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*Tomasz Raszkowski, Agnieszka Samson*

# APPLICATION OF GENETIC ALGORITHM AND SWARM INTELLIGENCE ALGORITHMS TO HEAT TRANSFER COEFFICIENT ESTIMATION

**Summary**

In this paper the dependence between heat transfer coefficient and temperature rise is considered. The results are obtained using the two different groups of algorithms. In the first group, swarm intelligence algorithms, the ant colony optimization and bee colony optimization algorithms are taken into consideration. In the second group, the genetic algorithms are presented. The received solutions are discussed in detail and compared between each other. Moreover, the evaluation time, accuracy and number of iterations of these algorithms are also demonstrated and compared.

*Keywords and phrases:* swarm intelligence agorithms, ant colony optimimization, bee colony optimization, artificial bee colony, genetic algorithm, heat transfer coefficient, temperature dependences

## 1. Introduction

The heat transfer problems are presently one of the most important issues during modern electronic appliances design process. This part of the research is particularly important due to the fact that the biggest number of electronic devices failures is caused by uncontrolled growth of their temperatures. The research related to malfunctions of electronic equipment indicates that most of the mentioned damages appear because of the meaningful temperature rise [1]. This situation is a result of the improper project of the final device, inappropriate arrangement of components of electronic integrated circuits and failure to take account all of the factors which have the biggest influence on the temperature rise value in analyzed devices.

All reasons described in the previous paragraph cause problems related to the proper operation of the electronic devices, shorter life span of the electronic appliances and even their destructions. Therefore, there exists a need for identification of all phenomena which have the significant influence on temperature distribution in electronic structures. One of the mentioned phenomena is the heat transfer between areas of different temperatures. The heat transfer is described by the heat transfer coefficient [2], [3].

Estimation of the heat transfer coefficient is very difficult because the value of this parameter depends on several factors. Among others, the shape of the analyzed structure, the surface temperature of this structure and external conditions, such as the temperature of the ambient, humidity or air condition, are taken into consideration [4], [5], [6], [7].

Apart from the identification of the phenomena influencing on the temperature distribution on electronic structures, the choice of the best possible methods to find the values of the parameters, describing these phenomena, is also crucial. In this paper, the average heat transfer coefficient and approaches to obtain its values are taken into account. Moreover, the natural convection and radiation, which determine the value of the heat transfer coefficient, are considered.

Regarding the fact that values of the parameters which describe the heat transfer coefficient are unknown and the boundaries of intervals including their value are not also known, global methods which can help finding the estimated coefficient have to be employed. For this purpose, the algorithms which base on the observations of natural environment and creatures, which inhabit this environment, have been proposed. Among these algorithms there are the ant colony optimization, the bee colony optimization and the classical genetic algorithm. The first and the second ones belong to the larger class of algorithms which is usually called the swarm intelligence. The third one represents the class of genetic algorithms and it uses, inter alia, the inheritance mechanisms to adjust to the measured data.

The structure of this paper presents as follows. Firstly, the detailed description of methodology, used during the simulations, is presented. The mentioned description includes the classical ant colony optimization algorithm and its modified versions, the bee colony optimization, artificial bee colony algorithms and their modification as well as the classical genetic algorithms and its adaptation to the considered problem. Secondly, the description of the simulations, including all necessary parameters and their interpretations, are discussed. Then, the simulation results are demonstrated. Moreover, the comparison between results, which have been obtained, are shown. Finally, the conclusions are presented.

All simulations and simulation results, presented in this paper, are based on the real measurements related to the temperature responses.

## 2. Algorithms Descriptions

The swarm intelligence is the name of the artificial or natural systems which are characterized by the self-organization, decentralization and collective behaviour. The idea of swarm intelligence systems was drawn from natural environment and mechanism of biological systems. The swarm intelligence systems are usually composed of the population of single particles, for example boids or single representative of chosen population. These representatives communicate each other and they interact with surrounding environment. The single representatives are not controlled by the main control unit. They are independent and make decisions by themselves following some principles rules, however their behaviours result also from the observation of behaviour of other individuals. That kind of independent decision making, based on the knowledge about the environment acquired through the communication between other members of the population, creates the intelligent global system leading optimization of various processes, which is not achievable for the single units.

Among swarm intelligence systems based on the behaviour of such animals as ants or bees there are ant colonies and bee colonies systems. These systems were a basis for the creation of ant colony optimization, bee colony optimization or artificial bee colony algorithms.

On the other hand, in many optimization problems the genetic algorithms are employed. As opposed to swarm intelligence algorithms, the genetic algorithms are based on the observations of the natural selection processes. Genetic algorithm is kind of heuristic which searches the set of alternative solutions and chooses the best one. Genetic algorithms are the part of the greater class of algorithms, called the evolutionary algorithms. These algorithms can generate the solutions of the undertaken problems based on the natural evolution mechanisms, for instance the selection, mutation, crossover or inheritance.

Both class of the mentioned algorithms, swarm intelligence algorithms and genetic algorithms, have been used in this paper.

### 2.1. Ant Colony Optimization Algorithm

Classical ant colony optimization algorithm has been establish by Marco Dorigos doctoral dissertation in 1992 [8], [9]. That algorithm has been based on probabilistic techniques. That kind of techniques allow solving the complex problems which are related to obtain good or the best possible solutions from huge number of opportunities.

The ant colony optimiziation algorithm construction is based on the ant colony behaviour observation. This algorithm is characterized by several single rules. The main assumption is related to find the food source by the single ant. Before the food source will be found, the path between anthill and the place, where the food is located, have to be discovered. After finding the food, the ant follows to the anthill. During this journey the ant leaves the pheromene traces which are recognized by other ants from the colony. This pheromone traces inform them about the direction to the food source. Thus, thaking into account this information, the proces of making the decisions by other members of the ant population becomes easier. When the food source is found by other ants, the amount of the pheromones on the path toward anthill is getting bigger. On the areas and paths, which have been left by ants and they are not used, the amount of the pheromone traces is getting weak due to the pheromone vaporaizing process. That kind of ants communication allow finding the optimal, the shortest and the most convenience path from the anthill to the food location.

However, the classical ant colony optimization algorithm cannot be directly applied to obtain the values of the heat transfer coefficient, because the problem undertaken in this paper is not related to find the optimal way but it is connected to obtain coordintes of point where the walue of the objective function is minimal. Due to this fact, the classical ant colony optimization algorithm had to be modified.

Two modifications of the ant colony optimization algorithms have been prepared. The first one presents as follows. Primarily, the start poin is arbitrary chosen and the number of ants in population is set. The start poin corresponds to the place where the anthill is located. Secondly, the mesh consisting of the previously fixed number of nodes in each dimension is generated. It is assumed that in one-dimensional case, this mesh consists of points from closed interval. In two-dimensional case, the analyzed mesh is rectangular. When the number of dimensions is equal to three, the mesh has got rectangular cuboid shape. In the case of the bigger number of dimensions, the mesh shape is described analogously.

Then the matrix of possible moves of all ants is created. Is was assumed that the single move can be made only in one chosen dimension. It means that in the case of the one-dimensional space, the single ant has got two possible moves, to the left or to the right respectively. In the case of two-dimensional space, the ant has got four possibilities to make the move, two in each dimension. In the case of three-dimensional space, the number of possible moves, which can be make by the ant, is equal to six, including two moves in each of dimensions. Increasing the number of dimensions by one, the number of possible moves is increased by two each-time. However, the number of possible moves is decreased when the ant reaches the end node in analyzed dimension. For example, in one-dimensional case, reaching the end node means that the only possible move is the move toward opposite way. On the other hand, in the case of the two-dimensional case, when the end point is achieved only in one-dimension, the total number of possible moves is equal to three – one in the analyzed dimension and two in the second one. However, when the ant have gone to the point, which is the end node for both investigated dimensions, the number of possibilities to make the move decreases to two – one for each dimension. The bigger number of dimensions indicates that the greater number of exclusions have to be taken into consideration. For example, in three-dimensional case, the number of possible decisions related to ant moves is equal to:

- six, when the current ant location is inside the mesh and no edge or apex is reached,
- five, when the end node is reached only for one dimension,
- four, when the node belonging to the edge of the mesh is achieved; this situation indicates that end node has been reached in two of the three dimensions,
- three, when the apex of the generated mesh is achieved; this case means that the end node has been achieved in each dimension.

When the bigger number of dimensions is taken into considerations, ant move exclusions are constructed in similar way.

Then, the vector of probabilities of choice of possible nodes and making the move is constructed. The mentioned probabilities are calculated according to the formula presented below:

$$p_{ij}^{k}(t) = \frac{(\tau_{ij}(t))^{\alpha} \cdot (\eta_{ij}(t))^{\beta}}{\sum_{j \in N_i^k} \left( (\tau_{ij}(t))^{\alpha} \cdot (\eta_{ij}(t))^{\beta} \right)} \tag{1}$$

Symbols, which have been used in the formula above, have the meanings presented in the Table 1.

The possible node is chosen by the ant randomly according to vector of probabilities created using formula (1).

When the decision related to the move to the chosen node is made, the amount of the pheromone trace in the new location of the ant increase, while the amount of the pheromone traces in other surrounding nodes stay at the same level. This dependence can be written using the following formula:

$$\triangle\tau_{ij}^{k}(t) = \begin{cases} \frac{Q}{J^k}, & \text{when } j^{th} \text{ node is chosen} \\ 0, & \text{in other case} \end{cases} \tag{2}$$

Explanation of symbols used in expression above is presented in Table 2.

As it was indicated earlier, the amount of the pheromone changes dynamically with the passing of the time. Pheromone trace amount decreases due to the vaporising process when the nodes were left by ants. On the other hand, when the ants visit another nodes, the amount of the pheromones getting bigger. Thus, the update of the pheromone amount is needed. The expression (3) describes the updated matrix including pheromone traces which will be taken into consideration in the next

Table 1. *Parameters of the ant move probability function.*

| **Parameter** | **Parameter interpretation** | **Additional information** |
|---|---|---|
| $k$ | Number of the ant | $k \in \mathbb{N} \setminus \{0\}$ |
| $t$ | Number of iteration | $t \in \mathbb{N} \setminus \{0\}$ |
| $i$ | Number of current node occupied by the ant | |
| $j$ | Number of node which can be occupied by the $k^{th}$ ant in the next iteration | |
| $N_i^k$ | Set of nodes in the neighborhood of the current node | $i^{th}$ node neighborhood |
| $\tau_{ij}$ | The value of the pheromene trace in the $j^{th}$ nodes which is the naighbour of $i^{th}$ node | $\tau_{ij} \in \mathbb{R}_+$ |
| $\alpha$ | Parameter controlling the pheromone weight | $\alpha \in (0,1)$ |
| $\eta_{ij}$ | Value of heuristic function describing phenomena which can have the influence on the ant decision related to make a move | distance between $i^{th}$ and $j^{th}$ |
| $\beta$ | Parameter controlling the weight of the value of the heuristic function $\eta_{ij}$ | $\beta \geq 1$ |
| $p_{ij}^k$ | Probability of move from $i^{th}$ node to the $j^{th}$ one | |

iteration

$$\tau_{ij}\left(t+1\right) = \rho\tau_{ij}\left(t\right) + \sum_{k=1}^{m} \triangle\tau_{ij}^{k}\left(t\right) \tag{3}$$

Symbol used in the expression below are descibed in Table 3.

The remaining parameters have been described previously. The algorithm is stopped when the maximum number of iterations is reached or the demanded accuracy is achieved.

The second modification of the classical ant colony optimization algorithm has been also prepared. The main difference between this modification and that one described previously is the absence of the generated mesh. Instead of the mesh, the random number is generated. This number indicates the distance which will be

Table 2. *Parameters of the pheromone trace change formula.*

| **Parameter** | **Parameter interpretation** | **Additional information** |
|---|---|---|
| $\triangle\tau_{ij}^{k}$ | Change of the amount of the pheromone trace after move from $i^{th}$ node to the $j^{th}$ one | |
| $Q$ | Amount of the pheromone placed by the ant after move from $i^{th}$ node to the $j^{th}$ one | $Q \in \mathbb{R}_{+}$ |
| $J^k$ | Value of the objective function for the $k^{th}$ ant | $J^k \in \mathbb{R}_{+}$ |

Table 3. *Parameters of the pheromone traces matrix updating formula.*

| **Parameter** | **Parameter interpretation** | **Additional information** |
|---|---|---|
| $\rho$ | Pheromone vaporising coefficient | $\rho \in (0, 1)$ |
| $m$ | Total number of ants in the population | $m \in \mathbb{N} \setminus \{0\}$ |

travelled by the ant after choice the direction of move. It is assumed that ant can change only one of the coordinates of point which is currently occupied. It means that number of possible moves to the next location is the same as in the first modification of the analyzed algorithm. Thus, this number is equal to two – in the case of the one-dimensional space, to four – in the two-dimensional space, to six – when the three-dimensional case is considered, etc.

Another difference between prepared modification of the classical ant colony optimization algorithm is related to the construction of the heuristic function $\eta_{ij}$. Due to the randomization of the next coordinate of the ant location, the heuristic function does not take into account the distance between analyzed point. Instead, the value of the objective function $J^k$ is considered. In the case of the minimization problems, the inverse of the value of the objective function $J^k$ should be taken into consideration.

Other assumptions in both modified versions of the ant colony optimization algorithm are similar. Moreover, formulas presented in expressions (1), (2) and (3) are also applicable.

## 2.2. Bees' Algorithms

Bees algorithms are the class of algorithms which are based on the observation of the behaviour of the honey bees. The construction of these algorithms uses the knowledge about the intelligent behaviour of the honey bees during the food searching. Bees algorithms, similarly to ant colony algorithm, belong to the swarm intelligence algorithms.

Among bees algorithms, there exists some algorithms which have different assumptions. In this paper, the bee colony optimization and artificial bee colony algorithms have been taken into consideration. In both cases searching for the food by bees is primarily based on the probabilistic mechanisms. When the food source is found, bees communicate with other members of their population doing a waggle dance. This behaviour informs other bees about the location of the food. This information influences on the bees decisions about changing the direction of food searching.

The waggle dance provides three important messages for the members of the bee colony. They inform about:

- the distance between beehive and the food source,
- the direction of food searching,
- the quality of the nectar in food source which has been found.

This information and described model of communication between bees create the global intelligent system which can be used in various complex optimization problems.

However, some modifications of the classical bee algorithms have to be done due to the form of the problem which has been undertaken in this paper. Moreover, the idea of Dervis Karaboga has been used [10]. The proposed beehive model consists of three main parts:

- employed bees,
    - onlooker bees,
    - scout bees,
- unemployed bees:
- food sources.

Employed bees are related to the food sources. In the case when the food in one of the food sources is getting empty, the employed bee, which is related with the analyzed food source, becomes the unemployed bee. The unemployed bees do not have the information about the other food sources. Due to this fact, they have to find new food locations. The unemployed bee can belong to scout bees group or to the onlooker bees group. Scout bees find new food sources in the neighborhood of the beehive in the random way. On the other hand, the onlooker bees observe the waggle dance of the employed bees when they go back to the beehive. Based on the information given during the waggle dance, the onlooker bees choose the direction of food source finding.

Excluding the employed and unemployed bees, the very important part of the model is the wealth of the food source. It is assumed that the number of the food sources in bee colony is equivalent to the number of the solutions of analyzed optimization problem. Moreover, the food location can indicate the coordinates of the solution in optimization problem. The among of the nectar in the food source can be treated, as the value of the objective function related to the solution.

The process of the solution founding in proposed algorithm presents as follows. Firstly, the primary food sources are chosen according to the following formula:

$$x_{ij} = x_{j_{min}} + rand\,[0,1]\,(x_{j_{max}} - x_{j_{min}}) \tag{4}$$

In the formula above uses parameters which explanations are presented in the Table 4.

Table 4. *Parameters used in food source coordinates formula.*

| **Parameter** | **Parameter interpretation** | **Additional information** |
|---|---|---|
| $i$ | Number of food source | $i \in \{1, 2, \ldots, P\}$, $P \in \mathbb{N} \backslash \{0\}$,<br>$P -$ number of food sources |
| $j$ | Analyzed dimension | $j \in \{1, 2, \ldots, D\}$, $D \in \mathbb{N} \backslash \{0\}$,<br>$D -$ number of dimensions |
| $x_{ij}$ | Coordinate of the food source calculated in regard to the $j^{th}$ dimension and $i^{th}$ food source | |
| $x_{j_{min}}$ | Minimum possible value for the coordinate related to the $j^{th}$ dimension | |
| $x_{j_{max}}$ | Maximum possible value for the coordinate related to the $j^{th}$ dimension | |
| $rand\,[0,1]$ | Function generating the random values from the range $[0,1]$ | |

The chosen coordinates of the food source comprise the set of the potential solutions of the investigated optimization problem. This set will be cyclically updated in the next iterations by the employed, onlooker and scout bees.

Secondly, the initial choice of the employed bees, onlooker bees and scout bees is made according to assumptions which have been previously undertaken. The employed bees go to the food sources and they make the verification of the quality of the food sources. After that, the coordinates of the food sources are updated based on the coordinates of analyzed bees and coordinates of other employed bees according to the expression presented below:

$$x_{ij_{new}} = x_{ij} + rand\,[-1,1]\,(x_{ij} - x_{kj})\,, \quad i,k \in \{1,2,\ldots,P\}, P \in \mathbb{N} \setminus \{0\}, i \neq k \quad (5)$$

Table 5 includes the explanations of parameters used in the formula above.

Table 5. *Parameters used in updating process.*

| **Parameter** | **Parameter interpretation** |
|---|---|
| $x_{ij_{new}}$ | Updated coordinate of the food source calculated in regard to the $j^{th}$ dimension |
| $rand\,[-1,1]$ | Function generating the random values from the range $[-1,1]$ |

For all new coordinates of the food source, the verification of the quality of the nectar is made. For this purpose, the objective function is calculated and its value is compared to the value of the objective function computed in the previous location. When the better quality of the nectar is reached, the food source coordinates are changed.

Then, the update of the location of the onlooker bees is made. This process occurs when all employed bees go back to the beehive and give other bees information about the food locations and quality of the nectar. Onlooker bees make the decision related to the choice of the food source based on the values of the objective function calculated previously for all food locations. When the quality of the food in the selected food source is greater than in other location, the probability of the choice of that food source is also greater. This probability can be described according to the following formula:

$$p_i = \frac{F\,(x_i)}{\sum_{i=1}^{P} F\,(x_i)}, \quad i \in \{1,2,\ldots,P\}, P \in \mathbb{N} \setminus \{0\} \quad (6)$$

Parameters used in the formula presented above have the meanings shown in the Table 6.

Table 6. *Parameters used in updating process.*

| **Parameter** | **Parameter interpretation** |
|---|---|
| $p_{ij}$ | Probability of the choice of the $i^{th}$ |
| $F$ | Objective function |
| $x_i$ | Vector of coordinates of $i^{th}$ food source |

According to the calculated probabilities, onlooker bees go the chosen food sources. However, onlooker bees make some corrections during their flights because they take into account their own observations. The mentioned corrections are made according to the expression (5). Then, they verify the qualities of the nectar in chosen locations and compare them to the values of objective function calculated for locations visited by the employed bees. If the decision of the change the food source was good, the food source coordinates are changed.

If the quality of the solution is not getting better after fixed number of attempts to change the coordinates of the current food source, the employed bee, related to the analyzed food location, becomes the scout bee and the investigated food location is treated as empty. The empty food source is replaced by the other location which is chosen randomly according to the expression (4).

The algorithm is stopped after maximum number of iterations or when the required accuracy is obtained.

### 2.3. Genetic Algorithms

Taking into consideration the form of the problem undertaken in this paper and its complexity, the genetic algorithm had to be adjusted. Due to this fact some modifications have been applied. Thus, the simplified scheme of the genetic algorithm presents as follows. Firstly, the new population is generated randomly. The population consists of fixed number of chromosomes. On the other hand, each chromosome consists of fixed number of parts. Each part of chromosome contains, in turn, previously definied number of genes. It is assumed that the single gene can be characterized by one of two possibles values: 0 or 1. Due to this fact each part of chromosome can is described by the binary string and each chromosome is represented by the vector of binary string. Taking into consideration that the primarily generated numbers are real numbers, they have to be transformed into binary ones.

The second task is related to calculation the value of the objective function for each chromosome. The obtained values are also known as the match rate of the chromosome. Then, the probabilities of chromosome selection is determinated according to the formula presented below:

$$p_i = \frac{F\left(x_i\right)}{\sum_{i=1}^{P} F\left(x_i\right)} \tag{7}$$

The parameters used in formula above have the meanings presented in the Table 7. Chromosomes are chosen using the roulette wheel or tournament selection method according to values of prababilities presented above.

The next step provide the selection of genes of chromosomes which will be mutated. The mutation is related to the change of the binary value of single gene in the following way. If the value of selected gene is equal to 1, it is transformed to 0. If its

Table 7. *Parameters used in the probabilities of chromosome selection formula.*

| **Parameter** | **Parameter interpretation** | **Additional information** |
|---|---|---|
| $i$ | Number of chromosome | $i \in \{1, 2, \ldots, NC\}$, $NC \in \mathbb{N}\backslash\{0\}$,<br>$NC$ – number of food sources |
| $p_i$ | Probability of the the $i^{th}$ chromosome selection | |
| $F$ | Objective function | |
| $x_i$ | Vector of genes of the $i^{th}$ chromosome | |

value is 0, it transforms into 1. However, the probability of the mutation is relatively small.

Then, the chromosomes which will be crossed are chosen. The probability of choice is fixed and it is usually assumed that its value belongs to the interval from 0.1 to 0.3. After the choosing process, the selected chromosomes are paired. The crossover process occurs for each pair. Primarily, the number of gene is randomly generated. After that, all genes of first chromosome of the pair which numbers are equal or greater than the drawn number are changed using the respective genes of the second chromosome of the analyzed pair. The genes changing in the second chromosome occurs in the similar way using the respective genes of the first chromosome. The scheme of the crossover process described above is presented in the Figure 1.

Moreover, the another version of the crossover process has been prepared. The principal difference beteween both investigated versions of the analyzed algorithm is related to the crossover process. Similarly to the previous case, the number og gene is randomly generated. However, after that process, only fixed number of next genes of the first chromosome of the investigated pair are changed using the respective genes of the second one. Analogously to the previous modification, the number of the first gene which will be changed during the crossover process is equal to the drawn number. The scheme of that version of crossover process is demonstrated in Figure 2.

The final part of the algorithm is related to generate of the new population, consisting of mutated, crossed and previously selected chromosomes.

## 3. Simulations and Their Results

This section presents the description of the simulations and main results which have been obtained. The simulations have been prepared in Matlab environment. The computational node which has been used during the simulation process includes the

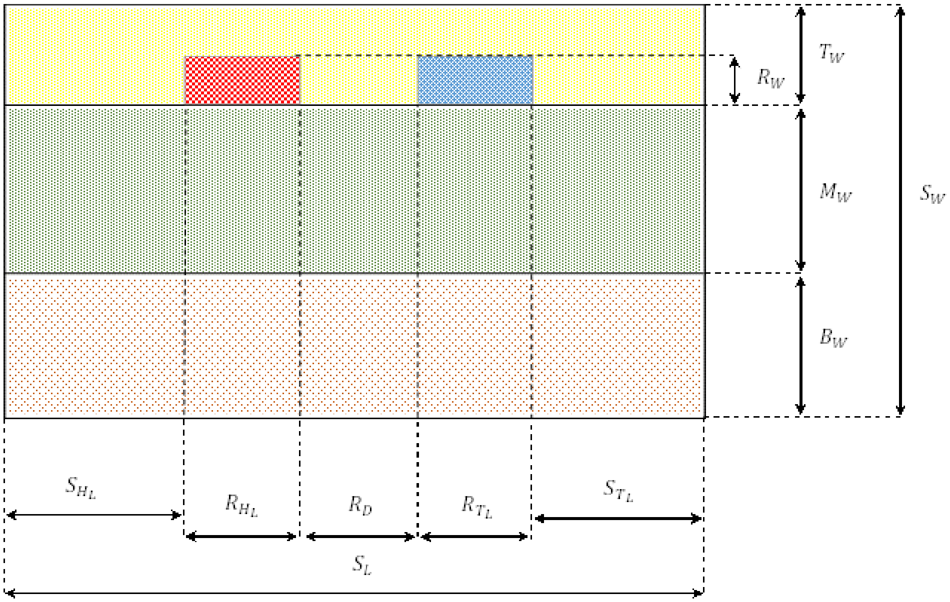

Fig. 1. *The scheme of the crossover process (version I).*

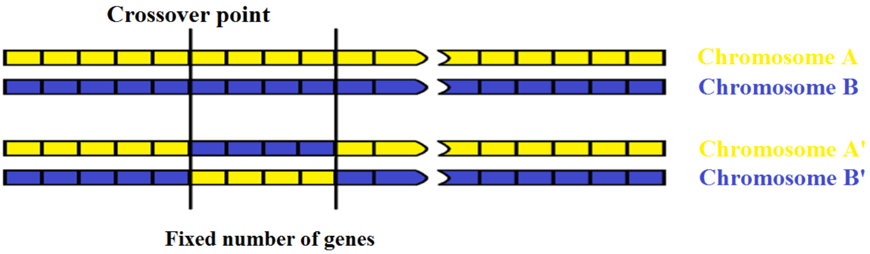

Fig. 2. *The scheme of the crossover process (version II).*

four-cores (eight logical threads) Intel®Core$^{TM}$ i7 2.5 GHz CPU (3.5 GHz in turbo mode), 16 GB of DDR3 memory and Microsoft Windows ver. 10 operating system. Moreover, the presented numerical algorithms are characterized by the sparse matrices implementation. As it was mentioned previously, the value of the heat transfer coefficient depends on many factors, however one of the most important one is the temperature rise above the ambient temperature. Moreover, in still air conditions, its value reflects the influence of two heat transfer mechanisms which occur simultaneously, the radiation and natural convection [11]. Taking into consideration these three significant factors, it can be assumed that the value of the average heat transfer coefficient can be evaluated using the following power function formula [12]:

$$h_{average} = a \cdot (\triangle T)^b + c \tag{8}$$

Symbol used in the expression (8) have the explanations presented in the Table 8.

Table 8. *Heat transfer coefficient formula.*

| **Parameter** | **Parameter interpretation** | **Additional information** |
|---|---|---|
| $h_{average}$ | Average heat transfer coefficient | $h_{average} > 0$ |
| $\triangle T$ | Temperature rise above the ambient temperature | $\triangle T \geq 0$ |
| $a$ | | $a > 0$ |
| $b$ | | $b > 0$ |
| $c$ | Parameter which reflects the value of the heat transfer coefficient when the temperature rise is not observed | $c > 0$ |

Parameters $a$, $b$ and $c$ have to be fitted using numerical methods. It means that the investigated heat transfer problem can treated as the three-dimensional problem and the values of the mentioned parameters can be identified as the coordinates of the optimal point. In order to determine the values of the three mentioned constants, the empirical values of the heat exchange coefficient have been needed. They have been obtained analytically based on the measurement carried out in still air conditions. Their values are presented in the Table 9.

Firstly, the simulation results of the heat transfer coefficient fitting formula determination based on the ant colony optimization algorithms will be presented. However, the objective function and all demanded parameters have to be defined. The objective function is presented by the following formula:

$$J(h, \triangle T, a, b, c) = \sum_{i=1}^{n} \left(h_i - \left(a \cdot (\triangle T)^b + c\right)\right)^2 \tag{9}$$

where $n$ means the total number of measurements. Values of the parameters $h_i$ and $\triangle T_i$, $i \in \{1, \ldots, n\}$, are presented in the Table 9. On the other hand, the Table 10 presents the parameters values which have been used during the simulations.

Based on parameters values presented in Table 10, the fitting plotted in the Figure 3 has been obtained.

Moreover, using parameters values prepared for the second version of the analysed algorithm, the result demonstrated in the Figure 4 has been obtained.

Table 9. *Measurement results.*

| **Number of measurement** | **Junction temp. rise** $[K]$ | **Heat transfer coeff. values based on measurements** $\left[\frac{W}{m^2 \cdot K}\right]$ |
|---|---|---|
| 1. | 3.5448 | 6.719518 |
| 2. | 6.3331 | 7.807035 |
| 3. | 9.2844 | 8.164184 |
| 4. | 11.6849 | 8.878489 |
| 5. | 14.4885 | 9.147993 |
| 6. | 17.1479 | 9.460037 |
| 7. | 20.2547 | 9.512457 |
| 8. | 22.7716 | 9.884705 |
| 9. | 26.0152 | 9.910199 |
| 10. | 27.9529 | 10.475383 |
| 11. | 30.5522 | 10.767441 |
| 12. | 33.2508 | 11.027259 |
| 13. | 35.9636 | 11.273734 |
| 14. | 38.8007 | 11.501820 |
| 15. | 42.1732 | 11.589751 |
| 16. | 45.4134 | 11.731151 |
| 17. | 48.6293 | 11.915853 |
| 18. | 51.6793 | 12.156714 |
| 19. | 54.3120 | 12.504787 |
| 20. | 59.3753 | 12.343296 |

Then, the bee colony algorithm has been used in order to fit the parameters described the heat transfer coefficient formula. The objective function J used in this algorithm is formulated similarly to previous cases and it can be formulated using equation (9). All significant algorithm parameters are presented in Table 11.
The fitting of the investigated parameters a, b and c is shown in Figure 5.

Finally, the genetic algorithm has been used. Accordingly to the previous analyzed algorithms, the objective function $J$ can be described using expression (9). Moreover, the parameters shown in Table 12 have been assumed.
Moreover, as it was mentioned in subsection 2.3 and shown in Figure 1 and Figure 2, two different mechanisms of crossover have been assumed. The fitting result based on the first assumption is presented in Figure 6.

On the other hand, the Figure 7 presents the fitting results when the second version of the crossover process is employed.

It is clearly visible that all results are very similar. Due to this fact, it is worth

Table 10. *Parameters values of the ant colony optimization algorithms.*

| **Parameter name** | **Value/expression** | | **Additional information** |
|---|---|---|---|
| | **Version I** | **Version II** | |
| Number of dimensions | 3 | | Number of dimensions is related to the number of parameters which have to be fitted. |
| Number of nodes in one dimension | 100 | n/a | The same number of nodes has been fixed for each dimension. |
| Total number of nodes | 1 000 000 | n/a | In the second version of the algorithm, the mesh is not assumed. |
| Start point coordinates | $a = 2.1$<br>$b = 0.5$<br>$c = 3.5$ | | Points chosen randomly. |
| Number of ants | 50 | | |
| Maximum number of iterations | 10 000 | | |
| Pheromone weight | 0.5 | | |
| Heuristic function weight | 5 | | |
| Primarily pheromone amount | 0.00001 | | |
| Pheromone vaporising coefficient | 0.1 | | |
| Pheromone amount coefficient | 1 | | |
| Heuristic function | $\eta = 0.01$ | $\eta = \frac{1}{J}$ | The constant value of the heuristic function in the first version of the algorithm is a result of the same differences between mesh nodes. |

analysing all of them in more detail. The Table 13 compares the main differences between results obtained all investigated numerical algorithms.

Based on the data presented in Table 13, it is visible that the better results has

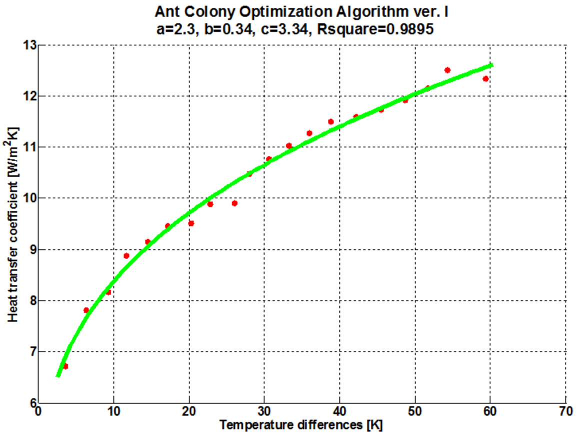

Fig. 3. *Fitting result of the ant colony optimization ver. I algorithm.*

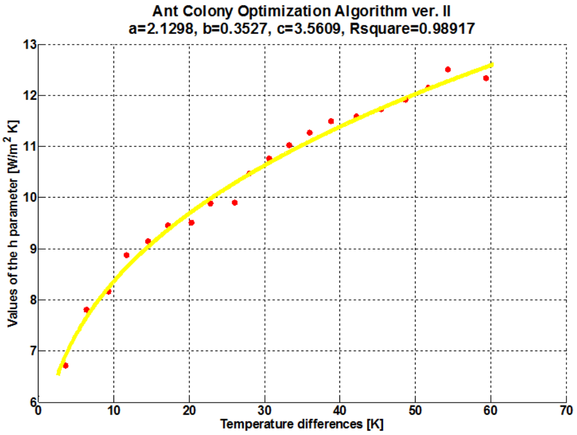

Fig. 4. *Fitting result of the ant colony optimization ver. II algorithm.*

been obtained using the second version of the ant colony optimization algorithm. It is indicated by the lowest number of algorithm iterations, the shortest evaluation time. Moreover, the goodness of the heat transfer coefficient parameters fitting is confirmed by the small value of the sum of squared errors, which is equal to 0.53513, and by the big value of the coefficient of determination, which almost equals the unity. On the other hand, results obtained using the first version of the ant colony optimization algorithm are also characterized by the good quality of fitting, however the number of iterations needed to obtain these results is significantly greater than

Table 11. *Parameters values of the bee colony optimization algorithm.*

| **Parameter** | **Value/expression** | **Additional information** |
|---|---|---|
| Number of dimensions | 3 | Number of dimensions is related to the number of parameters which have to be fitted. |
| Start point coordinates | | Different start points for each bee |
| Total number of bees | 100 | |
| Initial number of employed bees | 45 | It was assumed that number of employed bees and onlooker bees is equal. |
| Initial number of onlooker bees | 45 | It was assumed that number of employed bees and onlooker bees is equal. |
| Initial number of scaut bees | 10 | |
| Max. number of attempts to improve quality of nectar | 10 | |
| Max. number of iterations | 10 000 | |
| Objective function in probability formula | $F = \frac{1}{J}$ | |

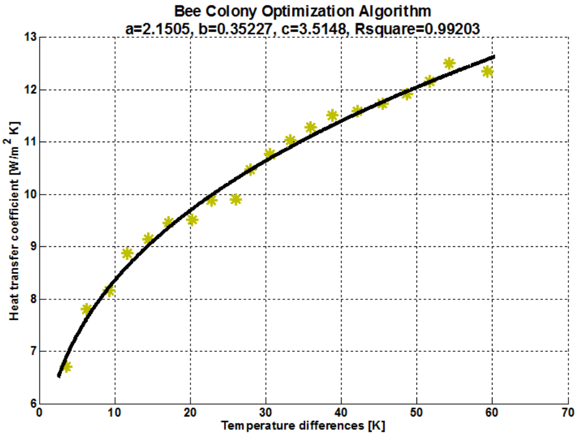

Fig. 5. *Fitting result of the bee colony optimization algorithm.*

Table 12. *Parameters values of the genetic algorithm.*

| **Parameter** | **Value/expr.** | **Additional information** |
|---|---|---|
| Number of chromosomes | 50 | Number of dimensions is related to number of parameters to be fitted. |
| Number of groups in each chromosome | 3 | Number of group is related to number of parameters to be fitted. |
| Number of genes in each chromosome | 39 | 13 genes for $a$, 13 genes for $b$ and 13 genes for $c$ parameters |
| Probability of mutation | 0.01 | It was assumed that number of employed bees and onlooker bees is equal. |
| Probability of crossover | 0.2 | It was assumed that number of employed bees and onlooker bees is equal. |
| Maximum number of iterations | 10 000 | |
| Objective function in probability formula | $F = \frac{1}{J}$ | |

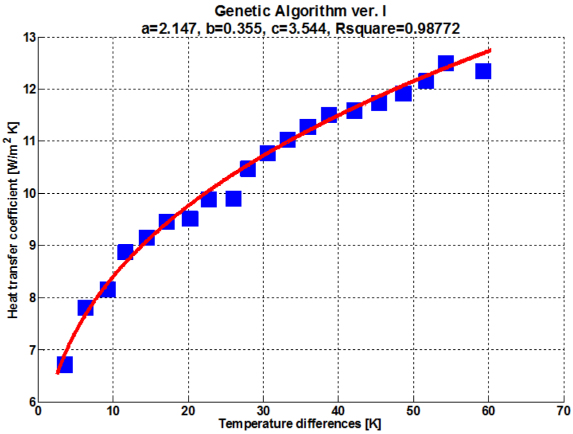

Fig. 6. *Fitting result of the genetic algorithm (version I).*

in the previously analyzed version. This meaningful difference is also shown in Figure 8 and 9.

They show the distance travelled by ants which reach the optimal point in the shortest time in the first and the second version of the ant colony optimization

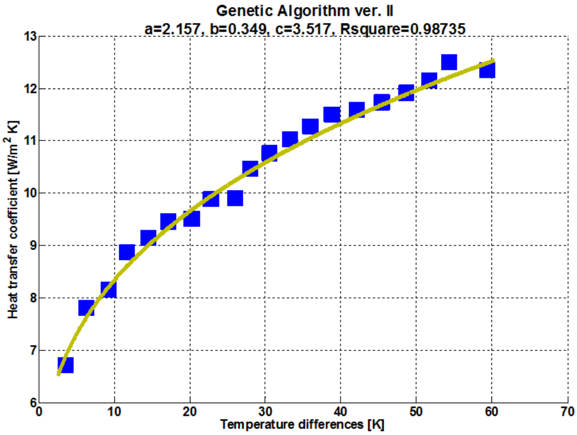

Fig. 7. *Fitting result of the genetic algorithm (version II).*

Table 13. *Results comparison.*

| **Parameter** | **Algorithm name** | | | | |
|---|---|---|---|---|---|
| | Ant Col. Opt. (ver. I) | Ant Col. Opt. (ver. II) | Bee Col. Opt. | Genetic (ver. I) | Genetic (ver. II) |
| Number of iterations | 3090 | **19** | 2837 | 781 | 952 |
| Evaluation time [$s$] | 9.3141 | **0.4509** | 19.6171 | 5.7230 | 7.9221 |
| Sum of squared errors | 0.52223 | **0.53513** | 0.52696 | 0.63360 | 0.61401 |
| Coefficient of determination | 0.98950 | **0.98917** | 0.99203 | 0.98772 | 0.98735 |

algorithm, respectively. It is shown that in the case, when the mesh of points is not used and the objective function in ant move probability formula is defined according to the expression presented in the Table 10, the results are obtained faster and in less number of iterations than in the opposite case.

## 4. Conclusions

This paper demonstrates the numerical approaches in determination of the dependence between heat transfer coefficient values and temperature rise above the ambient temperature values. This dependence is characterized by non-linear func-

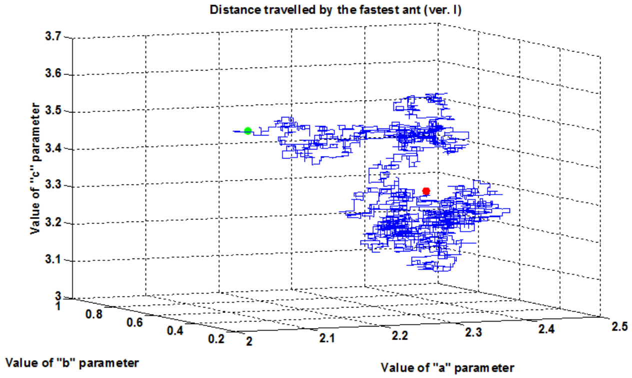

Fig. 8. *Path travelled by the fastest ant in the first version of the modified ant colony optimization algorithm.*

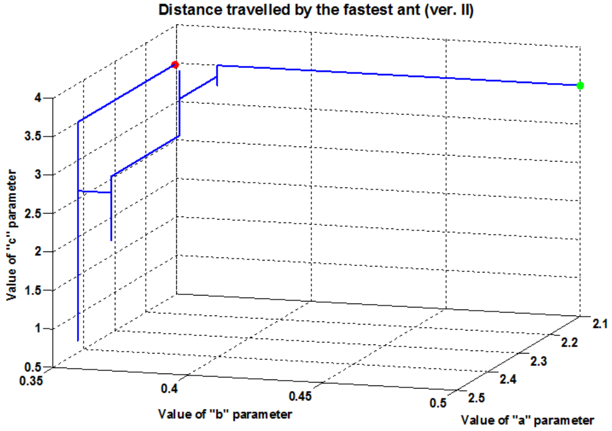

Fig. 9. *Path travelled by the fastest ant in the second version of the modified ant colony optimization algorithm.*

tion. Moreover, based on the literature, it can be assumed that this dependence can be expressed by the power function. This assumption has been confirmed by the simulation results.

The simulation results have been obtained using ant colony optimization, bee colony optimization and genetic algorithms. Results comparison suggests that definitely the fastest method among investigated ones is the second version of the ant colony optimization algorithm which do not assume the necessity of the mesh of points generation.

It is worth saying that presented results are very significant for designers of modern electronic circuits. Practical implementation of obtained solutions can improve the accuracy of the thermal simulations of complex electronic structures and optimize the reliability of these electronic appliances.

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Department of Microelectronics and Computer Sciences
Łódź University of Technology
Wólczańska 221/223, PL-90-924 Łódź
Poland
E-mail: traszk@dmcs.pl
asamson@dmcs.pl

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## ZASTOSOWANIE ALGORYTMU GENETYCZNEGO ORAZ ALGORYTMÓW ROJOWYCH DO ESTYMACJI WSPÓŁCZYNNIKA WYMIANY CIEPŁA

Streszczenie

W pracy przedstawiono zależność współczynnika wmiany ciepła od temperatury. Wyniki otrzymane zostały przy użyciu dwóch grup algorytmów. Z grupy pierwszej algorytmów rojowych, do obliczeń wybrane zostały algorytmy kolonii mrówek oraz roju pszczół. Z grupy trzeciej wybrany zostałalgorytm genetyczny. Otrzymane rezultaty zostały dokładnie opisane oraz porównane. Ponadto, czas symulacji, dokładność oraz liczba iteracji zastosowanych algorytmów także zostały zawarte w pracy.

*Słowa kluczowe:* algorytmy sztucznej inteligencji, algorytmy rojowe, algorytm roju pszczół, algorytm kolonii mrówek, algorytm genetyczny, współczynnik wymiany ciepła, zależność temperaturowa