A COMPETITIVE COMPARISON OF DIFFERENT TYPES OF EVOLUTIONARY ALGORITHMS

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Abstract
This paper presents comparison of several stochastic optimization algorithms developed by authors in their previous works for the solution of some problems arising in Civil Engineering. The introduced optimization methods are: the integer augmented simulated annealing (IASA), the real-coded augmented simulated annealing (RASA) [10], the differential evolution (DE) in its original fashion developed by R. Storn and K. Price [15] and simplified real-coded differential genetic algorithm (SADE) [6]. Each of these methods was developed for some specific optimization problem; namely the Chebychev trial polynomial problem, the so-called type 0 function and two engineering problems – the reinforced concrete beam layout and the periodic unit cell problem respectively. Detailed and extensive numerical tests were performed to examine the stability and efficiency of proposed algorithms. The results of our experiments suggest that the performance and robustness of RASA, IASA and SADE methods are comparable, while the DE algorithm performs slightly worse. This fact together with a small number of internal parameters promotes the SADE method as the most robust for practical use.

Keywords
optimization, evolutionary methods, genetic algorithms, differential evolution, engineering tasks

1 Introduction

Nowadays, optimization has become one of the most discussed topics of engineering and applied research. Advantages coming from using optimization tools in engineering design are obvious. They allow to choose an optimal layout of a certain structure or a structural component from the huge space of possible solutions based on a more realistic physical model, while the traditional designing methods usually rely only on some simple empirical formulas or guidelines resulting in a feasible but not necessarily an (sub-)optimal solution. Using optimization as a method of design can raise engineering job to a higher level, both in terms of efficiency and reliability of obtained results.

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Typically, optimization methods arising in engineering design problems are computationally demanding because they require evaluation of a quite complicated objective function many times for different potential solutions. Moreover, the objective function is often multi-modal, non-smooth or even discontinuous, which means that traditional, gradient-based optimization algorithms fail and global optimization techniques, which generally need even a larger number of function calls, must be employed. Fortunately, the rapid development of computational technologies and hardware components allows us to treat these problems within a reasonable time.

As indicated previously, the optimization methods can be divided generally into two groups: the gradient methods, that operate on a single potential solution and look for some improvements in its neighborhood, and global optimization techniques – represented here by so called evolutionary methods – that maintain large sets (populations) of potential solutions and apply some recombination and selection operators on them. During the last decades, evolutionary methods have received a considerable attraction and have experienced a rapid development. Good compendium of these methods can be found for example in [12] and references therein. Main paradigms are: genetic algorithm (binary or real coded), augmented simulated annealing (binary or real coded), evolution strategy and differential evolution. Each of these methods has many possible improvements (see, e.g., [1],[3]).

Many researchers all over the world are united in an effort to develop an evolutionary optimization method that is able to solve reliably any problem submitted to it. In present time, there is no such method available. Each method is able to outperform others for certain type of optimization problem, but it extremely slows down or even fails for another one. Moreover, many authors do not introduce the reliable testing methodology for ranking their methods. For example they introduce results of a single run of a given method, which is rather questionable for the case of stochastic algorithms. Finally, the methods are often benchmarked on some test functions, that even if presented as complicated, are continuous and have few local extremes.

This paper presents several optimization methods that were developed and tested for different types of optimization tasks. The integer augmented simulated annealing (IASA), derived from a binary version of the algorithm [9], was developed to optimize a reinforced concrete beam layout from the economic point of view. For solving the problem of a periodic unit cell layout [16], the real-coded simulated annealing was applied. Differential evolution arose to solve famous Chebychev polynomial problem [15],[4]. The last of the introduced methods is the so-called SADE technology. It is a simplified real-coded differential genetic algorithms that was developed as a specific recombination of a genetic algorithm and a differential evolution intended to solve problems on high-dimensional domains represented by the type 0 test function [6]. All these methods may aspire to
be a universal optimization algorithm. So, we have conducted a detailed numerical tests of all these four optimization methods for aforementioned optimization problems to examine their behavior and performance.

The paper is organized as follows. Section 2 provides brief description of each optimization task, while individual optimization algorithms are discussed in Section 3. Numerical results appear in Section 4. Summary on the performance of individual methods is presented in Section 5. For the sake of completeness, the parameter settings of algorithms is shown in the Appendix.

2 Optimization tasks

The optimization problems that are used as a set of test functions can be divided into two groups: the “test suite”, containing “artificial functions” and the “engineering problems”, which collect more (hopefully) practical optimization tasks. Specifically, these problems are:

- Test suite:
  - Chebychev trial polynomial problem,
  - Type 0 benchmark trial function.

- Engineering problems
  - Reinforced concrete beam layout,
  - Periodic unit cell problem.

The following section provides description of selected functions in more details.

2.1 Chebychev problem

Chebychev trial polynomial problem is one of the most famous optimization problems. Our goal is to find such coefficients of a polynomial constrained by the condition that the graph of the polynomial can be fitted into a specified area (see Fig. 1).

Thus, the optimized values are the parameters $a_i$ of a polynomial expression:

$$f(x) = \sum_{i=0}^{n} a_i x^i,$$  \hspace{1cm} (1)

and the value of objective function is determined as a sum of the areas, where the function graph exceeds a given boundary (hatched areas in Fig. 1).
2.2 Type 0 function

This trial optimization problem was proposed by the first two authors to examine the ability of the optimization method to find a single extreme of a function with a high number of parameters and growth of computational complexity with the problem dimension. For this reason, we used a function with a single extreme on the top of the high and narrow peak:

$$f(x) = y_0 \left( \frac{\pi}{2} - \arctan \frac{\|x - x_0\|}{r_0} \right),$$

(2)

where \(x\) is a vector of unknown variables, \(x_0\) is the point of the global extreme (the top of the peak) and \(y_0\) and \(r_0\) are parameters that influence the height or the width of the peak, respectively. Example of such a function on one dimensional domain is shown in Fig. 2.

Although this example function has only a single extreme, to find it even with a moderate precision is a non-trivial task for several reasons. First, in the very neighborhood of the extreme the function is so steep that even a futile change of the coordinates cause a large change of the function value; in such a case it is very difficult for the algorithm to determine what way leads to the top. Second,
the peak is located on a very narrow part of a domain and this disproportion increases very quickly with the problem dimension.

2.3 Reinforced concrete beam layout

An effort to create an optimal design of a steel-reinforced concrete structure is as old as the material itself. In present times an emphasis is put on this problem due to widespread use of RC structures in Civil Engineering. Frame structures are major part in this field with beams playing an important role as one of the basic building block of this construction system. An objective is to choose the best design from all possible configurations that can create the requested structure – in our case a continuous beam (see Fig. 3).

The total cost of the structure is used as a comparison factor. An advantage of the financial rating is its natural meaning to non-experts and easiness of constraints implementation. In our particular case, the objective function reads

\[ f(X) = V_c P_c + W_s P_s + \sum p f_i , \]  

(3)
where $V_c$ is the volume of concrete and $W_s$ is the weight of steel; $P_c$ and $P_s$ are the price of concrete per unit volume and steel per kilogram, respectively. From the mathematical point of view the penalty function $p_{f_i}$ is a distance between a solution and the feasible space, or equivalently, a price spent on the fulfillment of the condition $i$. Suppose that a variable $\Phi_i$ should not exceed a certain allowable limit $\Phi_{i,max}$. Then, the penalty $p_{f_i}$ assumes the form

$$p_{f_i} = \begin{cases} 0 & \text{if } \Phi_i \leq \Phi_{i,max}, \\ w_i \cdot (\Phi_i/\Phi_{i,max})^2 & \text{otherwise,} \end{cases}$$

(4)

where $w_i$ is the weight of the $i$-th constraint.

The constraints in this procedure deal with allowable strength and serviceability limits given by a chosen standard – in our case EUROCODE 2 (EC2) [2]. An interested reader can find implementation details for example in [9].

Consider a rectangular cross-section of a beam. There is the width $b$ and the
height \( h \) to optimize. Other variables in \( \mathbf{X} \) come from a model of a general RC beam which was presented in \([10]\): the beam is divided to three elements between supports with the same diameter of longitudinal reinforcement along the top surface and another one along the bottom. The differences are only in numbers of steel reinforcement bars in particular elements. The shear reinforcement is designed alike. There are three shear-dimension parts - each of them with different spacing of stirrups but the same diameter in the whole element. This partitioning reflects the characteristic distribution of internal forces and moments in frame structures, where the extremal values usually occur at three points—at mid-span and two end joints. The novelty of our approach is the assumption that length of parts may attain only the discrete values, in our case corresponding to 0.025 m precision. The same principle is used for the cross-section dimensions \( b \) and \( h \).

### 2.4 Periodic unit cell construction

The motivation for this problem comes from the analysis of unidirectional fiber composite materials. Such materials consist of a large number of fibers (which serve as a reinforcement) embedded in the matrix phase. The goal is to determine the overall behavior of such a material system provided that material properties of the matrix and fibers are known. It turns out that for this prediction, geometrical arrangement of fibers must be taken into account.

Unfortunately, the distribution of fibers in real composite materials is quite complex (see Fig. 4). To avoid such an obstacle, we attempt to replace a complicated microstructure with a large number of fibers by a certain periodic unit cell, which resembles the original material sample. More specifically, we describe the actual distribution of fibers by a suitable microstructural function and then determine the parameters of the periodic unit cell such that the difference between the function related to the periodic unit cell and function related to the original microstructure is minimized (for detailed discussion see \([16]\)).

The microstructural function used in the present approach is the second order intensity function \( K(r) \), which gives the number of further points expected to lie within a radial distance \( r \) of an arbitrary point divided by the number of particles (fibers) per unit area \((14)\)

\[
K(r) = \frac{A}{N^2} \sum_{k=1}^{N} I_k(r),
\]

where \( I_k(r) \) is the number of points within a circle with center at the particle \( k \) and radius \( r \), \( N \) is the total number of particles (fibers) in the sample and \( A \) is the sample area. An objective function related to this descriptor can be defined
as

$$F(x^N, H_1, H_2) = \sum_{i=1}^{N_m} \left( \frac{K_0(r_i) - K(r_i)}{\pi r_i^2} \right)^2,$$

(6)

where vector $x^N = \{x^1, y^1, \ldots, x^N, y^N\}$ stands for the position of particle centers of the periodic unit cell; $x^i$ and $y^i$ correspond to $x$ and $y$ coordinates of the $i$-th particle, $H_1$ and $H_2$ are the dimensions of the unit cell (see Fig. (5a)), $K_0(r_i)$ is the value of $K$ function corresponding to the original medium calculated in the point $r_i$ and $N_m$ is the number of points, in which both functions are evaluated. Throughout this study, we assume square periodic unit cell ($H_1 = H_2$) and determine its dimensions in such a way that the volume fraction of the fiber phase in the periodic unit cell is the same as in the original micrograph. An example of the objective function is shown in Fig. 5(b).

3 Applied methods

During last few years, we have developed and tested several evolutionary optimization methods that are based on both binary/integer and real-valued representation of searched variables. Each of them was primarily applied to one
Figure 5: (a) Geometry of a periodic unit cell, (b) An example of the objective function.

particular optimization problem of the four introduced above. These methods are (in order of appearance):

- Differential evolution, developed by R. Storn and K. Price [15],[4] to solve the Chebychev trial polynomial problem.

- Simplified differential genetic algorithm, developed by authors for research on high-dimensional problems [6],[5].
- Integer augmented simulated annealing - IASA (a combination of integer coded genetic algorithm and simulated annealing); it was primarily applied to the reinforced concrete beam layout optimization problem.

- Real-coded augmented simulated annealing - RASA (a combination of real-coded genetic algorithm by Michalewicz [13] and simulated annealing); it was developed for solving the periodic unit cell problem.

3.1 Differential evolution

The differential evolution was invented as the solution method for the Chebychev trial polynomial problem by R. Storn and K. Price in 1996. It operates directly on real valued chromosomes and uses the so called differential operator, which works with real numbers in natural manner and fulfills the same purpose as the cross-over operator in the standard genetic algorithm.

The differential operator has the sequential character: Let $CH_i(t)$ be the $i$-th chromosome of generation $t$

$$CH_i(t) = (ch_{i1}(t), ch_{i2}(t), ..., ch_{in}(t)), \quad (7)$$

where $n$ is the chromosome length (which means the number of variables of the fitness function in the real encoded case). Next, let $\Lambda$ be a subset of $\{1, 2, ..., n\}$. Then for each $j \in \Lambda$ holds

$$ch_{ij}(t+1) = ch_{ij}(t) + F_1 (ch_{pj}(t) - ch_{qj}(t)) + F_2 (ch_{bestj}(t) - ch_{ij}(t)), \quad (8)$$

and for each $j \notin \Lambda$ we get

$$ch_{ij}(t+1) = ch_{ij}(t), \quad (9)$$

where $ch_{pj}$ and $ch_{qj}$ are the $j$-th coordinates of two randomly chosen chromosomes and $ch_{bestj}$ is the $j$-th coordinate of the best chromosome in generation $t$. $F_1$ and $F_2$ are then coefficients usually taken from interval $(0, 1)$. Fig. 6 shows the geometrical meaning of this operator. The method can be understood as a stand-alone evolutionary method or it can be taken as a special case of the genetic algorithm. The algorithmic scheme is similar to the genetic algorithms but it is much simpler:

1. At the beginning an initial population is randomly created and the fitness function value is assigned to each individual.

2. For each chromosome in the population, its possible replacement is created using the differential operator as described above.

\footnote{The determination of $\Lambda$ is influenced by the parameter called \textit{crossrate} ($CR$), see [15].}
3. Each chromosome in the population has to be compared with its possible replacement and if an improvement occurs, it is replaced.

4. Steps 2 and 3 are repeated until some stopping criterion is reached.

As it could be seen, there are certain different features in contrary to the standard genetic algorithm, namely:

- the crossing-over is performed by applying the differential operator $\text{(8,9)}$,
- the selection operation like the roulette wheel, for example, is not performed, the individuals that are going to be affected by the differential operator, are chosen purely randomly,
- selection of individuals to survive is simplified to the mentioned fashion: each chromosome has its possible replacement and if an improvement occurs, it is replaced,
- the mutation operator is not introduced as authors of DE claim that the differential operator is able to replace both mutation and uniform crossover known from basic GAs.

Further details together with the source codes of DE can be obtained from web page [4].
3.2 Simplified atavistic differential evolution (SADE)

This method was proposed as an adaptation of the differential evolution in order to acquire an algorithm which will be able to solve optimization problems on real domains with a high number of variables. This algorithm combines features of the differential evolution with classical genetic algorithms. It uses the differential operator in the simplified form and an algorithmic scheme similar to the standard genetic algorithm.

The differential operator has been taken from the differential evolution in a simplified version for the same purpose as the cross-over is used in the standard genetic algorithm. This operator has a sequential fashion: Let (again) $CH_i(t)$ be the $i$-th chromosome in generation $t$,

$$CH_i(t) = (ch_{i1}(t), ch_{i2}(t), ..., ch_{in}(t)), \quad (10)$$

where $n$ is the number of variables of the fitness function. Then, the simplified differential operator can be written as

$$ch_{ij}(t + 1) = ch_{pj}(t) + CR(ch_{qj}(t) - ch_{rj}(t)), \quad (11)$$

where $ch_{pj}$, $ch_{qj}$ and $ch_{rj}$ are the $j$-th coordinates of three randomly chosen chromosomes and $CR$ is the so called cross-rate. Due to its simplicity this operator can be rewritten also in the vector form:

$$CH_i(t + 1) = CH_p(t) + CR(CH_q(t) - CH_r(t)). \quad (12)$$

Contrary to the differential evolution, this method uses the algorithmic scheme very similar to the standard genetic algorithm:

1. As the first step, the initial population is generated randomly and the fitness function value is assigned to all chromosomes in the population.

2. Several new chromosomes are created using the mutation operators - the mutation and the local mutation (number of them depends on a value $a$ of parameter called radioactivity, which gives the mutation probability).

3. Other new chromosomes are created using the simplified differential operator as was described above; the whole amount of chromosomes in the population doubles.

4. The fitness function values are assigned to all newly created chromosomes.

5. The selection operator is applied to the double-sized population, so the amount of individuals is decreased to its original value.

6. Steps 2-5 are repeated until some stopping criterion is reached.
Next, we introduce the description of the mentioned operators in detail:

**Mutation:** If a certain chromosome $CH_i(t)$ is chosen to be mutated, a new random chromosome $RP$ is generated and the mutated one $CH_k(t+1)$ is computed using the following relation:

$$CH_k(t+1) = CH_i(t) + MR(RP - CH_i(t)),$$

(13)

where $MR$ is a parameter called *mutation-rate*.

**Local mutation:** If a certain chromosome is chosen to be locally mutated, all its coordinates have to be altered by a random value from a given (usually very small) range.

**Selection:** This method uses modified tournament strategy to reduce the population size: two chromosomes are randomly chosen, compared and the worse of them is rejected, so the population size is decreased by 1; this step is repeated until the population size reaches its original size\(^2\).

Detailed description of the SADE method including source codes in C/C++ and the tests documentation for the high-dimensional problems can be obtained from the article [6] and on the web-page [5].

### 3.3 Real-valued augmented simulated annealing (RASA)

The augmented simulated annealing method is the combination of two stochastic optimization techniques – genetic algorithm and simulated annealing. It uses basic principles of genetic algorithms (selection, recombination by genetic operators), but controls replacement of parents by the Metropolis criterion (see Eq. (15)). This increases the robustness of the method, since we allow a worse child to replace its parent and thus escape from local minima, which is in contrary with DE methods described in Section 3.1.

The algorithmic scheme of the present implementation is summarized as follows.

1. Randomly generate an initial population and assign a fitness to each individual. Initial temperature is set to $T_0 = T_{max} = T_{frac}F_{avg}$ and minimal temperature is determined as $T_{min} = T_{frac\_min}F_{avg}$, where $F_{avg}$ is the average fitness value of the initial population.

2. Select an appropriate operator. Each operator is assigned a certain probability of selection.

\(^2\)Contrary to the classical tournament strategy this approach can ensure that the best chromosome will not be lost even if it was not chosen to any tournament.
3. Select an appropriate number of individuals (according to the operator) and generate possible replacements. To select individuals, we apply normalized geometric ranking scheme ([11]): The probability of selection of the $i$-th individual is given by

$$p_i = q'(1 - q)^{r-1}, \quad q' = \frac{q}{1 - (1 - q)^{\text{pop.size}}},$$

where $q$ is the probability of selecting the best individual in the population, $r$ is the rank of the $i$-th individual with respect to its fitness, and $\text{pop.size}$ is the population size.

4. Apply operators to selected parent(s) to obtain possible replacement(s).

4a. Look for an individual identical to possible replacement(s) in the population. If such individual(s) exists, no replacement is performed.

4b. Replace old individual if

$$u(0, 1) \leq e^{(F(I_{old}) - F(I_{new}))/T_t},$$

where $F(\cdot)$ is the fitness of a given individual, $T_t$ is the actual temperature and $u(\cdot, \cdot)$ is a random number with the uniform distribution on a given interval.

5. Steps 2–4 are performed until the number of successfully accepted individuals reaches $\text{success_max}$ or selected number of steps reaches $\text{counter_max}$.

6. Decrease temperature

$$T_{t+1} = T_{\text{mult}} T_t.$$  

If actual temperature $T_{t+1}$ is smaller than $T_{\text{min}}$, perform reannealing – i.e. perform step #1 for one half of the population.

7. Steps 2–6 are repeated until the termination condition is attained.

List of operators  The following set of real-valued operators, proposed in [13], was implemented. In the sequel, we will denote $L$ and $U$ as vectors of lower/upper bounds on unknown variables, $u(a, b)$ and $u[a, b]$ as a real or integer random variable with the uniform distribution on a closed interval $[a, b]$. Otherwise we use the same notation as employed in Sections 3.1 and 3.2.

**Uniform mutation:** Let $k = [1, n]$

$$\text{ch}_{ij}(t + 1) = \begin{cases} u(L_j, U_j), & \text{if } j = k \\ \text{ch}_{ij}(t), & \text{otherwise} \end{cases},$$

where $\text{ch}_{ij}(t + 1)$ is the new value of the $i$-th variable for the $j$-th individual at the $t+1$ iteration, and $u(\cdot, \cdot)$ is a random number with the uniform distribution on the interval $[L_j, U_j]$. If $j \neq k$, the old value is retained.

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Boundary mutation: Let \( k = u[1, n] \), \( p = u(0, 1) \) and set:

\[
ch_{ij}(t + 1) = \begin{cases} 
L_j, & \text{if } j = k, p < .5 \\
U_j, & \text{if } j = k, p \geq .5 \\
ch_{ij}(t), & \text{otherwise}
\end{cases}
\]  
(18)

Non-uniform mutation: Let \( k = [1, n] \), \( p = u(0, 1) \) and set:

\[
ch_{ij}(t + 1) = \begin{cases} 
ch_{ij}(t) + (L_j - ch_{ij}(t))f, & \text{if } j = k, p < .5 \\
ch_{ij}(t) + (U_j - ch_{ij}(t))f, & \text{if } j = k, p \geq .5 \\
ch_{ij}(t), & \text{otherwise}
\end{cases}
\]  
(19)

where \( f = u(0,1)(T_t/T_0)^b \) and \( b \) is the shape parameter.

Multi-non-uniform mutation: Apply non-uniform mutation to all variables of \( CH_i \).

Simple crossover: Let \( k = [1, n] \) and set:

\[
ch_{il}(t + 1) = \begin{cases} 
ch_{il}(t), & \text{if } l < k \\
ch_{jl}(t), & \text{otherwise}
\end{cases}
\]

\[
ch_{jl}(t + 1) = \begin{cases} 
ch_{jl}(t), & \text{if } l < k \\
ch_{il}(t), & \text{otherwise}
\end{cases}
\]

Simple arithmetic crossover: Let \( k = u[1, n] \), \( p = u(0, 1) \) and set:

\[
ch_{il}(t + 1) = \begin{cases} 
pch_{il}(t) + (1 - p)ch_{jl}(t), & \text{if } l = k \\
ch_{il}(t), & \text{otherwise}
\end{cases}
\]  
(20)

\[
ch_{jl}(t + 1) = \begin{cases} 
pch_{jl}(t) + (1 - p)ch_{il}(t), & \text{if } l = k \\
ch_{jl}(t), & \text{otherwise}
\end{cases}
\]  
(21)

Whole arithmetic crossover: Simple arithmetic crossover applied to all variables of \( CH_i \) and \( CH_j \).

Heuristic crossover: Let \( p = u(0,1) \), \( j = [1, n] \) and \( k = [1, n] \) such that \( j \neq k \) and set:

\[
CH_i(t + 1) = CH_i(t) + p(CH_j(t) - CH_k(t)).
\]  
(22)

If \( CH_i(t + 1) \) is not feasible then a new random number \( p \) is generated until the feasibility condition is met or the maximum number of heuristic crossover applications \( \text{num\_heu\_max} \) is exceeded.

3.4 Integer augmented simulated annealing.

Before presenting the actual optimization procedure we first introduce the mapping between representation and search spaces for individual design variables. Consider \( X = \{x_1, x_2, \ldots, x_n\} \) as a vector of \( n \) variables, integer or real numbers.
defined on a closed subset of an appropriate domain $D_i \subseteq \mathcal{N}, \mathcal{R}$. Further assume that each variable $x_i$ is represented with some required precision $p_i$, defined as the smallest unit the number $x_i$ can attain. Then, each variable $x_i$ can be transformed into an integer number $y_i \in \mathcal{N}$ as

$$y_i = \left\lfloor x_i p_i^{-1} \right\rfloor,$$

where $\lfloor x_i p_i^{-1} \rfloor$ denotes the integer part of $x_i p_i^{-1}$. An inverse transformation is given by

$$x_i = y_i p_i.$$

For instance, the real number 314.159 with precision $p_i = 0.001$ is transformed into the integer number 314159. An important aspect of this methodology is that the encoded number $y_i$ can be treated either as a binary string using bit-based operations or as a vector of integer numbers.

Integer augmented simulated annealing method is based on the same ideas as the previously mentioned RASA algorithm. This procedure effectively exploits the essentials of GAs (a population of chromosomes, rather than a single point in space is optimized) together with the basic concept of simulated annealing method guiding the search towards minimal energy states. To avoid well-known problems with binary coding the integer coding was used. Together with new operators such as differential crossover and a new mutation operator encouraging results were obtained.

The description of the algorithm does not substantially differ from the RASA algorithm, but for the sake of completeness all steps are briefly reviewed here.

1. Initial population consisting of OldSize individuals is created randomly and fitnesses are assigned to each individual. Starting and ending temperatures $T_{\text{min}}$ and $T_{\text{max}}$ are set by the user.

2. If a real random number $p = u(0, 1)$ is smaller than CrossoverProb the crossover is used, otherwise the mutation is applied. This step is repeated until the number NewSize of new solutions is obtained.

3. For each individual in a “new” population one “parent” from “old” part is selected. The “old” solution is replaced if

$$u(0, 1) \leq \frac{1}{1 + e^{(F(I_{\text{old}}) - F(I_{\text{new}}))/T_t}},$$

where $F(\cdot)$, $T_t$ and $u(\cdot, \cdot)$ have the same meaning as in the previous section. Equation (25) ensures the 50% probability of survival when comparing two solutions with the same fitness.

4. Steps 2–3 are performed until the number of successfully accepted individuals reaches SuccessMax or the selected number of steps reaches CounterMax.
5. The actual temperature is decreased by
\[
T_{t+1} = T_t \left( \frac{T_{\text{min}}}{T_{\text{max}}} \right) \left( \frac{\text{CounterMax}}{\text{TminAtCallsRate} \times \text{MaxCalls}} \right),
\]
(26)
where \(\text{TminAtCallsRate}\) determines a fraction of the maximum allowable number of function calls \(\text{MaxCalls}\) in which the minimum temperature \(T_{\text{min}}\) will occur. Reannealing step is represented here by setting actual temperature \(T_{t+1}\) equal to \(T_{\text{max}}\).

6. Steps 2–5 are repeated until the termination condition is attained.

In connection with the notation and principles mentioned in previous sections, integer operators within IASA algorithm have the following form:

**Differential crossover:** This operator is inspired by the DE. A new individual \(CH_j(t)\) is created from three randomly selected solutions \(CH_p(t), CH_q(t)\) and \(CH_r(t)\) according to
\[
CH_j(t+1) = CH_p(t) + u(0.0, CR)(CH_q(t) - CH_r(t)).
\]
(27)
Note that all vectors \(CH_i\) are integer numbers and also that the influence of the difference on the right-hand side randomly varies between zero and cross-rate \(CR\).

**Mutation:** Mutation operator is provided by modifying each variable in \(CH_j(t)\) to
\[
ch_{ij}(t+1) = ch_{ij}(t) + N(0, \left\lfloor \frac{ch_{ij}(t) - ch_{pj}(t)}{2} \right\rfloor + 1),
\]
(28)
where \(N(\cdot, \cdot)\) is a random integer number derived from the Gauss normal distribution and \(ch_{pj}(t)\) is the \(j\)-th variable of a randomly selected vector \(CH_p(t)\).

4 Test computations and results

Each of the methods introduced in the previous section was tested on all presented optimization problems. The methodology that has been used for our computations is based on the following criteria:

- For each problem and each method the computation was run 100 times to avoid an influence of random circumstances.
- For all cases, the number of successful runs (which can be traded as a probability of success or the reliability of the method) is presented.
• If the number of successful runs is non-zero, the average number of fitness calls of all successful runs is also presented.

Further details of individual function settings and methodology for results evaluation can be found in the next subsections.

4.1 Results for the Chebychev problem

The computations were performed for the Chebychev problem with a degree of the polynomial expression \( n = 8 \) (the T8 problem), which corresponds to the dimension of the problem 9. The computation was terminated if the algorithm reached a value of the objective function smaller than \( 10^{-5} \) or the number of function evaluations exceeded 100,000. Upper bounds on individual coefficients were set to 512, while lower bounds were equal to \(-512\). The results of individual algorithms are shown in Table 1 and Figure 7.

| Method                     | IASA | RASA | DE   | SADE |
|----------------------------|------|------|------|------|
| Successful runs            | 100  | 100  | 100  | 100  |
| Average number of fitness calls | 10342 | 47151 | 25910 | 24016 |

Table 1: Results for the Chebychev polynomial problem.

4.2 Results for the type 0 trial function

Test computations for the type 0 problem were performed for a wide set of problem dimensions, ranging from 1 to 200. The upper bound on each variable was set to 400, while the lower bound value was \(-400\). For each run, the position of the extreme was randomly generated within these bounds and the height of the peak \( y_0 \) was generated from the range 0–50. The parameter \( r_0 \) was set to 1. The computation was terminated when the value of the objective function was found with a precision greater than \( 10^{-3} \). The results are given in the form of the growth of computational complexity with respect to the problem dimension. For each dimension, the computation was run 100 times and the average number of fitness calls was recorded (see Fig. 8 and Table 2).

4.3 Results for the reinforced concrete beam layout problem

The basic parameters subjected to optimization were the beam width \( b \), which was assumed to take discrete values between 0.15 m and 0.45 m with the step 0.025 m and the beam height \( h \) ranging from 0.15 m to 0.85 m with the step
0.025 m. For each of the three parts of a beam, the diameter and the number of longitudinal reinforcing bars located at the bottom and the top of a beam, spacing and the diameter of stirrups and the length of the corresponding part were optimized. Lower bounds were selected for the sake of structural requirements; solutions exceeding upper bounds are considered to be irrelevant for the studied examples. However, from the optimization point of view, bounds can be easily adjusted to any reasonable value. The number of longitudinal bars was restricted to the range 0–15, the spacing of stirrups was assumed to vary from 0.05 m to 0.40 m with the 0.025 m step. The profiles of longitudinal bars were drawn from the list of 16 entries while for the stirrups, only 4 diameters were considered. This finally results in 18 independent variables. Note that the maximal number of longitudinal bars presents only the upper bound on the searched variable; the specific restrictions given by Codes of Practice are directly incorporated in the objective function. For more details see [9, 10]. The computation was terminated if an individual with price smaller than 573.5 CZK was found or the number of objective function calls exceeded 1,000,000. Table 3 stores the obtained results of different optimization algorithms, see also Figure 7.
4.4 Results for the periodic unit cell problem

Test computations for the periodic unit cell construction were performed for the 10-fiber unit cell (i.e. the dimension of the problem was 20). The computation was terminated if algorithm returned value smaller than $6 \times 10^{-5}$ or a number of function calls exceeded 400,000. Variables were constrained to the box $0 \leq x_i \leq H_1 \approx 25.8$ (see Section (2.4)). The required numbers of function are stored in Table 4 and displayed in Figure 7.

5 Conclusions

**Differential Evolution.** The Differential Evolution algorithm showed to be very efficient and robust for moderate-sized problems, but its performance for higher dimensions deteriorated. Moreover, the small number of parameters is another advantage of this method. However, the results suggest that the absence of mutation-type operator(s) is a weak point of the algorithm.

**Simplified Atavistic Differential Evolution.** The SADE algorithm was able to solve all problems of our test set with a high reliability and speed.
Although it needed larger number of function calls than other methods (see Table 5), the differences are only marginal and do not present any serious disadvantage. Another attractive feature of this method is relatively small number of parameters.

**Real-valued Augmented Simulated Annealing.** The RASA algorithm was successful for all presented problems; the average number of function calls was comparable to the other methods. The obvious disadvantage of this algorithm is a large number of parameters, which can results in a tedious tuning procedure. On the other hand, as follows from the Appendix, only two types of parameter settings were necessary – one for the continuous and one for discrete functions.

**Integer Augmented Simulated Annealing.** The IASA algorithm was the most successful and fastest method on problems with small dimensions. But on the problems with larger dimensions and with a higher number of local minima, the algorithm suffers from premature convergence and limited precision due to integer coding of variables. In addition, initial tuning of individual presents another drawback of this method.

Summary results are given in Table 5 to quantify the overall performance of individual methods. Each of the method is ranked primarily with respect to its success rate and secondary with respect to the average number of fitness calls. The sum then reveals the overall performance of the method.

**Final comments.** According to our opinion, several interesting conclusions and suggestions can be made from the presented results. Each of them is dis-
| Method                        | IASA | RASA | DE  | SADE |
|-------------------------------|------|------|-----|------|
| Successful runs              | 100  | 100  | 100 | 100  |
| Average number of fitness calls | 13641 | 12919 | 93464 | 55262 |

Table 4: Results for the periodic unit cell problem

| Method                        | IASA | RASA | DE  | SADE |
|-------------------------------|------|------|-----|------|
| Chebychev problem            | 1    | 4    | 3   | 2    |
| Type 0 test function         | 3    | 1    | 4*  | 2    |
| Concrete beam layout         | 1    | 2    | 4   | 3    |
| Periodic unit cell           | 3    | 1    | 4   | 2    |
| Σ                             | 8    | 8    | 14  | 9    |

Table 5: Overall performance of methods. (* : Not successful for all runs)

cussed in more detail.

- The performance and robustness of SADE method was distinguishably better than for DE algorithm. This supports an important role of a mutation operator(s) in the optimization process.

- Although algorithms were developed independently, all use some form of differential operator. This shows the remarkable performance of this operator for both real-valued and discrete optimization problems.

- The most successful methods, SADE and RASA algorithms, both employ a variant of “local mutation”. This operator seems to be extremely important for higher-dimensional type-0 functions, where these methods clearly outperform the others.

- Slightly better results of RASA method can be most probably attributed to the reannealing/restarting phase of the algorithm (a trivial but efficient tool for dealing with local minima) and to the search for an identical individual. The procedure for local minima assessment was implemented to SADE method (see [7, 8] for results), incorporation into IASA algorithm is under development.

- When comparing methods based on the discrete coding of variables with real-encoded ones it becomes clear that for continuous functions the methods with the real coding perform better. Nevertheless, after implementing new features, like those mentioned before, the performance is expected to be similar. On the other hand, the advantage of IASA algorithm is the possibility of its use for discrete combinatorial problems like the Traveling salesman problem.
Therefore, from the practical point of view, the SADE method seems to be the most flexible alternative due to its simplicity and small number of parameters.

Acknowledgement. We would like to thank an anonymous referee for his careful revision and comments that helped us to substantially improve the quality of the paper. The financial support for this work was provided by the Ministry of Education, projects No. MSM 210000003 and MSM 210000015 and by GAČR grant 103/97/K003.

Appendix

See Tables 6–9.

| Parameter | Chebychev, Type 0 | Beam | PUC |
|-----------|------------------|------|-----|
| pop_size  | $10 \times \text{dim}$ | $11 \times \text{dim}$ | $10 \times \text{dim}$ |
| $F_1 = F_2$ | 0.85 | 0.85 | 0.75 |
| $CR$ | 1 | 0.1 | 1 |

Table 6: Parameter settings for DE

| Parameter | Chebychev, Type 0 | Beam | PUC |
|-----------|------------------|------|-----|
| pop_size  | $10\times\text{dim}$ | $25\times\text{dim}$ | $10\times\text{dim}$ |
| $CR$ | 0.44 | 0.1 | 0.3 |
| radioactivity | 0 | 0.05 | 0.05 |
| $MR$ | 0.5 | 0.5 | 0.5 |

Table 7: Parameter settings for SADE

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| Parameter          | Beam      | Others    |
|--------------------|-----------|-----------|
| pop_size           | 64        | 32        |
| q                  | 0.04      | 0.04      |
| p_uni_mut          | 0.525     | 0.05      |
| p_bnd_mut          | 0.125     | 0.05      |
| p_nun_mut          | 0.125     | 0.05      |
| p_mnu_mut          | 0.125     | 0.05      |
| p_smp_crs          | 0.025     | 0.15      |
| p_sar_crs          | 0.025     | 0.15      |
| p_war_crs          | 0.025     | 0.15      |
| p_heu_crs          | 0.025     | 0.35      |
| b                  | 0.25      | 2.0       |
| T_frac             | $10^{-2}$ | $10^{-10}$|
| T_frac_min         | $10^{-4}$ | $10^{-14}$|
| T_mult             | 0.9       | 0.9       |
| num_success_max    | $10 \times \text{pop}_\text{size}$ | $10 \times \text{pop}_\text{size}$ |
| num_counter_max    | $50 \times \text{pop}_\text{size}$ | $50 \times \text{pop}_\text{size}$ |
| num_heu_max        | 20        | 20        |
| precision (step 4a)| see Section 4.3 | $10^{-4}$ |

Table 8: Parameter settings for RASA

| Parameter          | Chebychev | Type 0     | Beam    | PUC     |
|--------------------|-----------|------------|---------|---------|
| OldSize            | 80        | 900        | 180     | 200     |
| NewSize            | 5         | 600        | 250     | 100     |
| T_max              | $10^{-5}$ | $10^{-5}$  | $10^{-4}$ | $10^{-1}$ |
| T_min              | $10^{-7}$ | $10^{-10}$ | $10^{-5}$ | $10^{-5}$ |
| SuccessMax         | 1000      | 1000       | 1000    | 1000    |
| CounterMax         | 5000      | 5000       | 5000    | 5000    |
| TminAtCallsRate    | 19%       | 100%       | 25%     | 20%     |
| CrossoverProb      | 97%       | 92%        | 60%     | 90%     |
| CR                 | 0.5       | 0.6        | 1.3     | 1.0     |

Table 9: Parameter settings for IASA

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