant. In contrast to the descreasing schedules used in [14] [3] no decomposition of the Pareto-set can be observed (see Figure 2 right column). This leads to the hope that the controlling mechanism anticipates the trend to few single isolated set. Finally Figure 3 shows the resulting Pareto-fronts for the functions F_1 and F_3. Both Pareto-sets are well approximated. Summarizing one can state that the model is abel to solve multi-objective optimization problems, which have in general convex Pareto-Fronts.

6.3 Non-Convex Pareto-Fronts

In this section more complex functions are analyzed. F_4 is more difficult, because there are also locally efficient solutions that are not globally efficient. Function F_5 derives from the test suite of [40]. Here, the solutions are non-uniformly distributed along the non-convex Pareto-front. While the results of the function F_4 are ecouraging, here, the control mechanism of the mutation strength leads to a well approximated Pareto-set with a relative small number of dominated solutions. The same controlling mechanism works even well on theconcav function F_5. A limitation occurs at the borders of the Pareto-Front. Here, further reasons for this behaviour must be detected, especially in the field of finding the optimal parameterization for this heuristic-problem combination.

7 Summary

In this study the problem of adapting the well-known evolution strategy into the field of multi-objective optimization is treated. The modified evolution strategy

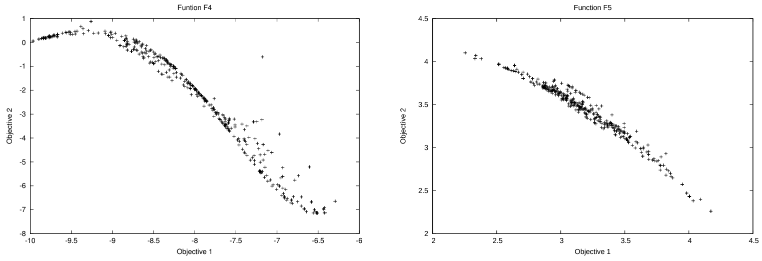


Fig. 4. Pareto-fonts of the test functions F_4 (a) and F_5 (b). The modified control mechanism of an ES leads to a well approximated Pareto-front in case of function F_4, but it fails by F_5.

adapted ideas of predator-prey models from ecology. In particular, this predator-prey approach enables the practitioner to change between single-objective optimization and multi-objective optimization in an easy manner. Questions about an appropriate controlling mechanism for the mutation strength in the case of multi-objective optimization are answered via a simple but efficient modification of the hitherto fix upper and lower bounds for the mutation strength. Experiments carried out with five test functions have shown that the predator-prey model is able to produce a good set of diverse solutions along the Pareto-front for convex as well as for non-convex test functions. Even in the case of single-objective optimization, the modified controlling mechanism still allows self-adaptation with equal and sometimes better rates of convergence. The hypothesis that structured populations preserve diversity in the set of non-dominated solutions can be confirmed. Unfortunately, a relativ great number of fitness evaluations is necessary in contrast to the well-known state-of-the-art heuristics. It might be speculated that an approximately optimal specification of the upper bound of the mutations strengths still remains to be done.

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