Genetic Algorithms in Electromagnetism: The Helmholtz Coils

Bożena Borowska

Institute of Computer Science, Technical University of Łódź
ul. Wólczańska 215, 93-005 Łódź, Poland
e-mail: bozena@ics.p.lodz.pl

Stefan Nadolski

Division of Computer Networks, Technical University of Łódź
ul. Stefanowskiego 18/22, 90-924 Łódź, Poland
e-mail: snadolski@zsku.p.lodz.pl

Abstract. *In this work, the modified genetic algorithm has been applied to solve the Helmholtz coil problem. The task of the algorithm was to determine the radius of the coils and the distance between them, which would assure that a priori assumed level of non-homogeneity of magnetic field is maintained. In the implemented genetic algorithm, the ternary system of representation has been used. Based on the results of performed experiments, the accuracy, efficiency and usefulness of the proposed algorithm has been assessed.*

1. Introduction

Helmholtz coils is a system of two identical coils placed at the distance d one from another, and each of them with current I and with a shape of circle with radius R. The system is characterized by mirror symmetry. This kind of coils is used with the purpose of obtaining (generating) relatively homogeneous magnetic field, in the space close to the center of symmetry of the system. Decomposition of the component vector of the magnetic field which is parallel to the symmetry axis of the system, as a function of its position on the symmetry axis, is described (and supported with examples) in [1]. Decomposition of the same component vector in the symmetry plane of the system is analyzed in [2]. The best results are obtained for the, so called, ideal coil, when d=R.

In this paper, the general case has been analyzed. For this purpose, the mathematical relationship has been derived, which permits to compute the

absolute values of magnetic field H (vector sum of three components) in an arbitrary point of three-dimensional space xyz. It has been assumed, that the radius of coils is constant as is equal to 1m (R=1m). The variable parameter is the distance between the coils, d=2Z (Fig.1).

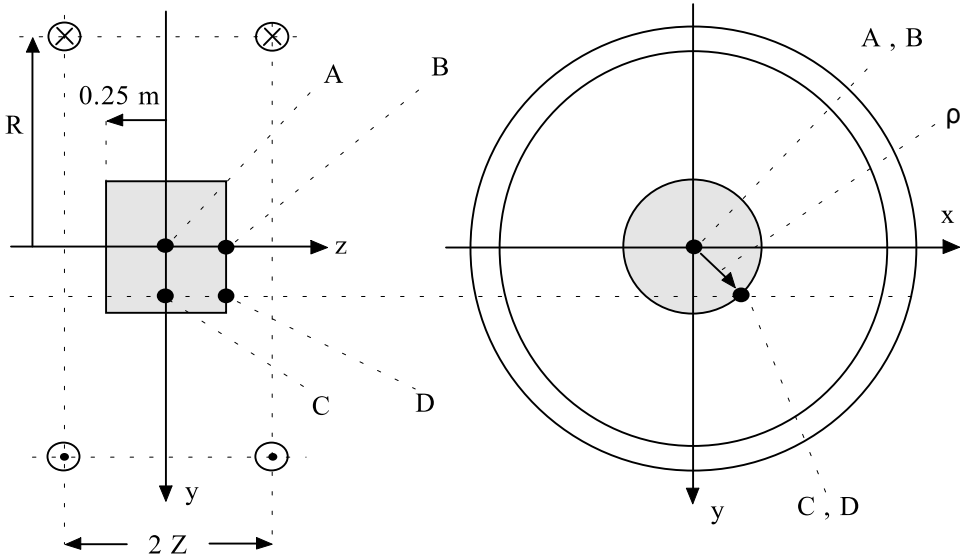Fig. 1. Helmholtz coil. R=1m – radius of the single circular loop with the current I=1A, 2Z – separation between current loops. The shadowed area represents the cylinder with selected points A, B, C, D for calculations.

The next step, taken in this investigation, was to define the space, in which non-homogeneity of magnetic field Δ should be determined, as a function of Z. This step has permitted to find the optimum value $Z = Z_{opt}$, for which $\Delta = \Delta_{min}$. Based on the obtained solution, the following research task has been formulated:

Applying optimization process which utilizes genetic algorithms, it is necessary to determine the minimum coil-radius R' and the distance between the coils 2Z' for which the level of non-homogeneity of magnetic field is Δ_{min} .

The idea of utilizing genetic algorithm in electromagnetism is known [3,4]. The purpose of present work has been to test how genetic algorithms perform in case of relatively simple system of Helmholtz coils. The a priori knowledge of the exact results (R=1m, $Z = Z_{opt}$) permits to analyze the accuracy and usefulness of results generated by genetic algorithms. It can be considered

as a base for further research on utilization of genetic algorithms in electromagnetism.

2. Helmholtz coil – parameter determination

A segment of infinitely thin conductor with current I and with length d**l** (vector) generates, in distance **r** (vector) from this segment, magnetic field equal to [5,6]:

$$d\mathbf{H} = \frac{I\,d\mathbf{l} \times \mathbf{r}}{4\pi\,r^3} \tag{1}$$

Assuming, that the symmetry axis of the coils coincides with the z-axis, and that the center of symmetry of the coils coincides with the center of xyz system (Cartesian system of coordinates), the following relation (known formula adopted for our case) is obtained for the absolute values of the magnetic field in the arbitrary point xyz.

$$
\begin{aligned}
H = \frac{IR}{4\pi} \\
\Bigg(\Bigg(\int_0^{2\pi} \frac{\sin(\phi + \pi/2)(z - Z)}{((x - R\cos\phi)^2 + (y - R\sin\phi)^2 + (z - Z)^2)^{3/2}}\,d\phi + \\
\int_0^{2\pi} \frac{\sin(\phi + \pi/2)(z + Z)}{((x - R\cos\phi)^2 + (y - R\sin\phi)^2 + (z + Z)^2)^{3/2}}\,d\phi \Bigg)^2 + \\
\Bigg(\int_0^{2\pi} \frac{\cos(\phi + \pi/2)(z - Z)}{((x - R\cos\phi)^2 + (y - R\sin\phi)^2 + (z - Z)^2)^{3/2}}\,d\phi + \\
\int_0^{2\pi} \frac{\cos(\phi + \pi/2)(z + Z)}{((x - R\cos\phi)^2 + (y - R\sin\phi)^2 + (z + Z)^2)^{3/2}}\,d\phi \Bigg)^2 + \\
\Bigg(\int_0^{2\pi} \frac{(\cos(\phi + \pi/2)(y - R\sin\phi) - \sin(\phi + \pi/2)(x - R\cos\phi))}{((x - R\cos\phi)^2 + (y - R\sin\phi)^2 + (z - Z)^2)^{3/2}}\,d\phi + \\
\int_0^{2\pi} \frac{(\cos(\phi + \pi/2)(y - R\sin\phi) - \sin(\phi + \pi/2)(x - R\cos\phi))}{((x - R\cos\phi)^2 + (y - R\sin\phi)^2 + (z + Z)^2)^{3/2}}\,d\phi \Bigg)^2 \Bigg)^{1/2}
\end{aligned}
\tag{2}
$$

The spaces in which non-homogeneity of magnetic field Δ is defined: cylinder, whose symmetry axis coincides with the z-axis, and whose center coincides with the symmetry center of the coils. The cylinder radius is equal to $\rho = (0.2^2 + 0.2^2)^{1/2}$, and its length is 0.5m (Fig.1). Non-homogeneity of absolute values of magnetic field is defined as:

$$\Delta = \frac{\left|H_{0,0.25} - H_{0,0}\right| + \left|H_{\rho,0} - H_{0,0}\right| + \left|H_{\rho,0.25} - H_{0,0}\right|}{H_{0,0}} \tag{3}$$

where $H_{0,0}$ is the absolute value of magnetic field in the center of cylinder (point A), $H_{0,0.025}$ is the absolute value of magnetic field on the axis of the cylinder in the distance of 0.25m from the center of the cylinder (point B), $H_{\rho,0}$ is the absolute value of magnetic field on the surface of the cylinder in the middle of its length (point C), $H_{\rho,0.025}$ is the absolute value of magnetic field on the cylinder surface in the distance of 0.25m from the symmetry plane (point D),(Fig.1).

The result obtained:

Δ, expressed as a function of Z, reaches the minimum value $\Delta = \Delta_{min} = 0.0165108$ for $Z_{opt} = 0.485$ m at R=1m (Fig.2)
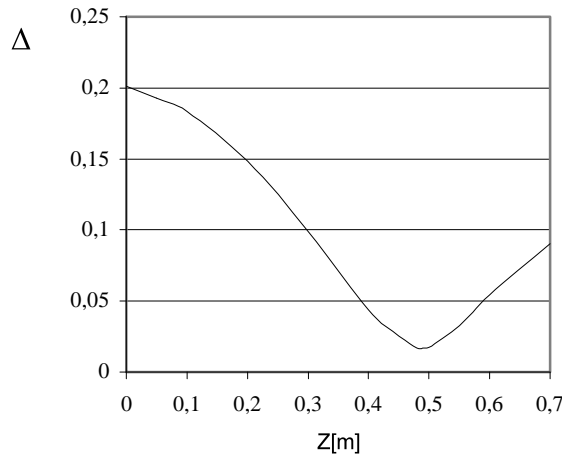

Fig. 2. Non-homogeneity of magnetic field versus a half of the distance between current loops Z.

3. Genetic algorithm used for investigation

In order to analyze the problem of the Helmholtz coil expressed in this work, a special genetic algorithm was proposed. This algorithm represents a modification of the classical genetic algorithms (GA) based on a ternary encoding system [7,8]. In this approach chromosomes are represented as strings of genes whose alleles can take values of 0, 1 and 2. Each chromosome consists of a few sub-chromosomes, each of which represents an individual parameter. The length of a sub-chromosome equals 8 genes. Gene values for each individual of the initial population are generated randomly. As a result, it is possible that multiple identical chromosomes could occur (but they need not). The quality measure of the solution represented by the chromosome is a fitness function, which is represented by the mathematical formula (3) depicted in chapter 2 of the following paper.

The choice of the individuals that participate in formation of a new (consecutive) generation is executed by means of the non-linear ranking selection method [9], according to which the chromosomes are ordered in a ranking list regarding their fitness function values. A specific number called "rank" is attributed to each individual. The individual with the largest value of the fitness function receives the highest value of the rank, whereas the lowest rank is attributed to the individual with the lowest value of the fitness function. The probability of the selection of an individual to the mating pool being formed can be calculated using the following nonlinear function (4):

$$F(k,s,n) = \frac{n \cdot s^{(k-1)}}{\sum\limits_{i=1}^{n} s^{i-1}} \qquad (4)$$

where: k – rank of the individual, n – number of selected individuals, s – selection coefficient

In the algorithm used for the investigation, a one-point crossover was used with the probability $p_c=1$, whereas the probability of the mutation operator was within the range $0 < p_m < 0.4$. The selection coefficient was $s=1.41$. The algorithm is stopped when consecutive iterations do not improve fitness (the results).

The investigation was performed for populations consisting of 20, 50, 100 and 200 individuals.

4. Results and discussion

The essential problem in this work was to determine the radius of the coils as well as the distance between them so as to maintain the established magnetic

field non-homogeneity. In order to evaluate the efficiency of the algorithm used to solve this problem, a special computer program was written in Java.

In the first stage of the investigations, an influence of the mutation probability p_m on the algorithm performance was determined. The computations were made for R, $Z \in [-10,10]$, and for the accuracy of 0.001. The exemplary results of these experiments are described below (Fig. 3-6). All the values are the average of 20 trials for each combination of parameters.
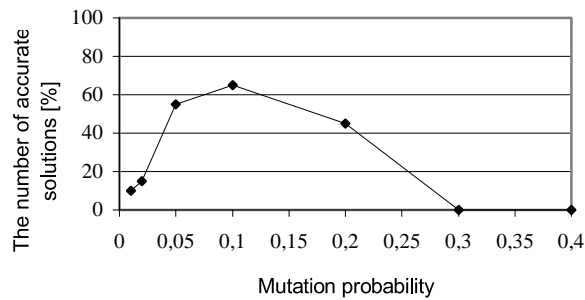

Fig. 3. The number of accurate solutions versus the mutation probability p_m, for the population of 20 individuals.
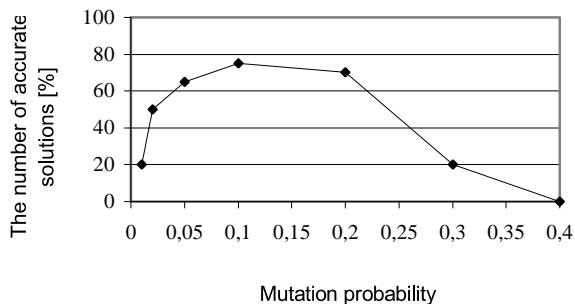

Fig. 4. The number of accurate solutions versus the mutation probability p_m, for the population of 50 individuals.
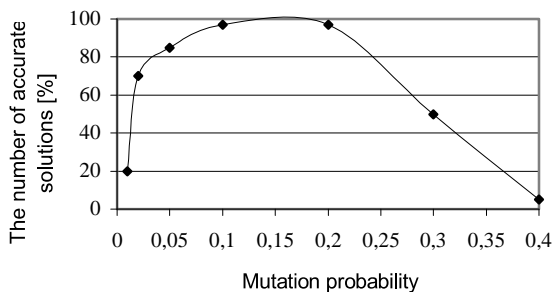
Fig. 5. The number of accurate solutions versus the mutation
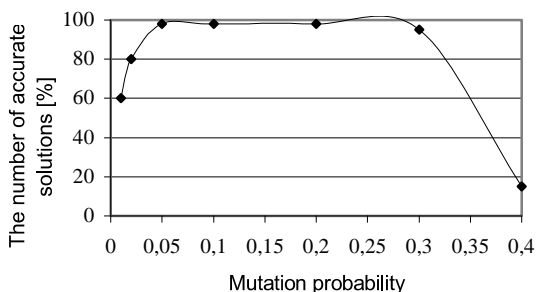probability p_m, for the population of 100 individuals.

Fig. 6. The number of accurate solutions versus the mutation
probability p_m, for the population of 200 individuals.

The analysis of the results clearly showed that the higher the probability value p_m the more accurate solutions were achieved. Moreover, the larger the cardinality of the initial population was, the more chances to find an optimal solution were. For the initial population of only 20 chromosomes, within 100 generations and the probability $p_m=0.02$, it was only 15 % of all trials that were carried out, that the algorithm found the accurate solution. Furthermore, where the same generation number and p_m value, were kept but the cardinality of the population was increased to 50 individuals, half of the solutions turned out to be accurate, whereas for the population of 200 chromosomes, the number of accurate solution reached 80 %. However, further increase of the mutation probability resulted in a deterioration of the genetic algorithm's performance, and this tendency was particularly visible for small populations. In case of the population comprising of 20 individuals, the best results were attained for $p_m=0.1$. For larger p_m-value, the algorithm was gaining and losing alternately best fit individuals in subsequent generations (Fig. 7) thus making the accurate

solution difficult or even impossible to achieve. When the initial population was more numerous, and comprised of 200 chromosomes, such behavior was observed for p_m=0.4.
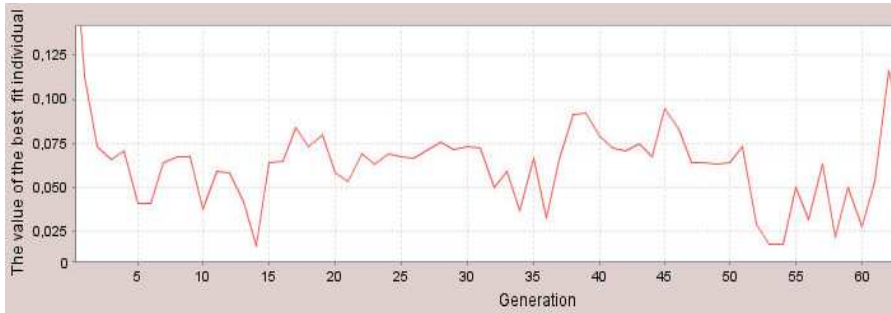

Fig. 7. Best fit individual values in subsequent generations of the initial population of 20 chromosomes and $p_m = 0.2$.

Poor results were also obtained for the mutation probability lower than 0.02, irrespective of the population quantity. This phenomenon resulted from a premature algorithm convergence.

In the following research, the best results – over 90 % of the accurate solutions – were achieved for the initial population comprising of 100 chromosomes and the probability within the range $0.1 \leq p_m \leq 0.2$ as well as for the population of 200 chromosomes and $0.05 \leq p_m \leq 0.3$. Best fit individual values in subsequent generations for the initial population comprising of 200 chromosomes and the probability p_m=0.2 were presented in Fig. 8.
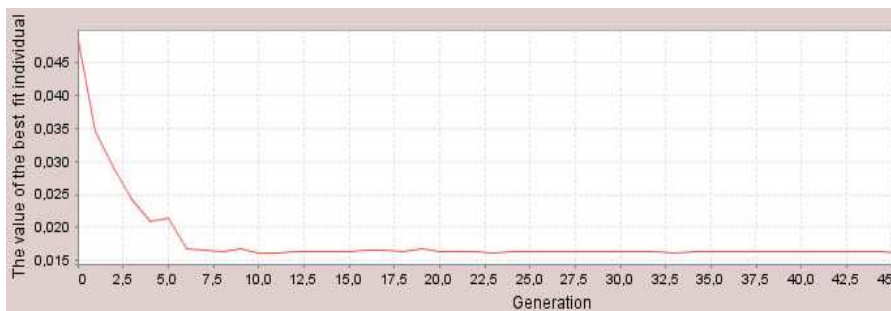

Fig. 8. Best fit individual values in subsequent generations for the population of 200 chromosomes and $p_m = 0.2$.

In the second stage of the research, an analysis to evaluate the influent of the cardinality of the initial population on the algorithm processing rate depending on the p_m-value was performed. The results of this investigation are shown

in Table 1. The values in each individual column depict average numbers of iterations after which accurate solutions were found for the initial populations of 20, 50, 100, and 200 chromosomes.

Table 1. The impact of the population cardinality on the algorithm processing rate for various p_m - values

P_m	The average number of iterations needed to achieve the accurate solutions depending on various p_m-values			
	20 chromosomes	50 chromosomes	100 chromosomes	200 chromosomes
0,4	-	-	43	12,2
0,3	-	48	13,5	6,57
0,2	23,2	18,67	7,22	6,83
0,1	21,56	13,93	7,15	4,9
0,05	21,9	16,71	10,53	6,29
0,02	36,33	16,42	15,7	15,14
0,01	53	19,4	17,1	13,33

The experiments showed that the larger was the cardinality of the initial population, the higher was the algorithm processing rate. For the population of 200 chromosomes and the probability p_m=0.05, the number of iterations (generations) necessary to achieve the accurate solution was over 3-times lower than for the population of 20 chromosomes, whereas the number of accurate solutions was almost 2-times larger respectively. However, when the mutation probability p_m is too large, the number of iteration significantly increases whereas the percentage of the accurate solutions decreases.

5. Summary

In this paper, a modification of the genetic algorithm employing the ternary representation of the Helmholtz coil problem was proposed. The algorithm task was to determine the radius and the distance between the coils, as these parameters ensure the established magnetic field to remain non-homogenic. A knowledge of the accurate solution enabled the precise analysis of the results achieved in the work. The experiments showed an advantageous effect of the larger cardinality of the initial population on the effectiveness of the proposed algorithm. It was found that the larger was the population cardinality the wider range of p_m as well as the lower number of iterations were obtained after which accurate solutions were found. An increase in the probability p_m may improve the algorithm effectiveness. However, for too large p_m-values the algorithm tends to lose best fit individuals in subsequent generations. As a result, a rapid increase of the iteration number accompanied with a decrease of the number of accurate solutions can be observed. Furthermore, when the mutation

probability is lower than p_m=0.02 a premature algorithm convergence is obtained.

A high efficiency of the genetic algorithm used for the problem of Helmholtz coils has sufficient grounds for further research on the application of GA methods in electromagnetism.

References

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