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ON ACCELERATION OF EVOLUTIONARY ALGORITHMS TAKING ADVANTAGE OF A POSTERIORI ERROR ANALYSIS

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Abstract. A variety of important engineering and scientific tasks may be formulated as non-linear, constrained optimization problems. Their solution often demands high computational power. It may be reached by means of appropriate hardware, software or algorithm improvements. The Evolutionary Algorithms (EA) approach to solution of such problems is considered here. The EA are rather slow methods; however, the main advantage of their application is observed in the case of non-convex problems. Particularly high efficiency is demanded in the case of solving large optimization problems. Examples of such problems in engineering include analysis of residual stresses in railroad rails and vehicle wheels, as well as the Physically Based Approximation (PBA) approach to smoothing experimental and/or numerical data. Having in mind such analysis in the future, we focus our current research on the significant EA efficiency increase. Acceleration of the EA is understood here, first of all, as decreasing the total computational time required to solve an optimization problem. Such acceleration may be obtained in various ways. There are at least two gains from the EA acceleration, namely i) saving computational time, and ii) opening a possibility of solving larger optimization problems, than it would be possible with the standard EA. In our recent research we have preliminarily proposed several new speed-up techniques based on simple concepts. In this paper we mainly develop acceleration techniques based on simultaneous solutions averaging well supported by a non-standard application of parallel calculations, and a posteriori solution error analysis. The knowledge about the solution error is used to EA acceleration by means of appropriately modified standard evolutionary operators like selection, crossover, and mutation. Efficiency of the proposed techniques is evaluated using several benchmark tests. These tests

indicate significant speed-up of the involved optimization process. Further concepts and improvements are also currently being developed and tested.

Keywords: Evolutionary algorithms, calculations efficiency increase, a posteriori error estimation, constrained optimization

Keywords: 68T99, 68W10, 68W15, 65B99, 65G99, 65K10

1 INTRODUCTION

1.1 Research Motivation

A variety of important engineering and scientific tasks may be formulated as non-linear constrained optimization problems. Their solution often demands high computational power. It may be reached by means od appropriate hardware, software or algorithm improvements. The Evolutionary Algorithms (EA) approach to solution of such problems is considered here. The EA are rather slow methods, however, the main advantage of their application is observed in the case of non-convex problems. Particularly high efficiency is demanded in the case of solving large optimization problems. Let us mention two of such problems here, namely railroad transport safety and experimental data smoothing. Evaluation of railway transport safety requires determination of service life and fracture mechanism both in railroad rails and vehicle wheels. Results of the extensive research problem carried out for the US DOT [11] clearly show that cracks nucleation and their development are mainly driven by residual tensile stress, the axial one in rails and the hoop one in wheels. Residual stresses analysis may be done using theoretical [12] and/or experimental approach [11]. Various experimental methods (like strain gauge techniques, neutronography, moire methods) may be applied in order to obtain the necessary data. Moreover, in a variety of experiments (not only referring to residual stresses) handling and smoothing of experimental data is needed. High quality final results may be obtained when using the Physically Based Approximation (PBA) method [6].

The PBA simultaneously uses all information available for the considered problem, in a way dependent on its credibility. All experimental data obtained by means of various measurement techniques may be used in the analysis at the same time then, taking into account their statistics, as well as our theoretical and/or heuristic knowledge about the problem in question. In this way smoothing of experimental data is done rather on physical than on mathematical basis. The same approach may be also applied to a discrete data obtained from any rough numerical solution of the boundary value problem.

Both residual stresses analysis (theoretical approach) and the PBA method, like many other problems, are formulated as non-linear constrained optimization ones [6, 12]. Their solution may be sought either by means of the deterministic

or by the stochastic methods, including the Artificial Intelligence (AI) approach, and in particular the EA methods [5]. In the case of the convex problems the deterministic methods (like the feasible directions or penalty methods) are faster, but their efficiency is significantly lower for problems of the other type. On the other hand, the speed of the EA, though relatively low, is not much diminished for the non-convex optimization problems. Several preliminary tests [13] indicate a reasonable hope that in the case of such problems the EA, especially when accelerated, may turn out to be faster than the deterministic methods. The considered problems are formulated as optimization of functionals, where a function $u(\mathbf{x}), \mathbf{x} \in \mathcal{R}^N$ is sought, usually in the discrete form of the vector $\mathbf{u} = \{u_i\}$ consisting of nodal values $u_i, i = 1, 2, 3, \ldots, n$. These are defined on a mesh that may be formed by arbitrarily distributed nodes. Here N is the dimension of the physical space (usually 1D, 2D or 3D), and n is a number of decision variables. In such case, usually a large number of decision variables is sought, so high efficiency of solving algorithm is strongly demanded.

1.2 Related Work

Having in mind the features of the optimization problems mentioned above, our research is focused, first of all, on efficiency increase of the EA. In general, it may be obtained by development of new algorithms, software improvements, and/or hardware acceleration (e.g. distribution and parallelization of calculations on multiprocessor systems, using GPUs or FPGA devices). Our research is mainly concentrated now on the first approach. Distributed and parallel computations are also used here, but in a non-standard way, as a support for new acceleration techniques.

Significant algorithmic acceleration of the optimization process may be obtained in several ways including introduction of new evolutionary operators, e.g. cloning or gradient mutation [4, 5], developing hybrid methods [4] like combinations of stochastic and deterministic approaches, application of standard parallelization and distribution of calculations [5, 7, 8], proceeded by a choice of the most efficient combination of particular variants of selection, crossover and mutation operators, and evaluation of the best values of the EA parameters [13].

In our recent research [13] we have preliminarily proposed several new acceleration techniques based on simple concepts such as step by step mesh refinement, a posteriori smoothing and balancing of rough results, solution averaging and a posteriori solution error analysis, supported by non-standard use of parallel and distributed calculations carried on a cluster. In this paper we mainly develop techniques based on using knowledge about a posteriori solution error in order to speed-up the optimization process involved. In the future, the existing, well known acceleration techniques, especially hybrid approach and standard parallelization of calculations, will also be combined with our accelerated EA. Moreover, other improvements of the EA, e.g. [10], will be analysed.

In the case of deterministic methods, the error estimation is well developed and widely used [1, 2, 9]. Our objective is to develop relevant efficient error estimation

technique for the EA, taking into account some concepts from the deterministic approach and some new ones. We may verify such approach using e.g. the residual stresses analysis and problems resulting from application of the PBA method. These are large optimization problems, that were successfully solved so far, however, only by means of the deterministic methods (e.g. feasible directions methods) [12, 15]. Use of the EA for the same problems provides means for examination of their efficiency.

1.3 Scientific Objective

The general objective of our research carried out in the recent years is development of highly efficient EA approach for solving large, non-linear, constrained optimization problems. Essential acceleration of the classic EA solution process is based on various simple concepts, some of them already preliminarily discussed [13].

In this paper, however, we mainly focus our attention on using our knowledge about the magnitude and distribution of a posteriori solution error for this purpose. In order to reach this goal we want to find possibly the most efficient modifications of the standard operators such as selection, crossover, and mutation.

2 PROBLEM SOLUTION DESCRIPTION

2.1 Optimization Problem Formulation

Considered is a wide class of large, non-linear constrained optimization problems, posed as follows:

Find a function $u = u(\mathbf{x})$, that yields the stationary point of the functional $\Phi(u)$ satisfying the equality

$$\mathbf{A}(u) = 0 \tag{1}$$

and inequality constraints

$$\mathbf{B}(u) \leq 0. \tag{2}$$

The PBA approach [6] is a specific example of the above general formulation. In the PBA all information available about the considered problem may be used. The functional is defined as the following combination:

$$\Phi = \lambda \overline{\Phi}^E + (1-\lambda)\overline{\Phi}^T, \quad \lambda \in [0,1]\,. \tag{3}$$

Here, $\overline{\Phi}^E(u)$ and $\overline{\Phi}^T(u)$ are the experimental and theoretical parts of the functional, scaled to be dimensionless quantities, u is the required solution, and $\lambda \in [0,1]$ is a dimensionless scalar weighting factor. Equality constraints $\mathbf{A}(u) = 0$ are mostly of theoretical nature, while inequality constraints $\mathbf{B}(u) \leq e$ are usually of experimental nature (e is an admissible tolerance, e.g. two standard deviations).

2.2 Error Analysis

Contemporary solutions of various engineering and scientific problems need reliable error analysis. Nowadays, in the case of the deterministic solution approach methods of such analysis and error estimation are well developed (e.g. [1, 2, 9]) especially for linear problems. These methods are mainly based on their ability to determine a high quality reference solution $\overline{u}$. Instead of the true local solution error

$$e = \widetilde{u} - u \tag{4}$$

we consider an estimated error

$$\overline{e} = \widetilde{u} - \overline{u} \tag{5}$$

where $u, \widetilde{u}, \overline{u}$ are functions (or vectors when discretized) representing the true, a rough, and an improved (used as the reference) solutions, respectively. Moreover, in the case of the local formulation of boundary value (b.v.) problems, involving the differential equation $Lu = g$ in the domain $\Omega \subseteq \mathcal{R}^N$, the residual error

$$\widetilde{r} = L\widetilde{u} - g \quad and \quad \overline{r} = L\overline{u} - g \tag{6}$$

could be used.

These local errors may be also used in order to evaluate the global ones. The following global error norms $\eta = \|\overline{e}\|$ are mostly applied:

$$\text{averaged mean square } \eta_{L2} = \sqrt{\frac{1}{\Omega}\int_{\Omega} \overline{e}^2 \, \mathrm{d}\Omega}, \tag{7}$$

$$\text{energy } \eta_E = \sqrt{b(\overline{e}, \overline{e})}, \tag{8}$$

$$\text{maximum } \eta_M = \max_{\Omega} |\overline{e}| \,, \tag{9}$$

where $b(\overline{e}, \overline{e})$ is the bilinear form dependent on the problem type considered. Integration is performed either over the whole domain Ω or over a chosen subdomain only (e.g. finite element).

The quality of the error estimation depends on the quality of the reference solution used. There are several types of the error estimators, like hierarchic (p – type, h – type or mixed), smoothing (zz), and residual (explicit, implicit) ones. So far the highest quality reference solutions have been obtained by means of the higher order ($2p$ – approximation order for p^{th} order operators) meshless finite difference method applied to the hierarchic type estimator, though a relevant version of finite element method could be also used [9].

However, all the above-mentioned considerations about the a posteriori error estimation are related to the deterministic type solutions of b.v. problems. In the case of the EA solutions such error analysis cannot be applied in exactly the same way. Though the similar general concept of a posteriori error analysis may also be used then, the reference solutions should be found in another way, taking advantage

of the EA specific features. The particular ways of generating reference solutions will be proposed in the next chapter.

In the case of benchmark problems, when the exact solution is known, the quality of all error estimators may be evaluated by means of the effectivity index

$$i = 1 + \frac{|\|e\| - \|\bar{e}\||}{\|e\|}, \tag{10}$$

that compares the true $\|e\|$ and estimated $\|\bar{e}\|$ error norms.

3 APPLIED ALGORITHMS AND METHODS

The EA form a wide group of AI methods, such as the Genetic Algorithms (GA), Genetic Programming, Evolutionary Strategies, and others [5]. In this paper the EA are precisely understood as the GA with decimal (floating-point) chromosomes. The standard EA include three basic operators: selection, crossover, and mutation [4, 5]. So far many various operators have been developed. In our research we analyse and use only few standard, popular operators.

The EA are stochastic methods; therefore, the best chromosomes obtained from various independent populations may differ from each other. For convex optimization problems a weighted averaged solution is expected to have a better chance to be closer to the exact one than any of particular solutions contributing to such average. Moreover, it may also be used as the reference solution for a posteriori error estimation. Knowledge about the magnitude and distribution of errors may be used in various ways in order to intensify calculations in large error zones.

3.1 Generation of Reference Solutions in the EA Method – Formulation

In the EA, high quality reference solutions may be obtained by weighted averaging of chromosomes followed by a data smoothing process. However, averaging may be successfully applied when there is only one maximum (minimum) in the considered domain. Thus, in the case of non-convex problems, the whole domain ought to be divided first into subdomains with only one maximum (minimum) in each. Some concepts of such domain division using the EA and data clustering algorithms [3] have been preliminarily tested. However, they are not discussed in this paper. In the future, a general approach for the generation of the EA reference solutions for non-convex optimization problems will be considered.

There are many ways how to average the EA results (chromosomes). For example, the following may be averaged:

1. all available data,
2. all data within each population,
3. all $n\,\%$ of the best chromosomes taken together from each independent population,

4. collection of such chromosomes, that each one of them presents the best solution in its population.

For averaging the standard arithmetic average, as well as a weighted (e.g. based on the fitness function values or on errors) one may be used. Moreover, the quality of a reference solution may be raised by means of an appropriate smoothing method. Assuming e.g. the case 4 for generation of reference solutions in the EA, the following procedure may be applied:

Use m independent populations simultaneously. After every a priori defined number of iterations, generate a new population of m solutions – find the best chromosomes taken from independent populations:

$$\left[u_1^1, u_2^1, u_3^1, \ldots, u_n^1\right], \left[u_1^2, u_2^2, u_3^2, \ldots, u_n^2\right], \ldots, \left[u_1^m, u_2^m, u_3^m, \ldots, u_n^m\right], \tag{11}$$

where:

- n – the number of decision variables,
- m – the number of independent solutions,
- u_k^i – the k^{th} decision variable from the i^{th} solution, $i = 1, 2, \ldots, m$, and $k = 1, 2, \ldots, n$.

Next, calculate the weighted average solution of these results over the whole new population:

$$\left[\overline{u}_1, \overline{u}_2, \overline{u}_3, \ldots, \overline{u}_n\right], \tag{12}$$

where:

- $\overline{u}_k = \frac{1}{W}\sum_{i=1}^{m} w_i u_k^i, \quad W = \sum_{i=1}^{m} w_i, \quad k = 1, 2, \ldots, n,$
- w_i – weighting factor for the i^{th} solution, w_i may be assumed e.g. as the fitness function value for each chromosome.

In the space of chromosomes each of them represents a point, while $[\overline{u}_1, \overline{u}_2, \ldots, \overline{u}_n]$ may be interpreted as a weighted center of gravity of the set of all m points (chromosomes). High quality postprocessing (higher order smoothing) may be applied next to this averaged discrete solution, e.g., by means of the Moving Weighted Least Squares [6, 14] approximation or the PBA [6, 14] approach.

Such averaged and smoothed solution may be used as a reference in order to estimate a posteriori error of each chromosome, and to calculate error maps in all populations:

$$E_j = \left[e_1^j, e_2^j, e_3^j, \ldots, e_n^j\right], \quad e_k^j = \left|u_k^j - \overline{u}_k\right|, \quad j = 1, 2, \ldots, J, \tag{13}$$

where J – number of all chromosomes in all populations (j – index of chromosome).

3.2 Research Strategy for A Posteriori Error Analysis

The following research strategy of a posteriori error analysis has been applied:

- use of the true solution error first, in order to find the most efficient modifications of the standard EA operators (selection, crossover, mutation) with influence of the quality and precision of the error evaluation excluded; this may be done when dealing with benchmark problems where the exact solutions are known,
- use of the best operator modifications found above, and repetition of the same analysis. However, this time the true solution error is replaced by its a posteriori evaluation based e.g. on the smoothed averaged solution assumed as the reference one.

3.3 Use of A Posteriori Error Analysis Results for Modification of the Standard EA Operators

3.3.1 Selection

The standard selection operator uses the fitness function f value to eliminate weak chromosomes. Beside this standard criterion, another one, based on solution error value e, may be also introduced. It may be used in several ways. Possible approaches include:

- alternate use of both criteria,
- choice of n chromosomes providing the smallest errors out of $m > n$ chromosomes with the best fitness function values,
- one resultant criterion composed of the normalized fitness function F and global error H such as

$$\text{find } \max(F^2 + H^{-2})^q, \quad q > 0. \tag{14}$$

  This approach may be applied to selection operators of any type.

3.3.2 Mutation

Knowledge about the distribution and magnitude of solution errors may influence the mutation probability. Increased probability may be proposed:

- in regions where error is larger than e.g. 1/2 maximum error (Figure 1 a)), or
- following the error level function, e.g. (Figure 1 b)–c)), where ε is local error value.

  Mutation probability may be increased in any mutation operator.

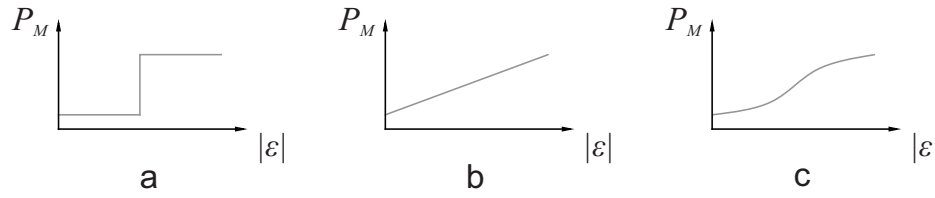

Figure 1. Function of the error level: a) Step function, b) Linear function, c) Any growing function

3.3.3 Crossover

Similarly to modification of mutation probability, also crossover probability may be increased in large-error zones. However, this time also other improvements are done in particular types of crossover operators. For instance, modification of heuristic crossover is presented here.

The standard heuristic crossover generates one offspring $\mathbf{Z}$ from two parents $\mathbf{X}$, and $\mathbf{Y}$ in the following way:

$$\text{If } f(\mathbf{X}) > f(\mathbf{Y}) : \mathbf{Z} = a(\mathbf{X} - \mathbf{Y}) + \mathbf{X}, \quad a \in [0, 1]\,, \tag{15}$$

where f – fitness function.

In such case, the new chromosome is created in the direction of better parent. The following modifications are applied:

- crossover in the direction of the best of three chromosomes: two parents and mean chromosome (averaged and smoothed),
- increasing value of the parameter a in large-error zones.

Other types of crossover operators, especially more complex ones, will also be analysed and modified in order to take advantage of the knowledge about the solution errors.

3.4 Other Chosen Acceleration Techniques

Acceleration may also be achieved by collecting the best chromosomes, taken from all populations, and generating new population of "representatives" (this may be done in several ways). New representatives are gathered constantly in a period of time.

The weighted averaged and smoothed solution is expected to have a better chance to be closer to the exact one than any of particular solutions contributing to such average. In order to speed up the optimization process a cloning strategy may also be used. Cloning may be applied to the weighted mean chromosome and/or to the best representatives. For instance, 20 % chromosomes in each population may be replaced by clones.

The possibility of carrying out efficient computations in multiple independent populations, applying solution error estimation and other related techniques is provided by multiprocessor systems and special software using parallel and distributed paradigm.

3.5 Hardware and Software Used

The results of calculations presented in this paper were obtained on a standard multiprocessor system with distributed memory (cluster). The authors prepared their own implementation of the EA and proposed acceleration techniques. Software was written using C++ (with standard libraries) and MPI library for parallel and distributed calculations. For pseudo-number generation the Mersenne-Twister algorithm was used.

4 RESULTS

Efficiency of the proposed techniques has been evaluated using several, carefully chosen benchmark problems. This chapter presents formulation of these problems and typical results obtained from their analysis.

The convergence rate of the standard EA is strongly dependent on the type of the evolutionary operators (selection, crossover, mutation) used, and the EA parameters values chosen for them (e.g. probability, population size). It is also worth mentioning here that we may deal with various variants, and combinations of the standard operators when switching from the binary representation of numbers to the decimal ones. In our recent work [13] we have preliminarily analysed several standard operators using six various, demanding benchmark tests, including problems formulated below. The following operators were considered: the ranking and tournament selection, arithmetic and heuristic crossover, uniform, non-uniform and border mutation, as well as various combinations of them. According to the results obtained, combination of the ranking selection, heuristic crossover, and non-uniform mutation was considered. These operators have been used therefore, in further research on investigation of the EA acceleration techniques.

This paper presents selected typical results of the tests executed in order to find the best acceleration of the convergence process. Variants and parameters of the a posteriori solution error estimation technique, as well as the methods related to non-standard distributed and parallel calculations were analysed. These results are compared with those obtained by using other acceleration techniques proposed in [13].

In order to evaluate the proposed acceleration techniques a speed-up factor S was defined [13] in four variants corresponding to four types of results presentation (Figure 2)

$$S_{e,n} = \left.\frac{n_{ref}}{n}\right|_{e=const}, \quad S_{F,n} = \left.\frac{n_{ref}}{n}\right|_{F=const}, \tag{16}$$

$$S_{e,t} = \left.\frac{t_{ref}}{t}\right|_{e=const}, \quad S_{F,t} = \left.\frac{t_{ref}}{t}\right|_{F=const}. \tag{17}$$

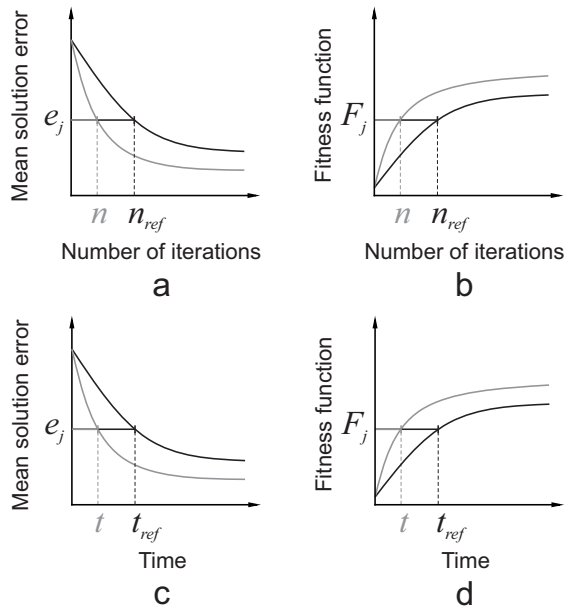

Figure 2. Definitions of speed-up factor: a) $S_{e,n}$, b) $S_{F,n}$, c) $S_{e,t}$, d) $S_{F,t}$

4.1 Formulation of the Benchmark Problems

Residual stresses analysis in a bar subject to cyclic bending is considered. Elastic – perfectly plastic material and rectangular cross-section of the bar are assumed. Main features of this benchmark include:

- formulation as constrained optimization problem,
- possibility of 1D or 2D analysis (bar model, and plate model),
- any number of decision variables may be chosen,
- the exact solution is known (Figure 3 c)).

This benchmark, formulated as a constrained optimization problem [15], has already been solved by means of deterministic methods [15]. However, the objective of the tests presented here is a comparison of various variants of the accelerated EA with the standard one, rather than with the deterministic methods. However, such comparison will also be done in future, especially for numerical solutions of complex optimization problems, where the exact results are not known.

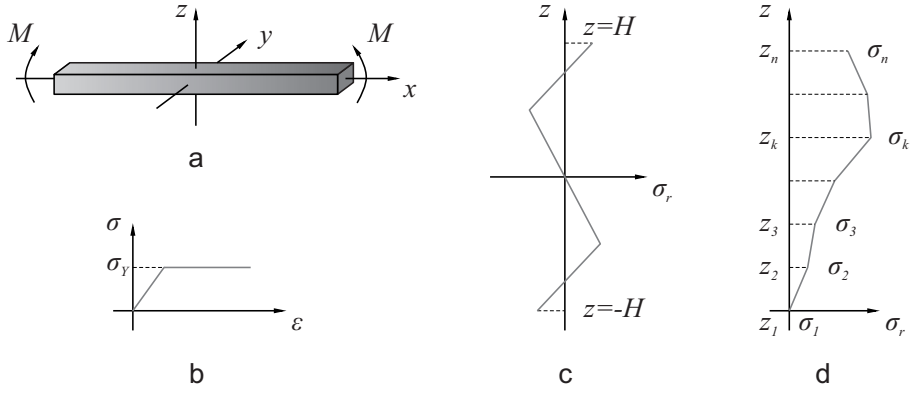

Figure 3. Benchmark problem: a) bending model, b) elastic-perfectly plastic material, c) the exact 1D solution, d) discrete 1D solution

4.1.1 1D Model – Formulation of the Optimization Problem

Find stresses $\sigma = \sigma(z)$ satisfying minimum of the total complementary energy [15]

$$\min_{\sigma} \int_0^H \sigma^2 \, \mathrm{d}z \tag{18}$$

and constraints

- global self-equilibrium equation

$$M = \int_0^H \sigma z \, \mathrm{d}z = 0, \tag{19}$$

- yield condition for total stresses

$$|\sigma + \sigma^e| \leq \sigma_Y, \tag{20}$$

where σ_Y – yield stress (plastic limit), σ^e – purely elastic solution of the problem.

Due to symmetry, only half of the cross-section is considered. After discretization, where the searched normal stress $\sigma = \sigma(z)$ is replaced by the piecewise linear function (Figure 3 d)) spanned over the nodal values σ_i, the following formulation is obtained:

Find stresses $\sigma_1, \sigma_2, \ldots, \sigma_n$ satisfying

$$\min_{\sigma_1,\sigma_2,\ldots,\sigma_{n-1}} \left(\sum_{k=1}^{n-1} \sigma_k^2 + \frac{1}{2}\sigma_n^2 \right), \quad \sigma_n = -\frac{2}{z_n} \sum_{k=1}^{n-1} \sigma_k z_k, \tag{21}$$

and inequality constraints

$$-\sigma_Y \leq \sigma_k + \sigma_k^e \leq \sigma_Y, \quad k = 1, 2, \ldots, n. \tag{22}$$

Though the simplest rectangle method for numerical integration is used in the above formulation, we used other methods in real calculations, giving the exact results for linear functions.

4.1.2 2D Model – Formulation and Discretization

In 2D model the fitness function (total complementary energy) is defined as follows:

$$I = \int_{-b/2}^{b/2} \int_{-H}^{H} \sigma^2 \, \mathrm{d}z \, \mathrm{d}y \approx \frac{h^2}{9} \left(\sum_{k=1}^{n} \sigma_k^2 \alpha_k \right), \tag{23}$$

where α_k are Simpson integration coefficients.

The sought solution has to satisfy the following constraints:

1. Global self-equilibrium equation

$$M = \int_{-b/2}^{b/2} \int_{-H}^{H} \sigma z \, \mathrm{d}z \, \mathrm{d}y \approx \frac{h^2}{9} \left(\sum_{k=1}^{n-1} \sigma_k z_k \alpha_k + \sigma_n z_n \alpha_n \right) = 0 \rightarrow \tag{24}$$

$$\sigma_n = -\left(z_n \alpha_n\right)^{-1} \sum_{k=1}^{n-1} \sigma_k z_k \alpha_k. \tag{25}$$

2. Yield condition for the total stresses

$$-\sigma_Y \leq \sigma_k + \sigma_k^e \leq \sigma_Y, \quad k = 1, 2, \ldots, n. \tag{26}$$

4.2 Typical Results

Using solutions of these two benchmark tasks several problems were investigated, briefly summarized in Table 1.

Test No.	Bench. No.	Test objective
1	1	Investigation of the best modifications of the mutation and crossover operators taking advantage of the knowledge about a posteriori solution error
2	1	Analysis of the impact of the number of iterations between subsequent refreshments of the reference solution
3	1	Comparison of various additional acceleration techniques related to the error estimation
4	1, 2	Analysis of the impact of the number of independent populations on the error estimation quality and the optimization process
5	1	Comparison of the results of all proposed acceleration techniques: mesh refinement, smoothing and balancing, error estimation

Table 1. Typical results – contents

Tests No. 1–4 present the results averaged over 10 independent solutions. Results in test No. 5 are averaged over 100 processes.

4.2.1 Modifications of the Mutation and Crossover Operators Based on a Posteriori Solution Error Analysis

The following approaches are chosen and compared:

- the standard algorithm (probability of mutation: 0.1, probability of crossover: 0.9),
- M – modification of mutation (probability of mutation is increased 5-times in regions, where the error is larger than 50 % of the maximum error in the chromosome examined),
- C1 – modification of the heuristic crossover type 1 (random value of the parameter a is increased twice in regions, where the error is larger than 50 % of its maximum value in the chromosome),
- C2 – modification of heuristic crossover type 2 (modification of direction of the crossover),
- combinations of the above two ones.

Figure 4 presents results obtained when using both the exact error maps (Figure 4 a)), and estimated errors (Figure 4 b)).

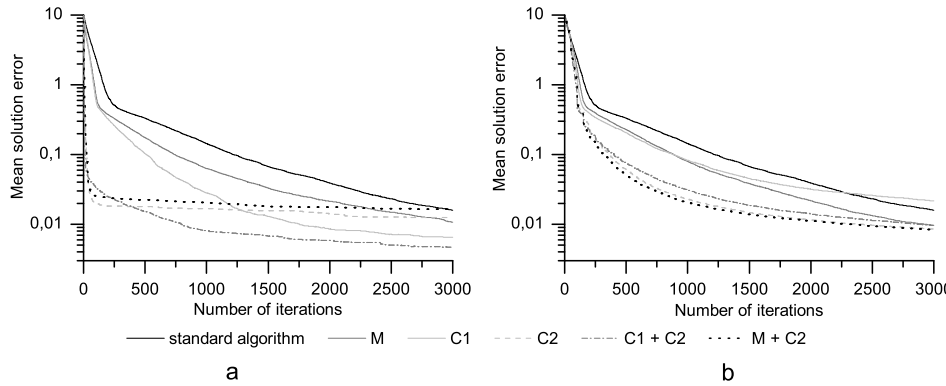

Figure 4. Comparison of various modifications of the mutation and crossover operators due to: a) the exact errors, b) estimated errors (estimation based on the best 12 independent solutions)

Each of the modifications proposed improves the convergence process. However, some of them do this only in the first stage of iterations. In the case of the estimated errors, the best results were obtained for the M + C2 case (Figure 4 b)). However, the same algorithm when using the exact errors (Figure 4 a)), very quickly reaches

certain, low level of errors, but later on it does not give further improvement of the solution process. The same situation occurs in the case of algorithm with C2 modification only; but if we join C1 with C2 we get the best results (for larger number of iterations) in the case of the exact errors, and not much worse than the best ones in the case of estimated errors.

4.2.2 Impact of the Number of Iterations Between Subsequent Refreshments of the Reference Solution

The objective of this test was to investigate the influence of refreshment of the reference solution on the convergence rate. The correlation found is simple – the more frequently the mean chromosome is updated and sent to all populations, the better results are obtained. However, the differences between results obtained for processes communicating each 5 to 25 iterations are not significant; therefore, 25 seems to be the most reasonable number. The results are shown as a function of time (Figure 5). Each process was executed for the same total number of iterations.

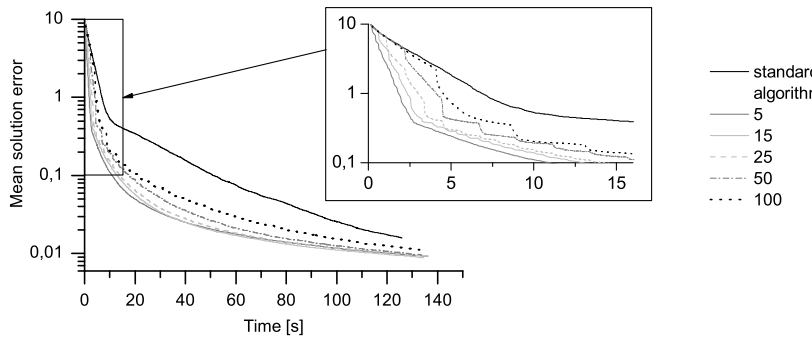

Figure 5. Impact of the number of iterations between subsequent refreshments of the reference solution

4.2.3 Comparison of Various Acceleration Techniques Related to the Error Estimation

Solution error estimation and operators modifications are compared here (Figure 6) with the other techniques supported by the parallel and distributed calculations. The best results were obtained for a simple technique, namely cloning of the averaged solution in all populations (cloning, and replacing 20 % of the worst chromosomes in each population by the mean one). The early stage of this research allows for the following preliminary conclusion: the standard operators working on improved populations give better results than modified operators. However, many other modifications of operators are still possible. Some of them will be investigated in our further research.

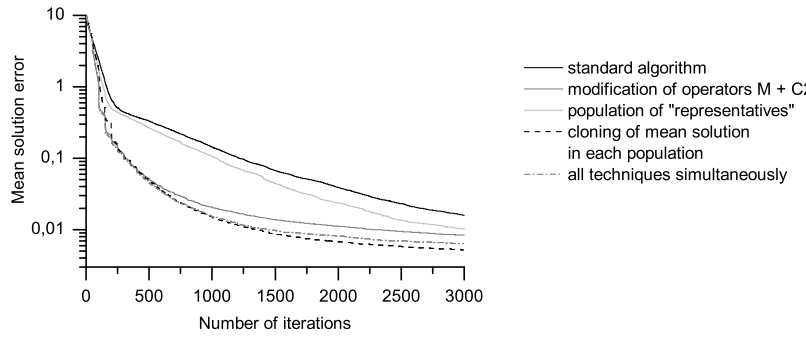

Figure 6. Comparison of various acceleration techniques related to the a posteriori error estimation

4.2.4 Impact of the Number of Independent Populations on the Error Estimation Quality and the Optimization Process

The impact of the number of independent populations involved in calculations on the convergence process is presented (for each population one processor is allocated, the standard parallelization, in which more than one processor is used for one population is also possible). This number influences the quality of the averaged solution used for the true solution error estimation. Besides, the results obtained in two benchmark problems are compared (Figure 7 a)–b)). Conclusions resulting from both benchmarks are similar. In the case of benchmark 2 the convergence of the fitness function is also presented (Figure 8). It is shown clearly how the analysed number of populations influences the optimization process. This is because of better quality of the reference solution resulting in better solution error estimation. The results are compared to those obtained in the process with the exact error map (uppermost left curve).

4.2.5 Results and Comparison of all Proposed Acceleration Techniques: Mesh Refinement, Smoothing and Balancing, Error Estimation

All speed-up techniques mentioned in this paper may be used simultaneously (this has already been shown in Figure 6). Such algorithm, using the solution error estimation, the additional population of representatives, and cloning of averaged chromosomes, was compared to other recently developed acceleration algorithms [13], such as mesh refinement, smoothing and balancing, and some combinations of them (Figure 9 a)). The variable speed-up factor corresponding to these results is shown in Figure 9 b).

The algorithm using the solution error estimation reached the acceleration factor about 2–4 times. With additional smoothing, the speed factor was about 7.5. This is not much when compared to mesh refinement. However, it is worth noticing that

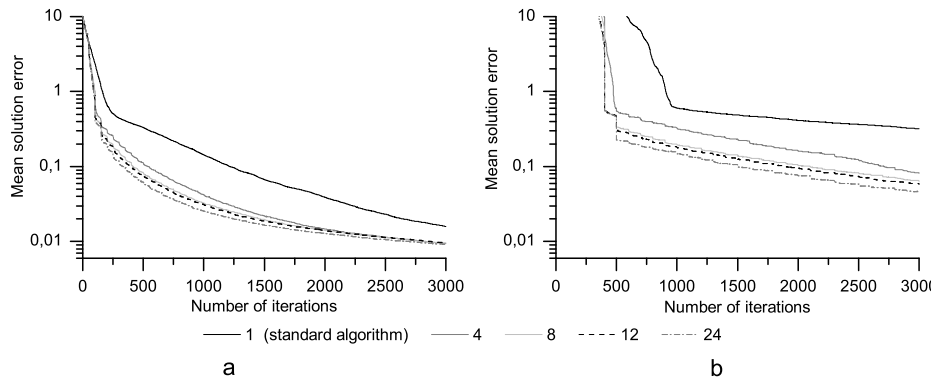

Figure 7. Impact of the number of independent populations involved on the convergence process: a) Benchmark 1 (1D model), b) Benchmark 2 (2D model)

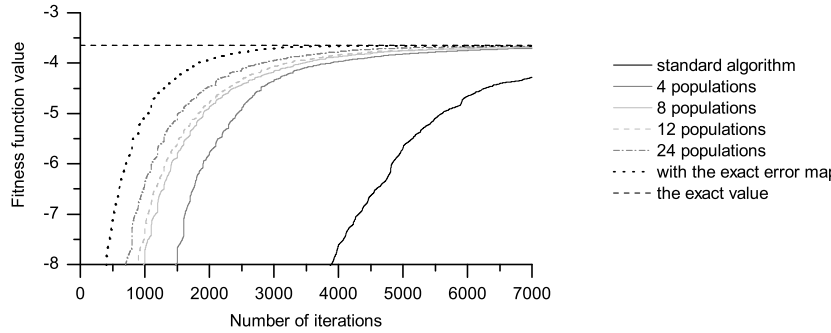

Figure 8. Impact of the number of independent populations involved – convergence of the fitness function, benchmark 2

excellent results obtained with that technique (combined speed up factor over about 650 times) may be a consequence of the specific features of the analysed problem (solution of the problem is a piecewise linear function). Error estimation technique proposed here does not take advantage of this feature.

Numerical benchmark tests considered in order to evaluate the acceleration indicate significant speed-up of the optimization process. The authors expect that the proposed techniques of taking advantage of the knowledge about errors may still be improved. Therefore, further modifications will be also examined and new concepts considered in order to achieve the very best acceleration of the optimization process.

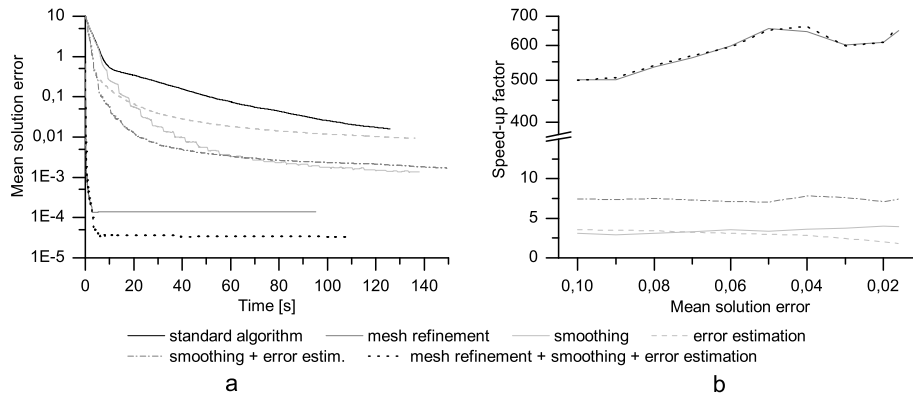

Figure 9. a) Comparison of the convergence process for all techniques, b) Comparison of the acceleration obtained for all techniques (speed-up factor calculated for the convergence of a mean solution error in a function of time)

5 FINAL REMARKS

5.1 Summary

Many scientific and technical tasks may be formulated in terms of non-linear, constrained optimization problems. In a wide class of such problems the objective is to find unknown function, mostly in a discrete form. They may be solved by means of either deterministic or probabilistic methods. The first ones are very efficient when dealing with the convex problems as opposed to usually slowly convergent probabilistic, type the EA methods, especially for large optimization problems. However, the EA efficiency does not change much for non-convex problems as opposed to the case of the deterministic methods.

Following engineering and scientific demands, the objective of this research is development of essential acceleration of the EA optimization method. Particular attention is paid here to use our knowledge about a posteriori solution error for such purpose. The proposed concepts are tested on various carefully selected benchmark problems, using the true solution error first, replaced later on by estimated errors. The strategy assumed relies on a modification of the standard selection, crossover, and mutation operators in a way relevant to the a posteriori solution error level and distribution.

Preliminary results of these tests are encouraging (speed-up factor about 2–4 for use of the error knowledge was reached). Together with previously tested mesh refinement concepts, as well as with solution smoothing and balancing, the overall factor up to about 650 times was reached.

5.2 Further Research

Further research is needed. It will be mostly concentrated on:

- continuation of various efforts oriented towards increasing of the EA efficiency, especially further development of a posteriori error analysis,
- analysis of further benchmarks,
- real engineering problems of residual stress analysis in railroad rails and vehicle wheels,
- analysis of large, non-linear, constrained optimization problems (convex and non-convex) resulting from the PBA applied to experimental measurements [6, 14].

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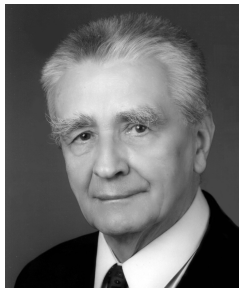

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