Proactive Evolutionary Algorithms for Dynamic Optimization Problems

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1 STAGE OF THE RESEARCH

The research is ongoing for nearly four years. The preliminary results and possible applications were presented on 6 international conferences and published in 10 papers available in: *Lecture Notes in Computer Science* (Filipiak et al., 2011; Filipiak et al., 2012a; Filipiak et al., 2012b; Michalak et al., 2013; Filipiak and Lipinski, 2014a; Filipiak and Lipinski, 2014b; Lancucki et al., 2014; Michalak et al., 2014), *Lecture Notes in Artificial Intelligence* (Filipiak and Lipinski, 2012) and *Lecture Notes in Mechanical Engineering* (Brzychczy et al., 2014) by Springer.

A completion of the PhD thesis is planned for the academic year 2014/2015.

2 OUTLINE OF OBJECTIVES

The aim of the research is to propose the anticipation strategies that are easily applicable to the contemporary Evolutionary Algorithms in order to improve their robustness in dealing with Dynamic Optimization Problems (defined in the next section).

A thorough examination of the suggested approach and the classification of optimization problems that are solvable with it are necessary to fill the research gap in this area.

Eventually, a comparison of the introduced algorithms with the state-of-the-art solutions, both *reactive* and *proactive*, needs to be done.

3 RESEARCH PROBLEM

Numerous real-world optimization problems are dynamic in a sense that their objective functions change as time goes by which makes them difficult to solve. Such dynamic objective function can be defined by

$$F^{(\alpha_t)} : \mathbb{R}^d \longrightarrow \mathbb{R}, \tag{1}$$

where $d > 0$ and (α_t) is a vector of parameters changing in time, indexed with $t \in T \subseteq \mathbb{N}$.

A solution to Dynamic Optimization Problem (DOP) is a set of pairs $S = \{(x,t) : x \in \mathbb{R}^d, t \in T\}$, where for all $(x,t) \in S$ holds

$$x = \arg\min\{F^{(\alpha_t)}(x) : x \in \mathbb{R}^d\}. \tag{2}$$

In other words, solving DOPs is not only about finding the biggest peak in the landscape yet also about tracking its movement and continuously exploring the search space looking for the newly appearing optima.

It has to be clarified that the vector of parameters (α_t) is not known for all $t \in T$. Let $t_{now} \in T$ encode the present moment which implies that only $(\alpha_{t_{now}})$ can currently be observed. It is often assumed that vectors $(\alpha_t)_{t\in T}$ for $t < t_{now}$ can also be accessible since one is usually able to keep the record of past observations (e.g. stock quotes, weather conditions) or events (e.g. alerts, system log files). However, the future values $(\alpha_t)_{t\in T}$ for $t > t_{now}$ clearly cannot be accessible until the t increases.

The above-defined DOPs are present in a wide range of academic and engineering fields, e.g. time series analysis (Box et al., 2011), decision support systems (Kim, 2006), inverse kinematics (Castellani and Fahmy, 2008), job scheduling and load balancing tasks (Jozefowiez et al., 2009).

3.1 Evolutionary Approach

Evolutionary Algorithms (EAs) are a class of easily applicable, self-adaptive heuristic optimization problem solvers that allow for a fast exploration of large parameter spaces aiming to find the (at least) suboptimal solutions. Even though EAs were originally designed for Stationary Optimization Problems (SOPs), their adaptation to the DOPs domain is rather straightforward (Branke, 2001). In the commonly used *reactive model* EAs probe for the landscape changes by triggering some simple actions in the synchronous manner, e.g. a re-evaluation of certain individuals in the population or a random sampling of the search space. Immediately after a change of the objective function is detected, a dedicated procedure aimed at localizing new optima is launched.

The main drawback of the above model is its inertia. Note that reactive EAs are always one step behind the changing environment since they can only respond to the changes that were already detected, providing that they were detected at all.

3.2 Improvement Due to Proactivity

A *proactive model* aims at acting *a priori* rather than *a posteriori*. It collects the past observations of the changing environment and utilizes them to anticipate the future landscape. This way, the EA can deal in advance with the changes to come, for instance by directing a part of the population towards the most probable future promising regions.

Although in theory the proactive model clearly seems much more robust then the reactive one, it is generally hard to achieve in practice since no anticipation mechanism can be fully reliable. Thus, a fundamental research problem is to propose a class of the forecasting models that the EAs can be equipped with and to analyze the applicability of the proposed proactive EAs to the certain types of DOPs.

Eventually, it has to be verified whether the suggested proactive algorithms indeed outperform the reactive ones as it is assumed in the theoretical model, and if so, then what is the obtained speed up.

4 STATE OF THE ART

Most EAs applied for SOPs follow the same two-stage pattern. They begin with the low-grained *exploration* of the search space aimed at localizing the most promising regions and then gradually switch to the *exploitation* stage when a fine-grained search is performed. Nevertheless, the above behaviour does not comply with DOPs. In the case of continuously changing environment both exploration and exploitation are carried on simultaneously since EA, during whole its run, has to probe for the new optima in parallel with tracking the ones that were already found. Otherwise, the population would soon converge to a small neighbourhood of some local optimum and thus immediately lose the ability to detect new optima emerging outside this neighbourhood.

4.1 Introducing Diversity

A number of EAs proposed by the researchers to address DOPs aim at forcing a diversification among tightly coupled individuals. Cobb proposed a Triggered Hypermutation (TH) mechanism that activates whenever a moving average of best individuals fitness deteriorates. The mutation rate is then increased to the predefined high level so that the individuals could be spread evenly across the search space (Cobb, 1990). An improved TH mechanism named Variable Local Search (VLS) was suggested in (Vavak et al., 1997). It performs a gradual increasing and decreasing of the mutation rate (rather than switching sharply between the two fixed levels) which improves the performance of VLS in DOPs with low severity of changes.

An alternative approach to diversifying the population on a triggered basis is to maintain a certain level of diversity throughout the whole run of EA. A popular Genetic Algorithm (GA) of this type, named Random Immigrants GA (RIGA), was first introduced in (Grefenstette, 1992). Near the end of each generation it selects a small fraction of individuals to replace them with the purely random ones. As a result a bunch of mediocre individuals is obtained each time yet the search space is relatively well covered and, what is more, there is no need for the environmental change detector. Another method for maintaining diversity was implemented in CHC (Simões and Costa, 2011), where only sufficiently distant individuals (in terms of a Hamming distance) are allowed for mating and crossing-over in order to prevent them from incest.

4.2 Memory Based Approach

In DOPs with periodical or recurrent changes it is often convenient to store the historical best solutions so that they can be re-used afterwards when the environment reaches the same state again. One possible approach to achieve this is through *polyploidy*, i.e. a collection of multiple information about each allel in the chromosome (Yang, 2006). Such chromosome is then additionally equipped with the adaptive mask that indicates which of the redundant allels dominates the others that are kept in the same locus. This way one genotype may encode various phenotypes depending on the current state of the adaptive mask.

The algorithms using memory *explicitly* were also proposed. A direct use of the previous good solutions stored in a buffer was well studied in (Yang, 2005). Alternatively, some indirect strategies for the use of a memory were suggested that either collect states of the environment (Eggermont et al., 2001), a probability vector that created best individuals (Yang and Yao, 2008) or a likelihood that an optimum would appear in a certain area (Richter and Yang, 2008).

4.3 Proactivity

Prediction approaches to DOPs are still not well studied. A "futurist" mechanism that empowered Simple GA (SGA) by directing the population into the future promising regions was signalized in (van Hemert et al., 2001) yet the author considered only the perfect predictor. A number of true anticipation models based on Kalman filter (Rossi et al., 2008), auto-regression (Hatzakis and Wallace, 2006) or time series identification (Zhou et al., 2007) were proposed to address some specific DOPs. An interesting approach using an auto-regressive model for predicting when the next change will occur and a Markov chain predictor for anticipating the future landscape was recently presented in (Simões and Costa, 2013). The latter approach was tested on the popular bit-string problems where it proved its rapidness in reacting to the recurring changes.

5 METHODOLOGY

A fundamental part of the research comprises of the three predictive strategies proposed for EAs so that they follow the proactive model in solving DOPs.

The first two strategies utilize the Auto-Regressive Integrated Moving Average model (ARIMA) (Box et al., 2011) frequently used in statistics and data analysis. Both of them focus on certain vectors of the search space that are somehow representative for the present landscape. The historical data associated to these vectors is collected in the form of time series. Later on, the ARIMA model is used for anticipating the future values of the time series so that EA can prepare for the next change of the environment that is likely to happen very soon. The strategies were employed in Infeasibility Driven Evolutionary Algorithm (IDEA) (Singh et al., 2009a) that, apart from dealing with DOPs, can also handle constraints which is a valuable asset in the field of real-world optimization problems (see: Appendix).

The third strategy is an extension of the anticipation mechanism based on a Markov chain predictor presented in (Simões and Costa, 2013). It makes a use of the ability of Univariate Marginal Distribution Algorithm (UMDA) (Liu et al., 2008) to build a probability model for distribution of good individuals within the search space. These models are further used as the parametrization of the states of the environment identified by the anticipation mechanism.

Detailed descriptions of the above strategies are given in the next sections accompanied with the preliminary results and indications of the future work.

5.1 Anticipation of Evaluations

In this anticipation strategy a dynamism of the environment is perceived through the recurrent evaluations of a finite set of samples $S \subset \mathbb{R}^d$, $d > 0$. Every

Algorithm 1: Pseudo-code of IDEA-ARIMA.

```
$S_1 = \emptyset$
$P_1$ = RandomPopulation()
Evaluate($P_1$)
for $t = 1 \to N_{gen}$ do
    if the function $F$ has changed then
        Re-evaluate($P_t$)
        $S_t$ = ReduceSamples($S_t \cup P_t$)
        Re-evaluate($S_t \setminus P_t$)
        if $t - 1 > N_{train}$ then
            $P_t$ = ReducePopulation($P_t \cup \widetilde{P}_t$)
        end if
    end if
    $P_{t+1}$ = IDEA$_t(P_t, F^{(t)})$
    if $t > N_{train}$ then
        $\widetilde{P}_{t+1}$ = RandomPopulation()
        $\widetilde{P}_{t+1}$ = IDEA$_1(\widetilde{P}_{t+1}, \widetilde{F}^{(t+1)})$
    end if
    $S_{t+1} = S_t$
end for
```

sample $s \in S$ is associated with the time series of its past evaluations $(X_t^s)_{t \in T}$, i.e.

$$\forall_{t \le t_{now}} \quad X_t^s = F^{(t)}(s). \tag{3}$$

In other words, all the historical values of the objective function F for all the samples $s \in S$ up to the present moment $t_{now} \in T$ are collected and made available at any time.

The ARIMA model is applied for predicting the future values of the objective function $\widetilde{X}^s_{t_{now}+1} = \widetilde{F}^{(t_{now}+1)}(s)$ based on the past observations $(X_t)_{t \le t_{now}}$. Then, the whole future landscape can be anticipated by extrapolating the set

$$\{\widetilde{F}^{(t_{now}+1)}(s)\,;\ s \in S\}, \tag{4}$$

using the $k > 0$ nearest neighbours method.

The above strategy was applied in IDEA and introduced as IDEA-ARIMA (Filipiak et al., 2011). The proposed algorithm maintains two concurrent populations P and $\widetilde{P}$. The first one is responsible for optimizing the objective function F while the latter optimizes the anticipated objective function $\widetilde{F}$.

Algorithm 1 presents the pseudo-code of IDEA-ARIMA. It begins with a random initialization of the population P_1 and the empty set of samples S_1. Then the main loop of the algorithm is run for $N_{gen} > 0$ generations. Whenever a change of the objective function F is detected (i.e. the evaluation of at least one of the randomly chosen individuals has just changed), the whole population P_t is re-evaluated and then added to the set of samples S_t. After that, the set S_t is reduced to the fixed maximum size and the rest of

Table 1: Numbers of matches in 10 runs of IDEA and IDEA-ARIMA for benchmarks $G24\_1$ and $G24\_2$ with $N_{gen} = 64$. The first $N_{train} = 16$ iterations were omitted since observable results of both algorithms do not differ within this time period.

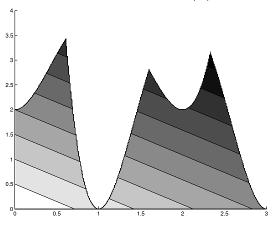
	$G24\_1$										$G24\_2$									
IDEA	21	23	13	19	19	15	22	16	22	21	5	9	19	10	9	14	11	12	18	14
IDEA-ARIMA	28	26	29	30	28	26	29	29	29	26	29	25	21	23	26	26	23	23	23	22

the samples $S_t \setminus P_t$ is also re-evaluated. Providing that the training period of the anticipation mechanism $t = 1, 2, \ldots, N_{train}$ is over, and thus the population $\widetilde{P}_t$ is ready, the individuals from P_t and $\widetilde{P}_t$ are grouped together and immediately reduced to the fixed population size $M > 0$. Eventually, regardless the changes of F, the t-th iteration of the original IDEA is invoked. Later on, the predictive population $\widetilde{P}_{t+1}$ is initialized randomly and used for the one iteration of IDEA with the anticipated objective function $\widetilde{F}^{(t+1)}$.

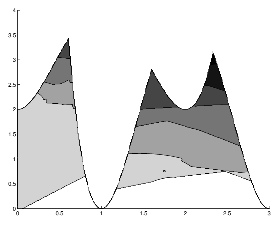
IDEA-ARIMA was tested on the dynamic constrained benchmark problems from the $G24$ family (Nguyen and Yao, 2009a) and the modified $FDA1$ (Farina et al., 2004; Filipiak et al., 2011). Figure 1 present the 2D-plots of the objective functions and their anticipated counterparts at the sample time steps. Darker shades represent lower values of $F^{(t)}$. It is clear that although the anticipations are not exact in every point of the search space, the promising regions (marked in black) are well identified.

Table 1 summarizes the numbers of matches (i.e. correct identifications of global optimum among local ones) at each time step $N_{train} < t \leq N_{gen}$ of $G24\_1$ and $G24\_2$ benchmark problems. An identification was

(a) Benchmark $G24\_1$

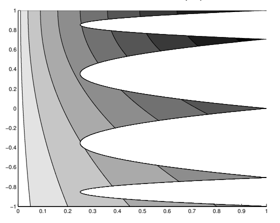


$F^{(25)}$

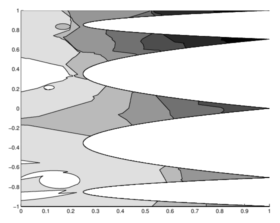


$\widetilde{F}^{(25)}$ seen at $t = 24$

(b) Benchmark $mFDA1$



$F^{(18)}$



$\widetilde{F}^{(18)}$ seen at $t = 17$

Figure 1: 2D-plots of the objective functions (left) and their counterparts anticipated with IDEA-ARIMA (right) at the sample time steps of benchmarks: (a) $G24\_1$ and (b) $mFDA1$. Darker shades represent lower values of $F^{(t)}$.

considered correct whenever the Euclidean distance between the global optimum and at least one feasible solution did not exceed $\delta = 0.1$. It is easy to see that IDEA-ARIMA outperformed IDEA in each run.

Finally, it has to be mentioned that IDEA-ARIMA was tested with no limitations on the size of the set of samples S (maximum size set to ∞). In the future an effective reduction mechanism on the set S ought to be proposed. Also the number of historical evaluations stored in time series needs to be limited due to the excessive memory usage.

5.2 Anticipation of Optima Locations

The second approach is an extension of the Feed-forward Prediction Strategy (FPS) proposed in (Hatzakis and Wallace, 2006). It assumes that the changes of spatial locations of optima inside the search space form a pattern that can be fitted with an AutoRegressive (AR) model. As a result, the location of future optimum can be anticipated using this model.

For all time steps $t \in T$, let $x_t^* \in \mathbb{R}^n$ be the argument minimizing $F^{(t)}$, i.e. the location of optimum of $F^{(t)}$. Let $\{X_t\}_{t \in T}$ be the n-dimensional time series of such optima locations, i.e. $X_1 = x_1^*$, $X_2 = x_2^*, \ldots$ Obviously, the exact values of x_t^* aren't known. Instead, an individual $p_t^* \in \mathbb{R}^n$ with the highest fitness among all specimens in a population P_t at time step t is used as the best available approximation of x_t^*. As a result, the accuracy of a prediction model is highly dependent on the efficiency of the EA used. It means that the closer a population can get to the actual optimum at each time step, the more exact locations of future optima can be anticipated. On the other hand, the less effectively EA performs at localizing current optima, the more erroneous anticipations it obtains in return.

The original FPS was based on a simple AR model parametrized with only a single positive integer determining the order of autoregression. In the proposed approach, the AR is extended into the more general ARIMA model that often guarantees more accurate forecasts. The suggested extension of FPS was applied to IDEA and introduced as IDEA-FPS (Filipiak and Lipinski, 2014a).

Apart from the prediction mechanism, IDEA-FPS provides a novel population segmentation on *exploring*, *exploiting* and *anticipating* fractions.

Algorithm 2: Pseudo-code of IDEA-FPS.

```
$X_0 = (\emptyset)$
$P_1$ = RandomPopulation()
for $t = 1 \to N_{gen}$ do
    Evaluate($P_t$)
    $P_t$ = InjectExploringFraction($P_t, size_{explore}$)
    $P'_t$ = IDEA$_t(P_t, F)$
    $p^*_t$ = BestIndividual($P'_t$)
    $X_t = (X_{t-1}, \{p^*_t\})$
    if $t > N_{train}$ then
        $\widetilde{p}^*_{t+1}$ = AnticipateNextBestIndividual($X_t$)
        $\Phi_{t+1} = \mathcal{N}(\widetilde{p}^*_{t+1}, \sigma^2_t)$
        $P_{t+1}$ = InjectAnticipatingFraction($P'_t$,
                    $\Phi_{t+1}, size_{anticip}$)
    else
        $P_{t+1} = P'_t$
    end if
end for
```

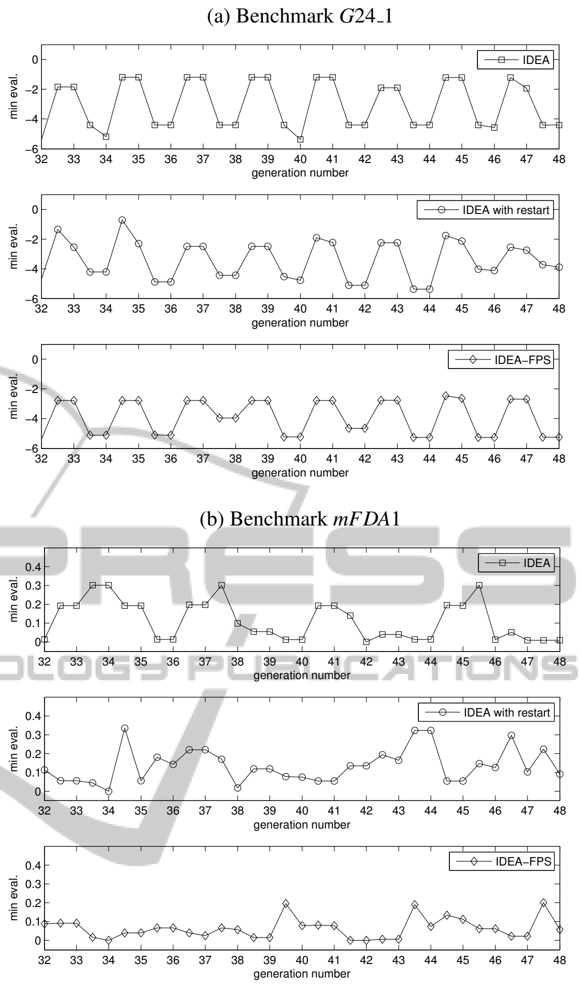


Figure 2: Comparison of the evaluations of best individuals during a sample run of IDEA-FPS vs. IDEA and IDEA with restart, tested in *G24_1* and *mFDA1*.

Exploring fraction is built up entirely with random immigrants that are uniformly distributed in the search space. Their randomness prevents a population from trapping into local optima and introduces diversity required for tracking changes in the landscape. *Anticipating fraction* is a group of individuals gathered in the nearest proximity of the predicted location of a future optimum. Providing that a forecast obtained with an anticipation model is accurate, these individuals become the most contributing ones just after the next environmental change. *Exploiting fraction* in turn is formed with offsprings of exploring and anticipating individuals from previous generations. It is responsible for a fine-grained search in the promising regions localized by other fractions.

A pseudo-code of IDEA-FPS is given in Algorithm 2. It begins with a random initialization of $M > 0$ individuals $x_1, \ldots, x_M \in \mathbb{R}^d$ and the empty time series $\{X_t\}_{t \in \mathbb{N}}$. Each iteration $t = 1, \ldots, N_{gen}$ starts with the evaluation of a population P_t. Later on, a new exploring fraction comprising of $size_{explore} \cdot M$ random immigrants (where $size_{explore} \in \{0\%, \ldots, 100\%\}$) is injected into P_t. These immigrants replace worst individuals in P_t. Next, the t-th iteration of IDEA is invoked and after that a *best-of-population* individual p^*_t is selected. A vector $p^*_t \in \mathbb{R}^d$ is then stored in $\{X_t\}$ as the best approximation of an optimum location at time step t.

For $t = 1, \ldots, N_{train}$ the anticipation mechanism of IDEA-FPS is inactive since best individuals from these generations are used for training the ARIMA model. During this initial period IDEA-FPS behaves like the original IDEA extended with random immigrants injections.

When the condition $t > N_{train}$ is finally satisfied, ARIMA is applied to $\{X_t\}$ in order to obtain a forecast concerning the next optimum location $\widetilde{p}^*_{t+1}$. As a result, the new anticipation fraction is created out of random individuals located in the proximity of $\widetilde{p}^*_{t+1}$. Virtually any continuous probability distribution function can be applied for that purpose. In the proposed approach the anticipation fractions are drawn with a d-dimensional Gaussian distribution $\mathcal{N}(\widetilde{p^*_{t+1}}, \sigma^2_t)$ where $\sigma_t = (\sigma_{t,1}, \sigma_{t,2}, \ldots, \sigma_{t,d}) \in \mathbb{R}^d$ with $\sigma_{t,i} = (x^{max}_i - x^{min}_i)/100t$ for $i = 1, \ldots, d$ and $x^{min}_i \leq x^{max}_i$. At the end of the main loop, $size_{anticip} \cdot M$ individuals (where $size_{anticip} \in \{0\%, \ldots, 100\%\}$) replace the worst ones from P_t just like in the case of exploring fraction.

In the experiments, all the combinations among $\{0\%, 10\%, 20\%, \ldots, 100\%\}$ were considered for both exploring and ancitipating fractions. Note that IDEA is a special case of IDEA-FPS with both fraction sizes set to 0% while IDEA-FPS with exploring fraction size = 100% and anticipating fraction size = 0% is indeed a sequence of independent IDEA runs — one run at each time step t or, in other words, it is the original IDEA with the full re-initialization of a population after each environmental change. For simplicity, the latter case will be referred to as *IDEA with restart*.

It turned out that the rate of exploration had a significant impact on the overall performance of IDEA-FPS. Particularly, the cases with $size_{explore} = 0\%$ performed the least effective every time. On the other hand, the best performances were obtained with $50\% \leq size_{explore} \leq 70\%$. Also the application of an anticipation mechanism noticeably influenced the results. It was especially visible after switching from $size_{anticip} = 0\%$ to $10\% \leq size_{anticip} \leq 30\%$.

Injections of exploring and anticipating fractions helped to avoid the risk of stagnation of a population. It is demonstrated in Figure 2 at the sample runs of the examined algorithms. Periodical fluctuations of best individuals that are visible on the plots relate to rapid reactivity to the environmental changes in *G24_1* whereas the distorted irregular variations indicate losing track of global optima. On the other hand, *mFDA1* is designed in such manner that the ideal run would result in the straight line at the 0 level. Thus, each deviation towards positive values visible on the plots signifies slow reaction to the environmental changes. Note that IDEA with restart hardly approached the 0 level. This implies that global optima in *mFDA1* are evidently less accessible by purely random individuals then in *G24_1*. However, an anticipation mechanism of IDEA-FPS allowed for handling with these difficulties.

In the experiments, the fixed sizes of the three fractions were used which required some prior examination of the optimized problems. For practical applications it would be more convenient to utilize a self-adaptation mechanism responsible for selecting the proper sizes. The future work should address that issue at first.

5.3 Anticipation of Landscape Changes

This anticipation strategy is based on a Markov chain model — a tool that is frequently applied in statistics and data analysis. In the most general form a *Markov chain* can be formulated as a sequence of random variables $(X_n)_{n\in\mathbb{N}}$, i.e. $X_1, X_2, X_3, \ldots$, such that for all $n \in \mathbb{N}$

$$\begin{aligned}\mathbb{P}(X_{n+1} = x \,|\, X_n = x_n, \ldots, X_1 = x_1) &= \\ = \mathbb{P}(X_{n+1} = x \,|\, X_n = x_n).\end{aligned} \tag{5}$$

It means that the instance of X_{n+1} depends only on its predecessor X_n, regardless the remaining of the history trail.

A *discrete chain Markov model* can be defined as a tuple (S, T, λ), where $S = \{S_1, S_2, \ldots, S_m\} \subset \mathbb{R}^d$ (for $d \geq 1$) is a finite set of possible states (i.e. a domain of X_n), $T = [t_{ij}]$ is a transition matrix containing probabilities of switching from state S_i to S_j (for $1 \leq i, j \leq m$), and $\lambda = (\lambda_1, \lambda_2, \ldots, \lambda_m)$ is the initial probability distribution of all the states in S.

Starting from the prior knowledge, which in practice is often a *zero knowledge*, where $\lambda = (1/m, 1/m, \ldots, 1/m)$, and by assuming that the variables X_n are sampled from some unknown stochastic process, the characterization of this process is built iteratively by observing instances of X_n and maintaining the transition matrix T as follows. Let $C = [c_{ij}]$ be an intermediary matrix for counting the past transitions. For all $1 \leq i, j \leq m$ the coefficients c_{ij} hold the number of transitions from state S_i to S_j that occurred so far. After each such transition the value of c_{ij} is incremented. The matrix T is then built up with the row-vectors $T_i = [c_{i1}/c, c_{i2}/c, \ldots, c_{im}/c]$ for $i = 1, \ldots, m$, where $c = \sum_{j=1}^{m} c_{ij}$.

The assumption stated in Equation 5 implies that any row T_i of matrix T indeed estimate the probability distribution of switching from the state S_i to any of the possible states $S_j \in S$. As a consequence, the model of changes encoded in T can be used further for predicting the future value of X_n for at least one step ahead by simply picking up the most probable transition originating at the present state. This mechanism is typically referred to as a *Markov chain predictor*.

The fundamental aspect in applying a Markov chain predictor is the definition of S. Ideally, the states $S_1, S_2, \ldots, S_m$ should play the role of *snapshots*, i.e. the exact models of the landscape at the given time. However, when dealing with optimization problems the main impact is on localizing the optimum, thus the quality of the model for the remaining part of the search space is negligible.

In (Simões and Costa, 2013), the authors applied a Markov chain predictor to the EA in order to improve its rapidness in solving the bit-string problems with the recurring type of changes. In this approach the applicability of the above mechanism is extended to the continuous domain. Note that, unlike bit-string problems where identifying the states of the environment is rather straightforward, in the case of continuous domain some parametrization is required for storing information about the landscape. For this purpose, a stochastic parametrization utilized in Estimation of Distribution Algorithms (EDAs) (Larrañaga and Lozano, 2001) seems most adequate since it models the exact spatial locations of the best candidate solutions.

EDAs are the class of EAs that search for the optima by building up a probabilistic model of the most promising regions in the vector space. They typically begin with a zero knowledge or a very rough estimation concerning the expected location of the optimum. Later on, the more exact model of the landscape is acquired iteratively by performing a random sampling in the area of interest and then narrowing down this area by cutting off the regions containing "the worst samples". Then, sampling it again and so on until convergence.

Univariate Marginal Distribution Algorithm (UMDA) (Liu et al., 2008) falls under the umbrella of EDAs. It estimates the distribution of the best individuals in the d-dimensional search space ($d > 1$) however the mutual independence of all d coefficients is assumed in order to simplify the computation.

In the proposed approach, the states of the environment are characterized with Gaussian distributions that model the spatial locations of best candidate solutions in the search space. For all $i = 1, \dots, m$ holds $S_i \equiv (\mu_i, \Sigma_i)$ where $\mu_i \in \mathbb{R}^d$ is a mean vector and $\Sigma_i = [\sigma_{kl}]_{1 \le k,l \le d}$ is a covariance matrix. These parameters are estimated and delivered by UMDA. Later on, the outputs of a Markov chain predictor are utilized by the same UMDA to direct the optimization towards the future promising regions.

The modification of UMDA equipped with the anticipation mechanism was named UMDA-MI[1] (Filipiak and Lipinski, 2014b). Similarly to IDEA-FPS, it maintains the three fractions of candidate solutions — *exploring*, *exploiting* and *anticipating*. Like before, the first one is filled up with random immigrants sampled with the uniform distribution across the search space. The remaining two fractions are formed with the individuals sampled as follows. Let Φ and $\widetilde{\Phi}$ be Gaussian distributions. The exploiting fraction uses the present distribution model Φ that is updated iteratively during the run of UMDA-MI whereas the anticipating fraction uses the foreseen distribution model $\widetilde{\Phi}$ obtained from the Markov chain predictor.

Algorithm 3 presents the main loop of UMDA-MI. It begins with a random selection of the distribution $\Phi_1 = (\mu_1, \Sigma_1)$ and defining the empty chain predictor $(S, T, \lambda) = (\emptyset, [\,], 1)$. The anticipated distribution $\widetilde{\Phi}_1$ is set to Φ_1 as for UMDA-MI it is established that in case of no clear forecast about the next environmental change, the best prediction available is in fact the present distribution Φ_t.

The algorithm runs for $N_{gen} > 0$ generations, each of which is split into $N_{sub} > 0$ intermediary steps called *subiterations*. Every k-th subiteration (for $k = 1, \dots, N_{sub}$) includes generating the three fractions of candidate solutions as follows. The exploring fraction is filled with $size_{explore}$ random individuals, while the exploiting and anticipating fractions are formed with $size_{exploit}$ and $size_{anticip}$ candidate solutions sampled with the distribution models Φ_{t_k} and $\widetilde{\Phi}_{t_k}$ respectively. Next, all the fractions are grouped together and evaluated. Among them the top $0 < M_{best} < M$ individuals $p_1, p_2, \dots, p_{M_{best}} \in \mathbb{R}^d$ are filtered out and utilized for updating the estimation of distribution $\Phi_{t_k} = (\mu_{t_k}, \Sigma_{t_k})$ using the following formula

$$\mu_{t_k} = \sum_{i=1}^{M_{best}} \frac{p_i}{M_{best}}, \quad \sigma_{t_k} = \frac{\sqrt{\sum_{i=1}^{M_{best}} (p_i - \mu_{t_k})^2}}{M_{best}}. \quad (6)$$

At the beginning of each generation, UMDA-MI sets all the fraction sizes to $1/3$ and then updates them automatically N_{sub} times, i.e. once per subiteration. The updating rule works as follows. It begins with finding a single best individual per fraction as its representative. Then, all the three fractions are given labels adequate to the fitness of their respective representatives. The fraction containing the best representative is labeled *best*, the second best is labeled

Algorithm 3: Pseudo-code of UMDA-MI.

```
Initialize estimation of distribution $\Phi_1$ randomly
Initialize Markov Chain predictor by setting:
    $(S, T, \lambda) = (\emptyset, [\,], 1)$ and $\widetilde{\Phi}_1 = \Phi_1$
for $t = 1 \to N_{gen}$ do
    $\Phi_{t_1} = \Phi_t$
    $size_{explore} = size_{exploit} = size_{anticip} = 1/3$
    for $k = 1 \to N_{sub}$ do
        $P_{explore}$ = RandomImmigrants($size_{explore}$)
        $P_{exploit}$ = GenerateFraction($\Phi_{t_k}, size_{exploit}$)
        $P_{anticip}$ = GenerateFraction($\widetilde{\Phi}_t, size_{anticip}$)
        $P_{t_k} = P_{explore} \cup P_{exploit} \cup P_{anticip}$
        Evaluate($P_{t_k}$)
        UpdateEstimation($\Phi_{t_k}, P_{t_k}$)
        UpdateFractionSizes($P_{explore}, P_{exploit}, P_{anticip}$)
    end for
    $S = S \cup \{\Phi_{t_k}\}$
    if size($S$) = max-size($S$) then
        Find a pair $\{S_i, S_j\}$ of the most similar states
            in the set $S$
        $\overline{S_{ij}}$ = AverageState($\{S_i, S_j\}$)
        Replace $\{S_i, S_j\}$ with $\overline{S_{ij}}$ in the set $S$
    end if
    Update transition matrix $T$
    Assign $\Phi_{t+1}$ to the most similar state to $\Phi_{t_k}$
        in the set $S$
    $\widetilde{\Phi}_{t+1}$ = PredictNextState($\Phi_{t+1}$)
end for
```

[1]The letter 'M' stands for a Markov chain predictor while 'I' for random immigrants.

Table 2: The best-of-generation results averaged over 50 independent runs for the compositions of Sphere, Rastrigin, Griewank and Ackley functions.

Dimensions		5				10			
Function	N_{sub}	2	5	10	20	2	5	10	20
Sphere	SGA-R	216.0	149.7	90.4	59.7	441.0	350.2	246.5	129.0
	UMDA	129.6	92.8	78.1	71.5	151.5	107.7	89.2	77.5
	UMDA-MI	94.4	62.1	57.7	56.5	109.8	77.4	62.2	59.0
Rastrigin	SGA-R	586.3	438.1	350.0	312.1	845.6	717.1	621.4	585.8
	UMDA	560.3	429.6	438.8	354.8	713.1	608.6	533.9	462.0
	UMDA-MI	370.9	312.1	263.7	229.5	532.9	488.0	441.7	409.2
Griewank	SGA-R	350.9	272.7	202.3	159.9	522.8	437.7	335.7	224.3
	UMDA	224.5	188.4	153.5	132.2	234.6	201.7	176.7	158.2
	UMDA-MI	203.9	160.7	129.9	113.2	205.4	172.0	148.9	140.2
Ackley	SGA-R	1687.4	1508.6	1176.4	665.5	1886.9	1831.2	1740.7	1507.2
	UMDA	1657.3	1613.6	1476.2	1364.6	1597.2	1587.4	1441.6	1343.2
	UMDA-MI	965.9	742.3	485.6	403.9	1093.4	858.9	645.7	516.0

medium and the last one — *worst*. Next, the size of the *best* fraction is increased by the small constant $\varepsilon > 0$. The remaining $1 - size_{best}$ "vacant slots" are disposed between the *medium* and *worst* fractions proportionally to the differences in fitness of their representatives and the representative of the *best* fraction. Clearly, all the three sizes must sum up to 1. They are also restricted to the range $[size_{min}, size_{max}]$ where $0 < size_{min} < size_{max} < 1$ in order to prevent from the excessive domination of a certain fraction causing the exclusion of the others.

After completing all of the N_{sub} subiterations, the Markov chain predictor is launched (once per generation). Firstly, it adds the obtained distribution Φ_{t_k} to the set of possible states S. Later, if the number of elements of S (after extending) reaches the predefined maximum size, the following replacement procedure is executed. Among all the elements in S a single pair of the two most similar states $\{S_i, S_j\} \subset S$ is identified and replaced with their average $\overline{S_{ij}}$. In order to find the most similar state to S_i, for all $i = 1, \ldots, \text{size}(S)$ a number of random samples is generated according to S_i and compared with $S \setminus \{S_i\}$. A Gaussian with the highest response to these samples is selected as S_j. In the case when S_i or S_j is the present state of environment, the state $\overline{S_{ij}}$ takes over its role.

The transition matrix T is built and maintained using the intermediary counting matrix C as described before. However, each time the two states S_i and S_j are unified, the corresponding j-th row and j-th column of C are removed while their values are added to the respective elements of i-th row and i-th column.

Finally, the most probable future state according to T is picked and used as the distribution model for the next anticipating fraction $\widetilde{\Phi}_{t+1}$.

UMDA-MI was tested on the DOPs generated with the Dynamic Composition Benchmark Generator (DCBG) (Li et al., 2008) which rotates and aggregates the functions given as input in a time-dependent manner. In the experiments the components of *Sphere*, *Rastrigin*, *Griewank* and *Ackley* functions were used.

Table 2 summarizes the best-of-generation results (i.e. mean evaluations of the best solutions found just before the next environmental change) averaged over 50 independent runs with various problem dimensions $d \in \{5, 10\}$ and numbers of subiterations $N_{sub} \in \{2, 5, 10, 20\}$. For comparison, also a Simple Genetic Algorithm with a complete re-initialization of a population after each change of the landscape (SGA-R) was run. It is evident that UMDA-MI outperformed both UMDA and SGA-R in all the examined cases.

The preliminary experiments revealed that the application of a Markov chain predictor together with the introduction of random immigrants into UMDA significantly improved the algorithm's reactivity to the recurrently changing environments in the continuous domain. However, it is probable that the accuracy of a Markov chain predictor may deteriorate in other than recurrent types of changes. The future work should cover that as well as dealing with the presence of constraints.

5.4 Time-linkage Aspect

The time-linkage aspect is an issue raised in (Bosman, 2005; Nguyen and Yao, 2009b). It assumes that any decision made at the given moment $t \in T$ may influence the states of the environment in the future. This implies that a solution which seemed optimal in the short-time perspective can unexpectedly become a sub-optimal one when perceived on the long term basis. For instance, a buy/sell decision of large amounts of assets on the stock market might affect the other players and result in a significant change of the prices.

The above aspect in DOPs is still not well studied. Moreover, it appears an extremely difficult issue to tackle in the proactive model since it requires the highly-accurate long-term forecasts.

It is very tempting to modify the three anticipation strategies presented in the previous sections such that they could try to deal with the time-linkage. However, this requires a slight redefinition of the solution to DOP. It should no longer be seen as the trajectory of moving optima, yet rather a more abstract entity like a consistent strategy or a classificator suggesting the behaviour in given states of the environment which can be further evaluated from the long-term perspective.

6 EXPECTED OUTCOME

The proposed anticipation strategies ought to be verified in the large set of both benchmark and real-world DOPs. It is expected that, after a thorough examination, the groups of problems that can be handled well with these strategies will be clearly identified.

It is also believed that at least some examples of the time-linkage can also be dealt with using the suggested anticipation strategies or their modifications.

Finally, one can expect that a comparison with other proactive approaches will result in some future improvements of IDEA-ARIMA, IDEA-FPS and UMDA-MI including an addition of auto-adaptation mechanisms, a reduction of the number of input parameters or an application of other prediction models.

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APPENDIX

Infeasibility Driven Evolutionary Algorithm

Infeasibility Driven Evolutionary Algorithm (IDEA) (Singh et al., 2009b) was originally proposed to address stationary constrained optimization problems. It maintains a certain fraction of “good” yet infeasible solutions within a population in order to improve an exploration of areas near constraint boundaries.

IDEA evaluates each individual under the two criteria. One criterion is simply an objective function. Another criterion, called *violation measure*, determines to what extent a given solution violates the constraints.

Algorithm 4: IDEA-Reduction of a union $C \cup P$ of children and parents populations respectively, producing an output population P' of $M > 0$ individuals.

```
$M_{infeas} = size_{infeas} \cdot M$
$M_{feas} = M - M_{infeas}$
$(S_{feas}, S_{infeas})$ = Split($C \cup P$)
Rank($S_{feas}$)
Rank($S_{infeas}$)
$P' = S_{feas}(1 : M_{feas}) + S_{infeas}(1 : M_{infeas})$
```

Algorithm 5: Sub-IDEA step.

```
$P_1 = P$
Evaluation($P_1$)
for $t = 1 \to N_{sub}$ do
    $P'_t$ = Selection($P_t$)
    $C_t$ = Crossover($P'_t$)
    $C''_t$ = Mutation($C'_t$)
    $P_{t+1}$ = IDEA-Reduction($P_t \cup C''_t$)
end for
Return $P_{N_{sub}}$
```

Algorithm 6: Main loop of IDEA.

```
$P_1$ = RandomPopulation()
for $t = 1 \to N_{gen}$ do
    Evaluation($P_t$)
    $C_t$ = Sub-IDEA($P'_t$)
    $P''_t$ = IDEA-Reduction($P'_t \cup C_t$)
end for
```

Since IDEA essentially reformulates a single-objective problem into a multi-objective one, any two individuals can no longer be compared according to their fitness. Instead, the ranking based on *non-dominated sorting* procedure with *crowding distance* metric (as a tie-breaking rule) is performed as in NSGA-II (Deb et al., 2002). It is important to note that crowding distance promotes individuals located in less crowded areas hence it introduces diversity within a population.

One of the key aspects of IDEA is the specific implementation of a reduction step. As it is seen in Algorithm 4, individuals from $C \cup P$ (a union of children and parents populations) are firstly split into two subsets containing feasible and infeasible solutions — S_{feas} and S_{infeas} respectively. Then, both subsets are ranked according to the mentioned NSGA-II ranking. Afterwards, the top M_{feas} individuals of S_{feas} and the top M_{infeas} individuals of S_{infeas} are chosen to form the new generation P'. Such separation is intended to promote the infeasible individuals which otherwise could be eliminated by the feasible ones due to their superiority in violation measure.

From the implementation perspective the heart of IDEA is Sub-IDEA step (Algorithm 5) which essentially runs the entire "evolutionary engine" of the algorithm. It consists of $N_{sub} > 0$ iterations of tournament selection, simulated binary crossover (SBX) and polynomial mutation (Singh et al., 2009b). In order not to confuse iterations of Sub-IDEA step with iterations of the main loop, the former ones are referred to as *subiterations*.

The main loop of IDEA (presented in Algorithm 6), apart from invoking Sub-IDEA step, consists only of one re-evaluation of a population and one IDEA-Reduction step per iteration.