APPLICATION OF ADAPTIVE STEP LENGTH BACTERIAL FORAGING ALGORITHM FOR PARAMETER IDENTIFICATION OF TRANSFORMER DETAILED MODEL

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Abstract: The R-L-C-M model of power transformer is obtained from geometrical structure and is extremely appropriate for studying transient phenomena in a transformer and detecting mechanical faults. The precision of this model depends strongly on the precision of its parameters. The accuracy of these parameters that are calculated by analytical formulas is limited due to different reasons. In this paper an adaptive step length bacterial foraging algorithm (ASBFA) is introduced as a method to identify the parameters of R-L-C-M Model without employing any analytical formulas.

1 INTRODUCTION

Power transformers are modelled diversely depending on the aim of simulation, conditions of transformer operation and the shape of input signals. The modelling of a complex arrangement such as a transformer active part is a compromise between accuracy and complexity. The number of definable basic elements and thus the accuracy of the modelling are limited. Among different proposed models, the following classification can be used:

- Black-Box models [1] and [2]
- Physical models [3], [4], [5], [6] and [7].
- Hybrid model [8]

The Black-Box models are inappropriate for the modelling of winding defects and inner physical phenomena such as transient voltage distribution, since they present just the behaviour of the transformer on its terminals. The physical models are based on the geometry of the winding and its lumped equivalent circuit. These models are also valid for higher frequencies.

The modelling of windings by the detailed model enables the calculation of the currents and voltages using common electrical network analyzing tools (e.g. ATP, Pspice, etc.). Complex windings can be modelled with several coils by this model, which is not possible for the multi-phase transmission line model.

Investigations show that among different approaches of the detailed modelling, the one which is based on the self and mutual inductances is the most appropriate for the description of the magnetic field behaviour [9]. Therefore, this model was applied in [10] and it was shown that:

- The detailed R-L-C-M model is determined exclusively from the geometrical dimensions and its validity is sufficient for the frequency range of a few kHz up to approximately 1 MHz.
- The description based on the winding's geometry enables a simple consideration of the dielectric failures in the winding and the determination of the failure location.

Therefore, the R-L-C-M model is a highly useful model for power transformer industry and has been used up to now for a wide variety of purposes by authors in [4], [8], [10] and [11]. However, the precision of this model is limited due to the following reasons:

- Using lumped elements for the presentation of distributed electric and magnetic field behaviour,
- Manufacturing tolerances and parameter dispersions of a real winding arrangement and therefore no precise geometry dimensions,
- Calculation of model parameters analytically after some simplifications of the geometrical structure of the winding.

Since the precision of the model depends on precision of calculated parameters of the model, these parameters must be calculated as precisely as possible.

On the other hand, because of the above mentioned reasons and non-existence of production geometry of transformer in some cases, it is necessary to improve the analytically

calculated values or to find a method other than analytical method to obtain the parameters of the R-L-C-M model. In the present work, it is attempted to solve this problem with the help of an ASBF optimization algorithm.

2 . ADAPTIVE STEP LENGTH BACTERIAL FORAGING ALGORITHM

Many bio-inspired computational methodologies such as Genetic Algorithm (GA), Ant Colony Optimization (ACO), Particle Swarm Optimization (PSO) and Chaos algorithm have been intensively studied and applied to various optimization problems. In recent years, a new and rapidly growing subject, Bacterial Foraging Algorithm (BFA), which is inspired by the behaviour that E-coil bacteria searching for food in human intestines, attracts more and more attention and shows its advantage in global optimization. This algorithm is consisting of 4 main operations called chemotaxis, cell-to-cell communication, reproduction and elimination dispersal which is described widely in [12] and [13].

In the bacterial algorithm, reproduction is used in order to have better search in the function domain and more accuracy. This can be achieved using bigger population. Higher population cause more computation and it affects the speed of the algorithm. To enhance the speed of the algorithm the simplest and easiest way is to use a small population. But it can cause accuracy reduction or loose of convergence.

In this paper, in order to increase the speed of algorithm a small population is used and the above mentioned problems are solved using two alternative methods which are explained in the following A and B sections[13].

2.1 Adaptive step length

One of the most important parameters which has great influence on rapid convergence of bacterial foraging algorithm and is less attended is the applied step length (C) to each bacterium.

At the beginning of the search on the function domain, for a quick search and visiting more regions, it is better to use high step size and while the bacteria is approaching to a region with sufficient nutrient, for more precision search, shorter step size should be taken. To aim this goal, exponential changes for step size seem to be a good idea. In this paper this is done in a way that each bacterium according to its position will get its appropriate exponential step changes.

At the beginning, the step size is high then if a bacterium has reached a nutrient region, the step size gets smaller for better search accuracy. By applying single exponential step, this bacterium has to wait until the step size becomes short enough to have an accurate search. To solve this problem we propose multi exponential step size as shown in Figure 2, Figure 3 and Figure 4. Now we define a method to make multi exponential step changes.

In the following function the step size is reduced as L (index of elimination and dispersal) increases.

$$C = C_h \times e^{(L^a)} \tag{1}$$

From the above equation we have Ch for L=1, and at the ending stages we want to have Cl, so:

$$Cl = C_h \times e^{(\beta \times Ned^a)} \tag{2}$$

Then we have:

$$\beta = (\frac{1}{Ned})^a \times \ln(\frac{C_L}{C_h}) \tag{3}$$

The parameter a causes a better control on step reduction with varying L. for having continuous exponential reduction we have to keep this reduction even in the interior loop (chemotactic loop). This is done by setting up the following equation:

$$C_h \times e^{(\beta \times L^a)} \times e^{(\theta \times Nc)} = C_h \times e^{(\beta \times (L+1)^a)} \tag{4}$$

Then we have:

$$\theta = \beta \times \frac{-L^a + (L+1)^a}{Nc} \tag{5}$$

It should be considered that the bacteria are sorted ascending according to their fitness value. By the following equations we define a boundary between the highest and the lowest step size.

The other bacteria get their suitable step size according to their fitness values bounded by the following equations:

$$C(i) = C1 + (i-1) \times (\frac{Cs - C1}{s-1}) \tag{6}$$

$$C1 = C_{1h} \times e^{(\beta 1 \times (L^{a1} - 1))} \times e^{(\theta 1 \times (j-1))} \tag{7}$$

$$Cs = C_{sh} \times e^{(\beta s \times (L^{as} - 1))} \times e^{(\theta s \times (j-1))} \tag{8}$$

$$\beta 1 = (\frac{1}{Ned})^{a1} \times \ln(\frac{C_{1L}}{C_{1h}}) \tag{9}$$

$$\beta s = (\frac{1}{Ned})^{as} \times \ln(\frac{C_{sl}}{C_{sh}}) \quad (10)$$

$$\theta 1 = K1 \times (\beta 1 \times \frac{-L^{a1} + (L+1)^{a1}}{Nc}) \quad (11)$$

$$\theta s = Ks \times (\beta s \times \frac{-L^{as} + (L+1)^{as}}{Nc}) \quad (12)$$

In the equations (11) and (12) 1 and Ks are used to change the speed of step size reduction. By applying K1=Ks=1 in the above equations, we will have single exponential step length. For k1 & ks >1 the speed of reduction will be increased and vice versa. Other parameters are as follow:

C(i) = adaptive step length applied to each bacterium.

C_{1h} and C_{1L} are the highest and lowest step size applied to the best bacterium respectively.

C_{sh} and C_{sL} are the highest and lowest step size applied to the worst bacterium respectively.

a_1 and a_s are the coefficients which determine the influence of L in step size reduction.

i = number of bacterium

j = Chemo tactic index

L = Elimination-dispersal index

S = population size

Ned = number of Elimination-dispersal

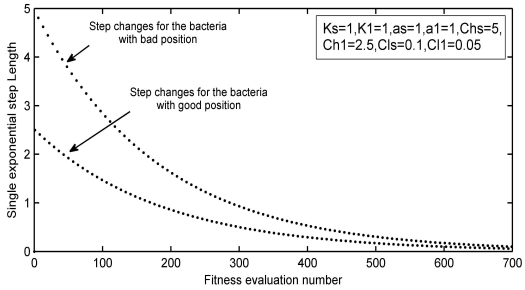

Figure 1: Single exponential step length

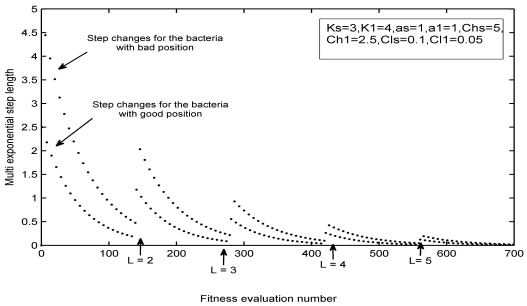

Figure 2: Multi exponential step length

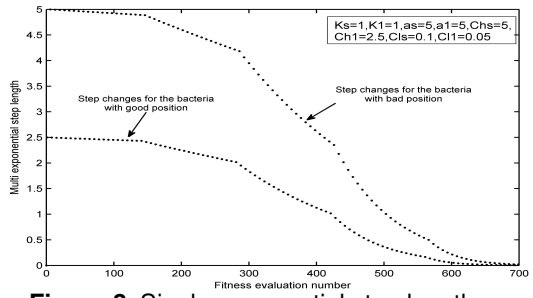

Figure 3: Single exponential step length

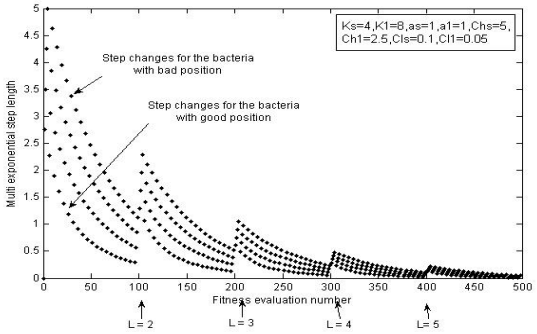

Figure 4: Multi exponential step length with S=4

2.2 New tumble method

In BFA, when the bacterium is close to global optimal some bad direction and tumbles on these directions can reduce the speed and accuracy of convergence. Sometimes movement on a bad direction has a benefit of escaping from local optimal. For keeping two above mentioned advantages of tumble while reducing its negative affects on the accuracy of convergence we propose a new tumble method.

In this method if $J^i(j+1,l) > J^i(j,l)$ the ith bacterium doesn't move and keeps its previous position $\theta^i(j+1,l) = \theta^i(j,l)$ and by using $J^i(j+1,l) = J^i(j+1,l)$.

We have increased the probability of the bacterium movement in the next chemotactic. By using this equation the bacterium thinks that is not in nutrient rich region therefore even for a not suitable proposed direction, the bacterium will move. This movement will not be too long because for a bad proposed direction, after a taken step the bacterium will understand that is placed near a nutrient rich region. Therefore the bacterium will not leave its previous good position so easily and also will not keep its position for too long.

The flowchart of the algorithm is shown in Figure 5.

3 PROPOSED PARAMETER IDENTIFICATION METHOD

The idea on which the method is based is to determine all the parameters of a mathematical

model of the transformer simultaneously, so that the model is capable of matching the input–output behaviour of the transformer. This can be achieved using the following approach.

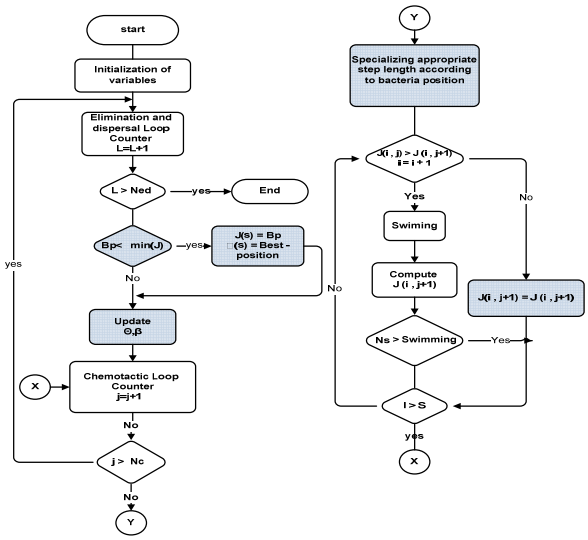

Figure 5: Adaptive step length BFA flowchart.

- **Step1:** An experimental test is carried out as in [14] and [15] consisting of an input excited by an impulse voltage, producing output voltage or current transfer function in frequency domain.
- **Step2:** Mathematical R-L-C-M detailed model of the transformer is implemented like [14] and [15] with the aim of simulating the experimental test of step1.
- **Step3:** A fitness function is computed as the inverse of the weighted sum of the square differences of the output variables acquired experimentally and those computed by simulation at the same frequencies.
- **Step4:** The unknown parameters of the transformer are iteratively updated so as to maximize the above fitness function.

To perform steps 3 and 4, an ASBFA optimization algorithm is used.

3.1 ASBFA for parameter identification

For identification of the unknown parameters of a model, parameters are regarded as the independent variables of the optimization problem and the fitness function that reflects the degree of goodness of the searched parameters is optimized (minimized).

The parameters of the previously presented mathematical model can be represented by the vector X1, in the case that the model contains 15 winding units.

$$\overline{X}_1 = (\mathrm{L_i}, \mathrm{L_{1,2}}, \mathrm{L_{1,3}}, ..., \mathrm{L_{1,15}}, \mathrm{C_i}, \mathrm{K_i}, \mathrm{Rs_i}) \qquad (13)$$

Practically, mutual inductance between two winding units by distance of greater than seven winding units is far too small and can be neglected. Under this condition, parameters of the model can be represented by vector P.

$$\overline{X} = (\mathrm{L_i}, \mathrm{L_{1,2}}, \mathrm{L_{1,3}}, ..., \mathrm{L_{1,8}}, \mathrm{C_i}, \mathrm{K_i}, \mathrm{Rs_i}) \qquad (14)$$

To identify the parameters, an impulse voltage applied on one terminal of winding is taken as the input and the short circuit current or open circuit voltage at the end terminal of winding are considered as the outputs of the system. Then the spectral distribution of the time domain signals is calculated using fast Fourier transformation (FFT). The quotient of output signal to input signal represents the transfer function in the frequency domain which is needed for identification purposes. So, the following vectors are defined to clarify the explanations:

$$H_I^M(i) = Measured\left|H_I(j\omega_i)\right| \qquad (15)$$

$$i=1,2,\ldots, n_1$$

$$H_I^C(i) = Calculated\left|H_I(j\omega_i)\right| \qquad (16)$$

$$i=1,2,\ldots, n_1$$

Where at i represent spectral frequency and H_I is the earth current transfer functions. The fitness of a particle used in the process of simulation is defined by equation (17).

$$fit = \sum_{i=1}^{n_1=54} [H_I^M(i) - H_I^C(i)]^2 \qquad (17)$$

3.2 ASBFA algorithm implementation

In the implementation of ASBFA optimization algorithm for transformer parameter identification, parameters of algorithm are taken as follow:

Nre=50,

Nc=55,

Ns=150,

S=10,

C1h=0.2, C1l=1e-4,

Csh=0.2, Csl=5e-4,

a1=1, as=1.

As the equation (17) shows, to calculate the fitness in each defined frequency, H_I^C must be calculated in that frequency from the model, while H_I^M is known experimentally.

Since H_I^M has 540 frequency points and simulation time of model equations in each frequency is about one second, calculation of the fitness will be an extremely time consuming process. To overcome this problem, in calculation of the fitness, some selected points of the transfer function are used instead of all points of the transfer function. The selected points of H_I^M , which are used in calculation of the fitness, are shown in Figure 6. It should be mentioned that the important points, such as resonance points, must be selected to get best results.

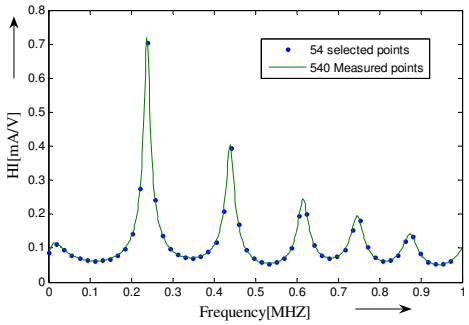

Figure 6: Selected points of the H_I

4 EVALUATION OF THE SCHEME AND EXPERIMENTAL RESULTS

Table 1 shows the calculated and identified parameters of the R-L-C-M model of the considered test object. In the first column of Table 1, the parameters of the R-LC-M model of the transformer are listed. The second column shows the computed parameters using common formulas [11] for the transformer studied in this paper.

The third to fifth columns show three sets of identified parameters. These three sets are obtained from the proposed scheme, using random initial values for $\overline{X}$ in three different runs of the algorithm. For these three and all other runs of the algorithm, the implemented ASBFA algorithm converged, the worst cast being 500 iterations. The third to fifth columns in Table 1 are just three samples of many runs carried out. As this table shows, the identified electrical parameters obtained from different runs are close enough to each other, while the identified and computed parameters have some differences with each other.

The effects of these differences between the computed and identified parameters, and the accuracy of the identified ones, are shown in Figure 7 and Figure 8. Figure 7 shows the H_I obtained from experiment and simulation using computed parameters. Figure 8 shows this transfer function obtained from experiment and simulation using the identified parameters with the help of the ASBFA algorithm.

These figures show the correctness and accuracy of the identified parameters and a noticeable error due to the error in computed parameters. It should be mentioned that the identified parameters can simulate behaviour of the transformer in high frequency better than the computed parameters. Especially the amounts of the resonance frequencies that are obtained by ASBFA algorithm are more precise than those obtained by the conventional analytical method.

5 CONCLUSION

This paper presents a systematic method for accurate parameter identification of the transformer R-L-C-M model. In this method a simple experimental set-up is used to conduct an easy test on the desired transformer, and then an ASBFA optimization algorithm identifies the parameters using the collected data. The validity of the scheme, the correctness and accuracy of the obtained parameters are shown by comparing the experimental and simulation results. The model based on identified parameters by ASBFA algorithm describes the transformer behaviour much better than the model based on calculated parameters by analytical formulas.

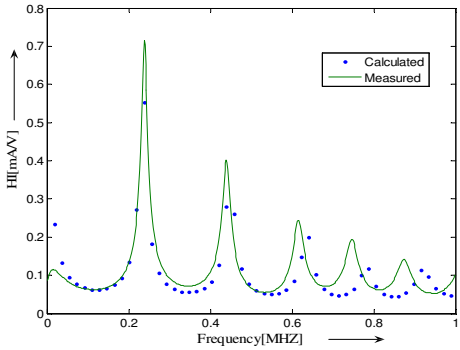

Figure 7: Comparison of the measured and calculated earth current transfer functions, in which the analytically calculated parameters are used by simulations

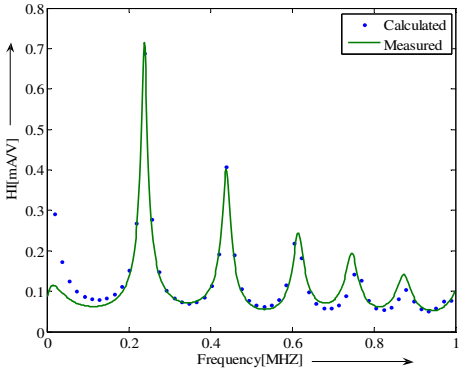

Figure 8: Comparison of the measured and calculated earth current transfer functions, in which the identified parameters with help of ASBFA are used by simulations

Table 1: The calculated parameters using common formulas and the identified parameters by ASBFA

Parameters of the R-L-C-M model	Calculated parameters by common formulas	Identified parameters by ASBFA (Set 1)	Identified parameters by ASBFA (Set 2)	Identified parameters by ASBFA (Set 3)
Li [mH]	0.6552	0.5173	0.5177	0.5181
L1,2 [mH]	0.3890	0.4183	0.4185	0.4186
L1,3 [mH]	0.2007	0.1515	0.1512	0.1514
L1,4 [mH]	0.1198	0.0953	0.0954	0.0951
L1,5 [mH]	0.0762	0.0761	0.0760	0.0762
L1,6 [mH]	0.0506	0.0389	0.0392	0.0391
L1,7 [mH]	0.0349	0.0262	0.0262	0.0264
L1,8 [mH]	0.0250	0.0173	0.0174	0.0172
Ci [nF]	0.0100	0.0109	0.0107	0.0108
Ki [nF]	0.0428	0.0530	0.0531	0.0532
Rs [kΩ]	0.1442	0.1331	0.1333	0.1332

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