The evolutionary algorithm in stochastic optimization and identification problems

Piotr Orantek[1] and Tadeusz Burczyński [1,2]

[1] Department for Strength of Materials and Computational Mechanics,
Silesian University of Technology, Konarskiego 18a, 44-100 Gliwice, e-mail: piotr.orantek@polsl.pl
[2] Institute of Computer Modelling, Artificial Intelligence Department,
Cracow University of Technology, Warszawska 24, 31-155 Kraków, e-mail: tadeusz.burczynski@polsl.pl

Abstract. This paper is devoted to the application of evolutionary computing in optimization and identification problems in uncertain random conditions. The algorithm is based on the stochastic representation of the data. Chromosomes are represented by multidimensional random vectors consisting of random genes in the form of independent random variables with the Gaussian density probability function. The stochastic optimization problem is replaced by a deterministic one by evolutionary computing for vector genes consisting of mean values and standard deviations. Special operators for mutation, crososver and selection are proposed. Two numerical tests are presented.

1 Introduction

The evolutionary algorithms, as global optimization techniques, have been applied in many optimization problems in which searching design variables are deterministic [1,9,12]. There are physical problems when systems and processes have some uncertain parameters, e.g. materials properties, boundary conditions or geometry. The granular type of information [2] about these parameters necessities using various models of uncertainty in the form of interval, fuzzy and rough sets and the theory of probability.

The concept of the interval and the fuzzy evolutionary algorithm and their applications in optimization and identification problems has been considered in [5,6].

In the present paper another form of granularity is analyzed - the probability approach to optimum design. The parameters of systems and processes are modelled by random variables determined by a probability density function. The classical approach to the solution of such problems is based on stochastic programming [3]. The application of evolutionary computation to such problems involves some modifications. Genes should be modelled by random numbers and potential solutions of the optimization problem should be represented by stochastic individuals in the form of random vectors. The evolutionary computing technique based on the random representation of data can be named as a stochastic evolutionary algorithm (SEA) but this term can cause controversy because evolutionary algorithms are considered in the literature as stochastic searching algorithms due to their random nature. The term SEA makes sense if one stress as the fact that it is applied to solving stochastic optimization problems.

2 The formulation of the stochastic optimization problem

In the theoretical model of random phenomena the basic role is played by the probability space (Γ, $\mathcal{F}$, P). The set Γ, called the space of elementary events (or sample space), represents all possible elementary outcomes of a trial associated with a given random phenomenon. $\mathcal{F}$ is a σ-algebra of subset of Γ. The elements of $\mathcal{F}$ are called random events, P is a probability measure defined of $\mathcal{F}$ ($0 \le P(A) \le 1$, $A \le \mathcal{F}$).

A general non-linear stochastic programming problem can be stated as follows:
Find a random vector $\mathbf{X}(\gamma)$

$$\mathbf{X}(\gamma) = [X_1(\gamma), X_2(\gamma), ..., X_i(\gamma), ..., X_n(\gamma)] \tag{1}$$

which minimizes the objective function $F(\gamma) = F(\mathbf{X}(\gamma))$ *subject to the constraints* $P\left[g_j(\mathbf{X}) \ge 0\right] \ge p_j, j = 1,2,...,m$. If the problem is solved by the evolutionary approach, the vector $\mathbf{X}(\gamma)$ is considered as the chromosome, where $X_i(\gamma)$, i=1,2,…,n, are random genes. A gene is represented by a random variable, which is a real function $X_i = X_i(\gamma)$, $\gamma \in \Gamma$, defined on a sample space Γ and measurable with respect to P: i.e., for every real number x_i, the set $\{\gamma : X_i(\gamma) < x_i\}$ is an event in $\mathcal{F}$.

The chromosome $\mathbf{X}(\gamma)$ is a function (measurable with respect to P) which takes every element $\gamma \in \Gamma$ into a point $\mathbf{x} \in R_n$.

The mean value of the chromosome $\mathbf{X}(\gamma)$ is given as follows

$$\mathbf{m} = \mathbf{E}[\mathbf{X}(\gamma)] = \left[m_1, m_2, ..., m_i, ..., m_n\right] \tag{2}$$

where:

$$m_i = \mathbf{E}\left[X_i(\gamma)\right] = \int_{\Gamma} X_i(\gamma) dP(\gamma) = \int_{-\infty}^{+\infty} x_i p_i(x_i) dx_i \tag{3}$$

is the mean value of the gene $X_i(\gamma)$ and $p_i(x_i)$ is the probability density function (PDF) of this gene:

$$\int_{-\infty}^{+\infty} p_i(x_i) dx_i = 1 \tag{4}$$

$$\mathrm{P}\left(a \le X_i(\gamma) \le b\right) = \int_a^b p_i(x_i) dx_i \tag{5}$$

The joint probability density function $p(x_1, x_2, ..., x_i, ..., x_n)$ for the chromosome $\mathbf{X}(\gamma)$ must satisfy the following conditions:

$$\text{(i)} \quad p(x_1, x_2, ..., x_n) \ge 0 \tag{6}$$

$$\text{(ii)} \quad \underbrace{\int_{-\infty}^{+\infty} \int_{-\infty}^{+\infty} ... \int_{-\infty}^{+\infty}}_{n-\text{fold}} p(x_1, x_2, ..., x_n) dx_1 dx_2 ... dx_n = 1 \tag{7}$$

$$\text{(iii)} \quad \begin{aligned} &P\left(a_1 \le X_1(\gamma) \le b_1, a_2 \le X_2(\gamma) \le b_2, ..., a_n \le X_n(\gamma) \le b_n\right) = \\ &= \int_{a_1}^{b_1} \int_{a_2}^{b_2} ... \int_{a_n}^{b_n} p(x_1, x_2, ..., x_n) dx_1 dx_2 ... dx_n \end{aligned} \tag{8}$$

The matrix of covariance is given as follows:

$$\mathbf{K} = [k_{ij}] = \mathbf{E}\left[\left(\mathbf{X}_i(\gamma) - \mathbf{m} \right) \left(\mathbf{X}_i(\gamma) - \mathbf{m} \right)^T \right] \tag{9}$$

where the covariance between $X_i(\gamma)$ and $X_j(\gamma)$ is defined by:

$$k_{ij} = \mathbf{E}\left[\left(X_i(\gamma) - m_i \right) \left(X_j(\gamma) - m_j \right) \right] = \int_{-\infty}^{+\infty} \int_{-\infty}^{+\infty} \left(x_i - m_i \right) \left(x_j - m_j \right) p\left(x_i, x_j \right) dx_i x_j \tag{10}$$

where $p\left(x_i, x_j \right)$ is the joint PDF of $X_i(\gamma)$ and $X_j(\gamma)$ given by:

$$p\left(x_i, x_j \right) = \underbrace{\int_{-\infty}^{+\infty} \int_{-\infty}^{+\infty} \ldots \int_{-\infty}^{+\infty}}_{(n-2)-\text{fold}} p\left(x_1, x_2, \ldots, x_n \right) dx_1 \ldots dx_{i-1} dx_{i+1} \ldots dx_{j-1} dx_{j+1} \ldots dx_n \tag{11}$$

If $i = j$, the covariance k_{ii} is represented by a variance:

$$k_{ii} = \sigma_i^2 = Var\left(X_i(\gamma) \right) = \mathbf{E}\left[\left(X_i(\gamma) - m_i \right)^2 \right] = \int_{-\infty}^{+\infty} \left(x_i - m_i \right)^2 p_i\left(x_i \right) dx_i = \mathbf{E}\left[X_i(\gamma) \right]^2 - \left(m_i \right)^2 \tag{12}$$

where:

$$\mathbf{E}\left[X_i(\gamma) \right]^2 = \int_{-\infty}^{+\infty} x_i^2 p_i\left(x_i \right) dx_i \tag{13}$$

In the present paper the random chromosome $\mathbf{X}(\gamma) = [X_1(\gamma), X_2(\gamma), \ldots, X_i(\gamma), \ldots, X_n(\gamma)]$ has an *n*-dimensional Gaussian distribution of the probability density function, given as follows:

$$p(x_1, x_2, \ldots, x_i, \ldots, x_n) = \frac{1}{(2\pi)^{n/2} \sqrt{|\mathbf{K}|}} \left[-\frac{1}{|\mathbf{K}|} \sum_{i,j=1}^{n} \left| K_{ij} \right| (x_i - m_i)(x_j - m_j) \right] \tag{14}$$

where $|\mathbf{K}| \neq 0$ is the determinant of matrix covariance, $\left| K_{ij} \right|$ the cofactor of the element k_{ij} of the matrix $\mathbf{K}$.

It is assumed that random genes are independent random variables. The joint probability density function is expressed by the probability density functions of single random genes as follows:

$$p(x_1, x_2, \ldots, x_i, \ldots, x_n) = p_1(x_1) p_2(x_2) \ldots . p_i(x_i) \ldots . p_n(x_n) \tag{15}$$

where

$$p_i\left(x_i \right) = N\left(m_i, \sigma_i \right) = \frac{1}{\sigma_i \sqrt{2\pi}} \exp\left[-\frac{\left(x_i - m_i \right)^2}{2\sigma_i^2} \right] \tag{16}$$

is the probability density function of the random gene $X_i(\gamma)$.

It can be seen that if the random genes $X_i(\gamma)$, *i*=1,2,…,*n*, are random independent Gaussian variables, two parameters: the mean value m_i and the standard deviation σ_i describe the probability density function.

3 The evolutionary algorithm based on the stochastic representation

Stochastic optimization problems emerge when some parameters of the objective function or constraints are probabilistic. The application of evolutionary algorithms to solve such problems requires some modifications of the traditional evolutionary approaches because chromosomes consist of random genes $X_i(\gamma)$, i=1, 2,…, n, described by moments, e.g. by the mean value m_i and the standard deviation σ_i in the case of Gaussian independent random genes. The mean idea of SEA is similar to the traditional evolutionary algorithm but all steps of algorithm must be modified to the stochastic data and their moments. Each individual expresses a stochastic solution. Each solution is evaluated, and a stochastic value of the fitness function is obtained as the result. The next generation is constructed on the basis of better stochastic chromosomes of the previous generation. In this case the special types of relations are defined. Also the stochastic types of operators (mutation and crossover) are constructed. It can be observe that the next population in the stochastic evolutionary algorithm is better than the previous one.

The stochastic problem is solved by using mathematical operations on moments (e.g. the mean value m_i and the standard deviation σ_i, etc.). Therefore, the original stochastic problem is considered as an equivalent deterministic problem. This technique is known very well in other problems, e.g. in solving the stochastic programming, stochastic differential equations, etc. Thus, the original stochastic problem can be reduced to a deterministic one. Instead of the random chromosome $\mathbf{X}(\gamma)$ one can consider a deterministic chromosome **chr** which consists of n-vector pars of genes $\mathbf{g}_i=(m_i,\sigma_i)$, i=1,2,…,n which correspond to random variable $X_i(\gamma)$

$$\mathbf{chr}=\left[\mathbf{g}_1;\mathbf{g}_2;...\mathbf{g}_i;...;\mathbf{g}_n\right]=\left[(m_1,\sigma_1);(m_2,\sigma_2);...;(m_i,\sigma_i);...;(m_n,\sigma_n)\right] \tag{17}$$

In more general cases the gene $\mathbf{g}_i$ consists of more moments of random variable $X_i(\gamma)$. Due to the Gaussian distribution two moments are sufficient to describe random genes.

In the presented SEA the evolutionary operations are applied to the random genes $X_i(\gamma)$ by modification of mean values m_i and standard deviations σ_i.

It is worth stressing some similarities between the proposed approach to the stochastic representation of the EA and the evolutionary strategies [9].

For each vector gene $\mathbf{g}_i=(m_i,\sigma_i)$ i=1,2,…,n, two kinds of constraints are imposed:

$$m_i^{\min}\le m_i\le m_i^{\max} \tag{18}$$

$$\sigma_i^{\min}\le \sigma_i\le \sigma_i^{\max} \tag{19}$$

where indices: *min* and *max* mean here the maximum and minimum values.

3.1 The mutation operators

Two types of the Gaussian mutation are introduced. The term – the *Gaussian mutation* means the type of the mutation, which is used in the traditional EA. The mutation probability is described by *pro_mut*.

In both cases the modified vector gene $\mathbf{g}_i=(m_i,\sigma_i)$ is randomly selected from the chromosome $\mathbf{chr}=\left[\mathbf{g}_1;\mathbf{g}_2;...\mathbf{g}_i;...;\mathbf{g}_n\right]$.

In the first type of mutation (*mutation I*) the mean value m_i of the random gene $X_i(\gamma)$ is modified. The operator is expressed by the following equation:

$$m_i^* = m_i + m_i^o \tag{20}$$

where m_i^o is a sampled value (with the Gaussian distribution).

If the value m_i^* does not fulfil the condition (18) the mutation is repeated.

In the second type of the mutation (*mutation II*) the standard deviation σ_i of the random gene $X_i(\gamma)$ is modified. The operator is expressed by the following equation:

$$\sigma_i^* = \sigma_i + \sigma_i^o \tag{21}$$

where σ_i^o is a sampled value (with the Gaussian distribution).

In the case when value σ_i^* does not fulfil the condition (19) the mutation is repeated.

Both kinds of mutations can work together or individually. In the present paper both kinds of mutations work together. The mean value m_i and the standard deviation σ_i, which describe the random gene $X_i(\gamma)$, can change during the mutation, thus the probabilistic characteristics of the random gene undergo modification.

3.2 The crossover operator

An arithmetic crossover operator is proposed in the stochastic evolutionary algorithm. Each chromosome in the population can be selected for the crossover with the probability *pro_cro*.

Consider two parent chromosomes:

$$\mathbf{chr\_a} = [\mathbf{g\_a}_i], \quad where \quad \mathbf{g\_a}_i = (m_i, \sigma_i)_{\mathbf{a}} \tag{22}$$

$$\mathbf{chr\_b} = [\mathbf{g\_b}_i], \quad where \quad \mathbf{g\_b}_i = (m_i, \sigma_i)_{\mathbf{b}} \tag{23}$$

They create two children $\mathbf{chr\_a}^* = [\mathbf{g\_a}_i^*]$ and $\mathbf{chr\_b}^* = [\mathbf{g\_b}_i^*]$ with the vector genes

$$\mathbf{g\_a}_i^* = \lambda \mathbf{g\_a}_i + (1-\lambda)\mathbf{g\_b}_i \tag{24}$$

$$\mathbf{g\_b}_i^* = \lambda \mathbf{g\_b}_i + (1-\lambda)\mathbf{g\_a}_i \tag{25}$$

where $\lambda \in [0,1]$ is a random value with uniform distribution.

As a result of the crossover operator the children contain genes with modified probabilistic characteristics described by moments of random genes $X_i(\gamma)$, i=1,2,…,n.

3.3 The selection

The selection is based on the tournament selection, which is used in traditional EA. A special criterion for comparing two random individuals is presented. Consider the fitness function for two different random chromosomes: $F_1(\gamma) = F(\mathbf{X}_1(\gamma))$ and $F_2(\gamma) = F(\mathbf{X}_2(\gamma))$. The random values $F_1(\gamma)$ and $F_2(\gamma)$ are described by the moments: $F_1(\gamma) \to (m_{F1}, \sigma_{F1})$ and $F_2(\gamma) \to (m_{F2}, \sigma_{F2})$, respectively. The minimization problem is considered. The parameters β_1 and β_2 decide the probability of survival of chromosomes: $\mathbf{X}_1(\gamma)$ and

$\mathbf{X}_2(\gamma)$, respectively. At the beginning the parameters β_1 and β_2 are equal to β_0 (in this work β_0=0.1). In the next step, the conditions:

$$m_{F1} < m_{F2} \tag{26}$$

$$\sigma_{F1} < \sigma_{F2} \tag{27}$$

are checked. If the conditions (26) and (27) are fulfilled, the probability of the survival of the first chromosome is bigger by $\Delta\beta_m$ and $\Delta\beta_\sigma$, respectively (in this work $\Delta\beta_m$ = 0.7, $\Delta\beta_\sigma$ =0.3). In the contrary cases the probability of the survival of the second chromosome is bigger by $\Delta\beta_m$ and $\Delta\beta_\sigma$, respectively. It is possible to observe that if the both stochastic values of the fitness functions are identical, the probability of the survival of both individuals is identical. Finally, the survived individual is sampled with respect to the survival parameters β_1 and β_2.
All individuals in the population are generated using the tournament selection. There is a possibility that the best individual will not survive.

3.4 Evaluation of the stochastic fitness function

One of the most important steps of the evolutionary algorithm is the evaluation of the fitness function. If the design variables are deterministic, the fitness function result is also deterministic. In the case of solving the stochastic optimization problem, the problem of evaluating the fitness function is much more complicated. A few ways to estimate the results in this case are possible. In the case of simple mathematical functions the basic arithmetic operators {+;-;*;/} for stochastic representation are used. Due to the use of the Taylor's expansion (for small fluctuations of design variables) and other techniques some basic bench-marks can be computed.

If the fitness function is the explicit function of stochastic design parameters, its value can be computed on the basis of the Taylor's extension. Unfortunately, in many cases the fitness function evaluation can be done after solving the stochastic boundary-value problem. The stochastic boundary-value problems can be solved by means of the stochastic boundary element method SBEM [4] or the stochastic finite element method SFEM [8].

4 The example of the stochastic optimization problem

The aim of the test is to find the vector $\mathbf{X}(\gamma)$ which minimizes the function:

$$F(\gamma) = F(\mathbf{X}(\gamma)) = \sum_{i=1}^{n}\left[\frac{1}{\pi}\left|X_i(\gamma)-0.7\right|^{\frac{\pi}{3}}\left(\frac{\pi}{2}-\cos\left(2\pi a\left|X_i(\gamma)-0.7\right|^{\frac{\pi}{3}}\right)\right)\right] \tag{28}$$

where: n – the number of random design variables $X_i(\gamma)$, a – the parameter, which determines the number of the optima.

The mean value and the standard deviation of the fitness function $F(\gamma)$ were computed using the stochastic arithmetic operators {+;-;*;/} and Taylor's extension (for small fluctuations).

The following constraints for the parameters of the random numbers were assumed: $0 \le m_i \le 1$ for the mean value and $0 \le \sigma_i \le 0.2$ for the standard deviation, where: i=1,2,…,n. The optimum solution is represented by chromosome: $\mathbf{chr} = [\mathbf{g}_i]$, where $\mathbf{g}_i$=(m_i,σ_i)=(0.7,0.0) for each gene. The minimum of the random value of the fitness function is described by the parameters: F_{opt}=(m_{opt},σ_{opt})=(0.0,0.0).

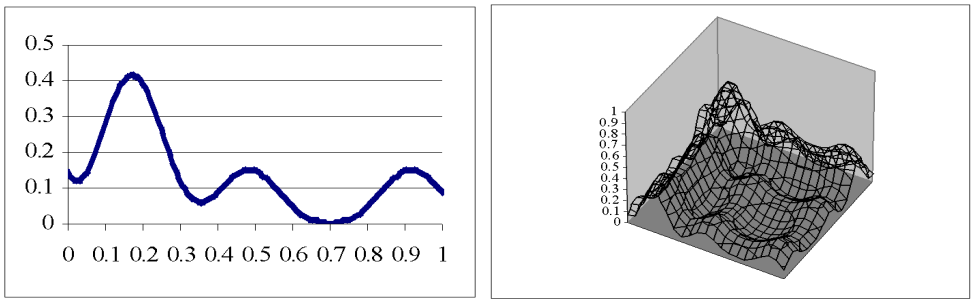

Figure 1. The mean value of the fitness function (28) for a=3, (n=1, n=2).

The finish condition depends on the found result. The special parameter: *distance* was introduced:

$$distance=\sqrt{distance_m^2+distance_\sigma^2} \tag{29}$$

where: $distance_m$ and $distance_\sigma$ are the differences between the parameters of the found results and the actual results ($\mathbf{g}_i=(m_i,\sigma_i)=(0.7,0.0)$, i=1,2,…,n). The following values of the parameters $distance_m$ and $distance_\sigma$ were assumed:

$$distance_m=\frac{1}{n}\sqrt[n]{\varepsilon_m} \tag{30}$$

$$distance_\sigma=\frac{1}{n}\sqrt[n]{\varepsilon_\sigma} \tag{31}$$

where: n – the number of design variables, ε_m - the parameters of differences of the mean value (ε_m=0.02), ε_σ - the parameter of the differences of the standard deviation (ε_σ=0.002). Table 1 contains the selected results for the following parameters: n=3, a=3.

In the first step of investigation, the optimal probabilities of mutation and crossover operators were searched. In the second stage the best population size was searched. The selected results (n=3, a=3) (mean value from 10000 independent experiments) are presented in Tables 1-3.

Table 1. The number of the fitness function computation (n=3, a=3).

The mutation probability (*pro_mut*)	The crossover probability (*pro_cro*)				
	0.1	**0.2**	**0.3**	**0.4**	**0.5**
0.1	426	589	774	972	1210
0.2	**387**	504	640	782	946
0.3	399	493	603	728	859
0.4	419	503	595	706	821
0.5	438	519	600	697	804

Table 2. The number of the fitness function computation (n=3, a=3).

The number of chromosomes (*pop_size*)	The number of the fitness function computation
3	338
4	313
5	**302**
6	304
7	308
8	319
9	333
10	342

The searching of the optimal parameters of the stochastic evolutionary algorithm for all combinations of parameters n and a were carried out. The results are included in Table 3.

Table 3. The optimal parameters of the stochastic evolutionary algorithm (*pro_mut/pro_cro/pop_size*)

The number of optimum a	The number of design variables n				
	1	**2**	**3**	**4**	**5**
1	0.4/0.1/4	0.4/0.1/5	0.3/0.1/4	0.2/0.1/4	0.2/0.1/4
2	0.3/0.1/4	0.3/0.1/6	0.3/0.1/9	0.3/0.1/10	0.2/0.1/12
3	0.2/0.1/4	0.2/0.1/5	0.2/0.1/5	0.2/0.1/5	0.2/0.1/5
4	0.2/0.1/4	0.2/0.1/5	0.2/0.1/5	0.2/0.1/5	0.1/0.1/5
5	0.2/0.1/4	0.2/0.1/5	0.2/0.1/4	0.1/0.1/5	0.1/0.1/5

5 Identification stochastic loads

Consider a two-dimensional elastic structure (plane stress) with prescribed boundary conditions (Figure 2). The following parameters of the structure: (i) geometry, (ii) material properties and (iii) boundary conditions, can be modelled by using the stochastic approach. In this example loads $X_i(\gamma)$ i=1,2,..,n, are random variables. The rest of the parameters are deterministic.

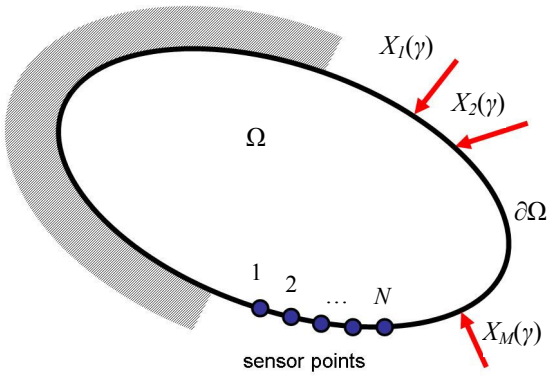

Figure 2. The elastic structure under random loads

The displacement $\mathbf{U}(\mathbf{x},\gamma)$ is the stochastic field, which is the solution of the boundary value problem of linear elastostatics [13]. This field can be found by using the *Stochastic Finite Element Method* (SFEM) [8] or the *Stochastic Boundary Element Method* (SBEM) [4]).

In the case of the SFEM, the displacements are obtained by solving the system of random equations:

$$\mathbf{A}\mathbf{U}(\gamma)=\mathbf{X}(\gamma) \tag{32}$$

where: $\mathbf{A}$ – the stiffness matrix, $\mathbf{U}(\gamma)$ – the vector of nodal displacements, $\mathbf{X}(\gamma)$ – the vector of random loads.

The problem of the identification of stochastic loads $X_i(\gamma)$ i=1,2,..,n, on the basis of the stochastic displacements measured in the boundary sensor points k=1,2,..,N, is considered.

From the mathematical point of view, the identification problem is expressed as the minimization of a special stochastic function:

$$F(\gamma)=\int_{\partial\Omega}\varphi\left(\mathbf{U}(\mathbf{x},\gamma)\right)d\partial\Omega(\mathbf{x}) \tag{33}$$

where $\mathbf{U}(\mathbf{x},\gamma)$ is a random displacement field on the boundary $\partial\Omega$.

The integrand φ is expressed as follows:

$$\varphi\left(\mathbf{U}(\mathbf{x},\gamma)\right)=\sum_{k=1}^{N}\left[\mathbf{U}(\mathbf{x},\gamma)-\hat{\mathbf{U}}(\mathbf{x},\gamma)\right]^2\delta(\mathbf{x}-\mathbf{x}_k) \tag{34}$$

$\hat{\mathbf{U}}(\mathbf{x},\gamma)$ - measured random displacements in sensor points $\mathbf{x}=\mathbf{x}_k$, k=1,2,..,N, δ - Dirac function. The formula (33) can be transformed to the simpler form:

$$F(\gamma)=\sum_{k}\left[\mathbf{U}_k(\gamma)-\hat{\mathbf{U}}_k(\gamma)\right]^2 \tag{35}$$

where: $\mathbf{U}_k(\gamma)=\mathbf{U}(\mathbf{x}_k,\gamma)$.

The aim of this test is to find n=2 random loads: $X_1(\gamma)$ and $X_2(\gamma)$ (Figure 3). The actual stochastic parameters of the load $X_1(\gamma)$ is described by: $\mathbf{g}_1=(m_1,\sigma_1)$, where: m_1=10.0 [kN], and σ_1=0.167 [kN]. The actual stochastic parameters of the load $X_2(\gamma)$ is described by: $\mathbf{g}_2=(m_2,\sigma_2)$, where: m_2=15.0 [kN], and σ_2=0.167 [kN]. The loads are independent random variables.

The stochastic chromosome $\mathbf{X}(\gamma)=[X_1(\gamma),X_2(\gamma)]$ is replaced by a deterministic one containing moments of $X_i(\gamma)$ $\mathbf{chr}=\left[\mathbf{g}_1;\mathbf{g}_2\right]=\left[(m_1,\sigma_1);(m_2,\sigma_2)\right]$.

As the sensor points N=21 boundary nodes were selected (Figure 3a).

The following parameter values of the stochastic evolutionary algorithm were assumed: the mutation probability *pro_mut*=0.4, the crossover probability *pro_cro*=0.1, the population size *pop_size*=5, the number of generations was equal to 500.

25 independent experiments were performed. The results (worst, average and best) are included in Table 4.

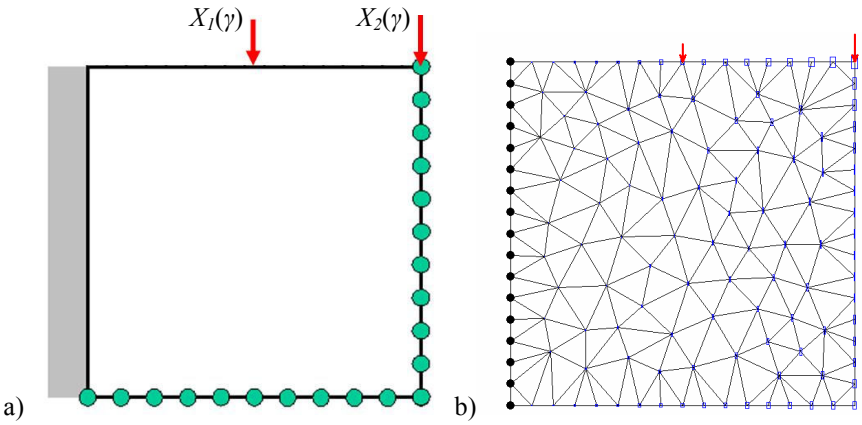

Figure 3. The 2-D elastic structure: a) the sensor points (gray points), b) the SFEM model.

Table 4. The found moments of the random loads

Results	The moments of random loads			
	m_1 [kN]	σ_1 [kN]	m_2 [kN]	σ_2 [kN]
worst	9.876	0.183	14.854	0.153
average	10.007	0.163	15.015	0.167
best	10.000	0.167	14.990	0.169

6 Conclusions

An effective intelligent technique based on the stochastic evolutionary algorithm has been presented. This approach can be applied in the optimization and the identification of systems that are in random conditions. This approach is very promising for reliability optimization in which the safety of a system is estimated and represented by the probability of its failure, i.e. the occurrence of an ultimate limit state manifesting itself.

The future task is testing the influence of the parameters on the sensitivity of the algorithm: the parameters of the evolutionary algorithm (the number of individuals, the probability of the operators), the control parameters of the selection (the probability of the comparison of two stochastic numbers). Coupling with the gradient method will be considered. The two-stage strategy will be taken into account. This approach has been applied for a real value problem and the fuzzy value problem [7] and the results have been satisfactory. The special type of the stochastic ANN can be applied for the computation of the sensitivity of the stochastic fitness function.

More general approaches will be developed in future. Other types of PDF functions with a greater number of moments will be examined. The dependences between random numbers will also be examined.

In the general case uncertain conditions have the granular form [2]. Models based on interval and fuzzy numbers were used instead of the stochastic approach presented in this paper. Models based on perturbation numbers will be presented in the future.

The granular evolutionary algorithm can be created as a general method for all models described.

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