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A NEW DYNAMIC GENETIC SELECTION ALGORITHM: APPLICATION TO INDUCTION MACHINE IDENTIFICATION

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Key words: Genetic algorithm, Selection pressure, Power ranking selection, Induction machine, Identification.

Premature convergence is known as a serious failure mode for genetic algorithms (GAs). This paper presents a new dynamic selection based on power ranking by varying gradually the selection pressure versus generations, in order to maintain a trade-off between exploitation and exploration in genetic algorithm and avoid premature convergence. The proposed dynamic genetic selection algorithm's performance was proven by identifying an induction machine's (IM) parameters, both electrical and mechanical, using only the starting current and the corresponding phase voltage. A comparison is established between the proposed dynamic genetic selection algorithms with other genetic selections algorithms. The evaluation is carried out on IM's (1.5 kW) parameters estimation by measured data. The matching in the transient and in steady state of computed currents with the measured ones confirms the accuracy of the identified parameters. The experimental results obtained indicate the superiority of the proposed dynamic genetic selection algorithm versus the other algorithms in terms of computing time and convergence speed.

1. INTRODUCTION

Several works on induction machine (IM) parameters identification based on the output error method have been proposed in the literature [1–4]. These methods differ from each other by the nature of the input–output signals, the adopted IM model, and the used optimization method. Many evolutionary techniques optimization like genetic algorithm [5,6], particle swarm optimisation [7] and bacterial foraging [8], have been successfully applied to IM parameter identification. The most part of papers only estimated the electrical parameters [9–11]. Usually, the mechanical parameters are separately determined by the slowing-down method. In this paper, all of the parameters are estimated at the same time, by the minimization of the quadratic error between the experimental current of the IM and the computed one from the adopted model. Genetic algorithms (GAs) are used as minimization technique to identify the IM parameters vector.

GAs are stochastic search and optimization techniques based on the principles of genetics and natural selection [12,13]. It is well known that, the premature convergence is a common problem in GAs [14] and their performance depends on the combination of the genetic operators (selection, crossover, mutation) and parameter settings. The selection operator deserves a special position in GA, because this determines the evolutionary search spaces. Many selection mechanisms have been proposed in the literature [15–17]. A selection is often recognized as the main cause of premature convergence. Baker [14] has introduced a ranking method for circumventing the problems of fitness proportionate selection methods [18] and avoids premature convergence. Furthermore, the selection should maintain the diversity in the population during the search. The diversity depends on the selection pressure (SP) which means a probability of the best individual being selected compared to the average probability of selection of all individuals. On one hand, higher SP causes a fast convergence with a risk of premature convergence. On the other hand, a lower SP leads to slower convergence. Baker [14] proposed the linear ranking selection to overcome premature convergence with bounded SP between 1 and 2. In order to increase the SP, a quadratic ranking selection is proposed in [19]. A trade-off to achieve a good search between the exploration and the exploitation of new and unknown areas is to make use of knowledge found at previously visited points to help find better ones. The dynamic control of SP maintains the balance between exploitation and exploration by using a quadratic dynamic selection, where the main limitation of this approach is the bounded SP between 1.4 and 2.9 [20]. This paper presents a new dynamic selection based on power ranking, allowing a progressive change of the SP *versus* generations. This provides an improvement of the SP variation range. A comparison of the proposed dynamic genetic selection algorithm with other genetic selections algorithms (linear ranking selection, nonlinear ranking selection, uniform ranking selection and tournament selection) is carried out for the estimation of an IM's (1.5 kW) parameters by measured data.

This paper is organized as follows. Section 2 describes the tournament, the linear-nonlinear-uniform ranking selections and the proposed selection based on dynamic power ranking. Those are coupled to the same crossover, mutation, and incorporated in different real-coded GAs, which are specified in Table 1.

Table 1

GAs with different selection methods

GAs	Coding	Selection	Crossover	Mutation	Elitism
GAP	Real-coded	Proposed	Continuous	Non-uniform	Yes
GAL	Real-coded	Linear ranking	Continuous	Non-uniform	Yes
GANL	Real-Coded	Nonlinear ranking	Continuous	Non-uniform	Yes
GAT	Real-coded	Tournament	Continuous	Non-uniform	Yes
GAU	Real-coded	Uniform ranking	Continuous	Non-uniform	Yes

Section 3 presents the induction machine model. Section 4 presents an identification method trough an output error method. The procedure is used to determine simultaneously the electrical and mechanical parameters of an induction machine from measurements of the starting current and the corresponding phase voltage. Section 5 confirms the identification method by experimental results carried out to study the performance of GAs. Finally, Section 6 draws some conclusion.

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2. GENETIC ALGORITHM

The Genetic Algorithm optimization process starts with a random population composed of a large number of individuals to evolve under specified selection rules to a state that minimizes the objective function. Each individual represents an IM, which is characterized by the following parameters vector $P = \left[\sigma \, \mathrm{T_r} \, \mathrm{L_s} \, \mathrm{T_s} \, \mathrm{J} \, \mathrm{B}\,\right]^T$ and a value of objective function, which represents the output quadratic error. The elements of the vector *P* are called genes. All genes are bounded in order to respect the space search. The new population is obtained iteratively applying the genetic operators (selection, crossover, mutation) and replacement strategy.

The following steps describe the tournament, the linear-nonlinear-uniform ranking selections and the proposed selection based on dynamic power ranking. Those are coupled to the same crossover, mutation, and incorporated in different real-coded GAs for IM parameters identification.

2.1. TOURNAMENT SELECTION

In the tournament selection [15,21] a set of *k* individuals are chosen randomly from population. These individuals are ranked according to their objective values, and the best individual is selected for reproduction. The whole operation is repeated times for the entire population. Therefore, the probability of each individual to be selected is given by the following expression:

$$p(i) = \begin{cases} \dfrac{C_{N-i}^{k-1}}{C_N^k}, & if\ 1 \le i \le N-k+1, \\ 0, & if\ N-k+2 \le i \le N, \end{cases} \tag{1}$$

where *N* is the population size and *i* is the rank of i^{th} individual.

In this paper, the particular case of the tournament of two individuals ($k = 2$), called a probabilistic binary tournament is used. Then, the eq. (1) reduces to the following equation:

$$p(i) = \frac{2}{N}\frac{(N-i)}{(N-1)}. \tag{2}$$

2.2. LINEAR RANKING SELECTION

The notion of linear ranking was introduced by Baker [14] to circumvent the problem of proportional selection. The linear ranking selection consists to sort the individuals in a decreasing order with respect to the value of their objective function following a linear distribution function for each generation. This distribution is used to map the rank of individuals in the sorted list as shown in eq. (3):

$$fit(i) = \left[\phi - 2(i-1)(\phi-1)/(N-1)\right], \tag{3}$$

where ϕ represents the selection pressure (PS), and is a chosen parameter that controls the evolution of individuals with $\phi \in [1,2]$.

The linear distribution function is illustrated in Fig. 1. Then the individuals are selected with a probability that is linearly proportional to the rank of the individuals in the population.

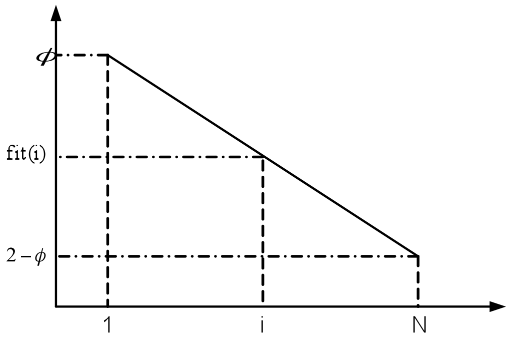


Fig. 1 — Linear dirstribution function.

The probability of selection *p*(*i*) for each individual is given by the following expression:

$$p(i) = \frac{fit(i)}{\sum\limits_{m=1}^{N} fit(m)}, \tag{4}$$

$$p(i) = \left[\phi - (i-1)(2\phi-2)/(N-1)\right]/N. \tag{5}$$

2.3. NONLINEAR RANKING SELECTION

Quadratic ranking is a case of nonlinear rankings. The fitness value attributes to each individual as a quadratic function of its rank *i*. The eq. (4) of the probability of selection is applied to each individual. After individuals sorting, the quadratic distribution function [19] is used to map the rank of individuals in the sorted list as shown in eq. (6):

$$fit(i) = A(i-N)^2 + B, \tag{6}$$

where $A = \dfrac{fit\,\max - fit\,\min}{(N-1)^2}$ and $B = fit\,\min$.

The quadratic distribution function is illustrated by Fig. 2.

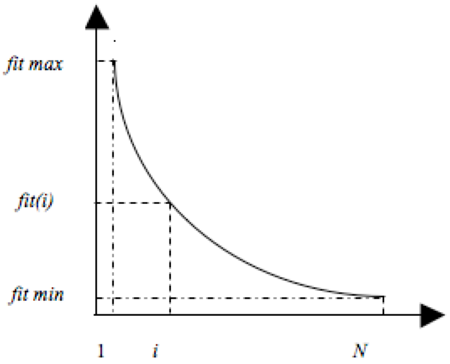


Fig. 2 — Quadratic distribution function.

The probability of selection to each individual is given by the eq. (4).

2.4. UNIFORM RANKING SELECTION

The uniform ranking selection consists in choosing equiprobably the individuals of rank less than or equal to μ (μ ≤ N). Other individuals are excluded from the population and cannot participate in reproduction [18]. The probability of selection is expressed by:

$$p(i)=\begin{cases}\dfrac{1}{\mu}, & si\ \ 1\le i\le\mu,\\ 0, & si\ \ \mu<i\le N.\end{cases} \tag{7}$$

2.5. PROPOSED SELECTION

In order to maintain the trade-off between exploration and exploitation, the SP is varied versus generations using a beam of power curves that are equidistant with respect to a vertical straight-line Δ. All beam curves pass through points P_1, P_2 and the intermediate point M of Δ between A and B as shown in Fig. 3. Additionally, the external curves of beam are characterized by the fixed SP (SP_1 and SP_{nc}) where *nc* represents the curves number of beams.

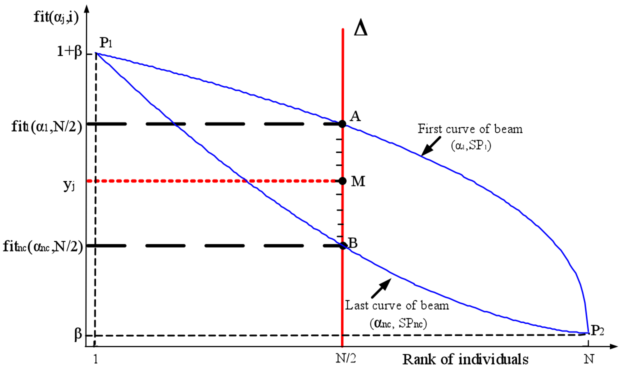


Fig. 3 — Intersection on the external curves with a vertical straight line.

The curves beam generation offer an interesting approach of changing the selective pressure (SP). Higher SP causes a fast convergence with a risk of premature convergence. A lower SP leads to slower convergence. SP is defined as:

$$SP_j=\frac{N.fit\left(\alpha_j,1\right)}{\sum\limits_{r=1}^{N} fit\left(\alpha_j,i\right)}, \tag{8}$$

where the subscript j represents the j^{th} curve of beam. However, each beam curve is given by:

$$fit\left(\alpha_j,i\right)=\left[1-\left(\frac{i-1}{N-1}\right)\right]^{\alpha_j}+\beta, \tag{9}$$

where β is a constant.

The coordinates of the points P_1 and P_2 are calculated from eq. (9), so that $P_1(1,1+\beta)$ and P_2 (N,β). The external curves PS (PS_1 and PS_{nc}) are fixed; α_1 and α_{nc} are numerically calculated by the Newton-Raphson method [22] using the following equations:

$$SP_1\sum_{i=1}^{N} fit\left(\alpha_1,i\right)-N fit\left(\alpha_1,1\right)=0 \tag{10}$$

$$SP_{nc}\sum_{i=1}^{N} fit\left(\alpha_{nc},i\right)-N fit\left(\alpha_{nc},1\right)=0 \tag{11}$$

The curve beam intersects with the vertical straight-line Δ, which is expressed as:

$$\Delta=\frac{N}{2} \tag{11}$$

The external curves at points A (*N*/2, y_1) and B (*N*/2, y_2) are defined by the following expressions:

$$y_1=fit\left(\alpha_1,\frac{N}{2}\right)=\left(1-\frac{\frac{N}{2}-1}{N-1}\right)^{\alpha_1}+\beta, \tag{12}$$

$$y_2=fit_{nc}\left(\alpha_{nc},\frac{N}{2}\right)=\left(1-\frac{\frac{N}{2}-1}{N-1}\right)^{\alpha_{nc}}+\beta. \tag{13}$$

All beam power curves pass through the points P_1, P_2 and M located on a vertical straight line Δ between A and B with the coordinates $\left(\frac{N}{2},y_j\right)$, where y_j is given by:

$$y_j=y_1+\left(\frac{y_2-y_1}{nc-1}\right)(j-1),\ \ 1\le j\le nc. \tag{14}$$

For each curve j, the corresponding α_j is numerically calculated by the Newton-Raphson method using the following equation:

$$y_1+\frac{y_2-y_1}{n_c-1}(j-1)-\left(1-\frac{\frac{N}{2}-1}{N-1}\right)^{\alpha_j}-\beta=0. \tag{15}$$

The evolution of α_j versus number j of the beam curves is illustrated in Fig. 4.

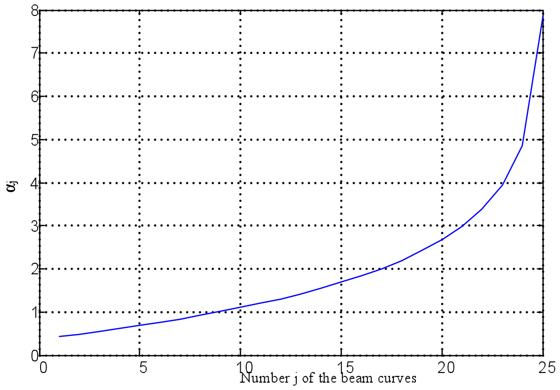


Fig. 4 — Evolution α_j versus number j of the beam curves.

The calculated α_j allow the generation of the equidistant curves beam related to the vertical straight line as shown in Fig. 5. Each beam curve is characterized by the α_j parameter, which allows computing the corresponding SP_j by eq. (8). The evolution of SP_j *versus* curves number of beams is shown in Fig. 6.

First the ranking selection is to sort the individuals in a decreasing order with respect to the value of their objective function, for each generation. Then, a selection probability $p\left(\alpha_j,i\right)$ is calculated for each individual, using a beam of power distributions $fit\left(\alpha_j,i\right)$ *versus* their rank *i* as follow:

$$p\left(\alpha_j, i\right) = \frac{fit\left(\alpha_j, i\right)}{\sum_{m=1}^{N} fit\left(\alpha_j, m\right)}. \qquad (16)$$

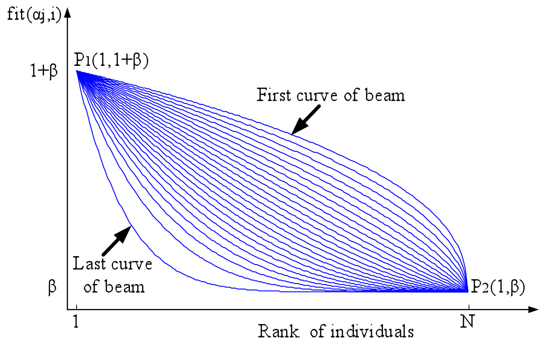


Fig. 5 — Power equidistant curve beam related to the vertical straight line for 25 values of the parameter α_j.

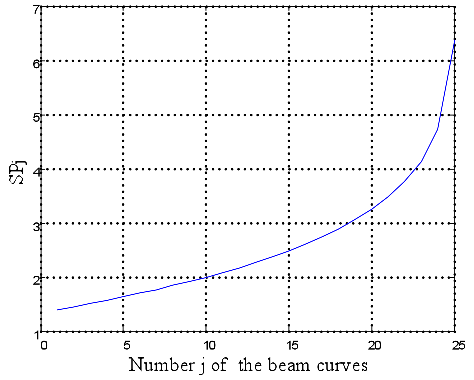


Fig. 6 — Evolution SP$_j$ versus number j of the beam curves.

2.6. CROSSOVER

Crossover consists to the mixing of information from both parents to create the children. The real and the continuous crossover are applied. The genes of child ‘a’ are chosen near those of the parents. The following equation is applied to each child’s gene born from "parent1" and "parent2"

$$a = a_{parent1} + \text{rand}^{*}\left(a_{parent2} - a_{parent1}\right), \qquad (17)$$

where rand is defined a random coefficient with a uniform distribution in the interval [-d, d+1], d $\in \Re$. The crossover range is governed how far a crossover between two individuals may be from its original value. If the crossover range is rand, the original value is a, and the allowable weight limits are $a_{k\min}$ and $a_{k\max}$. The crossover value is chosen from the range:

$$a_{new} \in \left\{ \begin{matrix} \max\left(a - rand * \left(\dfrac{a_{k\max} - a_{k\min}}{2}\right), a_{k\min}\right), \\ \min\left(a + rand * \left(\dfrac{a_{k\max} - a_{k\min}}{2}\right), a_{k\max}\right) \end{matrix} \right\}. (17)$$

2.7. MUTATION

The mutation operator [23] alters the parameters of selected individuals by a random change in predefined domains. Each gene is going to undergo an important modification during the first generation. The alteration rate will be decreased as long as the research progressively continues. For the t^{th} generation, the mutated parameter a'_k is given by:

$$a'_k = \begin{cases} a_k + \left(a_{k\max} - a_k\right)\left(1 - rand^{(1-t/T)^5}\right) \; if \; p_a < 0.5, \\ a_k - \left(a_k - a_{k\min}\right)\left(1 - rand^{(1-t/T)^5}\right) \; if \; p_a > 0.5, \end{cases} \qquad (19)$$

where rand $\in$ [0,1] is selected according to a uniform distribution which determines indirectly the alteration amplitude. $a_{\text{k min}}$ and $a_{\text{k max}}$ stand for the lower and upper bounds of a_k, and T is the generation index at which the mutation amplitude is canceled.

2.8. ELITISM REPLACEMENT

This elitism replacement copied the best individuals from the generation into successive one. The best child participated with the other child undergoing the genetic operations in the successive generation. This elitist model can accelerate the GA convergence.

3. **INDUCTION MACHINE MODEL**

Using the usual simplifying hypothesis, the saturation effect, core losses and skin effect are neglected, only first space harmonic is considered, and air gap is constant. In Park model, the dynamic equations of the IM [24] related to a reference linked to the stator are given by:

$$\frac{\mathrm{d}X_1}{\mathrm{d}t} = A_1 X_1 + A_2 U, \qquad (20)$$

where A_1 and A_2 are respectively given by:

$$A_1 = \begin{bmatrix} -\dfrac{1}{\sigma T_s} & \dfrac{1-\sigma}{\sigma} P_o \Omega & \dfrac{1-\sigma}{\sigma T_r} & \dfrac{1-\sigma}{\sigma} P_o \Omega \\ -\dfrac{1-\sigma}{\sigma} P_o \Omega & -\dfrac{1}{\sigma T_s} & -\dfrac{1-\sigma}{\sigma} P_o \Omega & \dfrac{1-\sigma}{\sigma T_r} \\ \dfrac{1}{\sigma T_s} & -\dfrac{1}{\sigma} P_o \Omega & -\dfrac{1}{\sigma T_r} & -\dfrac{1}{\sigma} P_o \Omega \\ \dfrac{1}{\sigma} P_o \Omega & \dfrac{1}{\sigma T_s} & \dfrac{1}{\sigma} P_o \Omega & -\dfrac{1}{\sigma T_r} \end{bmatrix}, (21)$$

$$A_2 = \begin{bmatrix} \dfrac{1}{\sigma L_s} & 0 & -\dfrac{1}{\sigma L_s} & 0 \\ 0 & \dfrac{1}{\sigma L_s} & 0 & -\dfrac{1}{\sigma L_s} \end{bmatrix}^T, \qquad (22)$$

where σ is the leakage coefficient, T_r is the rotor time constant (s), T_s is the stator time constant (s), P_o is the number of pole pairs and L_s is the stator inductance (H)

$$X_1 = \left[I_{ds} \; I_{qs} \; I'_{dr} \; I'_{qr} \right]^T, \qquad (23)$$

where

$$I'_{dr} = \frac{I_{dr}}{L_r}, \quad I'_{qr} = \frac{I_{qr}}{L_r}, \quad U = \left[V_{ds} V_{qs} \right]^T, \qquad (24)$$

The mechanical equation is given by:

$$J \frac{\mathrm{d}W}{\mathrm{d}t} = T_{em} - T_l - T_{res}, \qquad (25)$$

where T_l is the load torque and J is the rotor inertia [Kg.m^2] T_{em} is the electromagnetic torque given by:

$$T_{em} = \left(1 - \sigma\right) L_s \left(I_{qs} I'_{dr} - I_{ds} I'_{qr} \right), \qquad (26)$$

and T_{res} is the friction torque assumed to be:

$$T_{res} = \mathrm{B}\Omega\,, \tag{27}$$

and B is the viscous friction coefficient (N.m.s/rad). So, the mechanical equation becomes:

$$\frac{\mathrm{d}\Omega}{\mathrm{d}t} = \frac{1}{J}(1-\sigma)L_s\left(I_{qs}I'_{dr} - I_{ds}I'_{qr}\right) - \frac{\mathrm{B}\Omega}{J} \tag{28}$$

The machine is governed by the nonlinear equations (20) and (28). So, the IM is completely characterized by the parameters vector $P = [\sigma\ \mathrm{T_r}\ \mathrm{L_s}\ \mathrm{T_s}\ \mathrm{J}\ \mathrm{B}\ ]^T$, which can be determined from the measurement of the starting current and the corresponding simple voltage applied to the machine.

4. IDENTIFICATION METHOD

The idea on which the method is based consists in simultaneously determining the electrical and mechanical parameters of a mathematical model of the IM. So, the model is able to match the input–output behavior of the IM. This can be achieved from the measurement of the current and the corresponding voltage applied to machine on transient from standstill to steady state.

The identification method used in this paper is illustrated in Fig. 7. In order to estimate the vector of parameters $P = [\sigma\ \mathrm{T_r}\ \mathrm{L_s}\ \mathrm{T_s}\ \mathrm{J}\ \mathrm{B}\ ]^T$, the quadratic error Fo between the measured values I_{mi} and the computed ones I_{ci} from the model adopted at the same instants is minimized by the GA

$$Fo = \sum_{i=1}^{n}\left(I_{m_i} - I_{c_i}\right)^2, \tag{29}$$

where n is the number of the measured values.

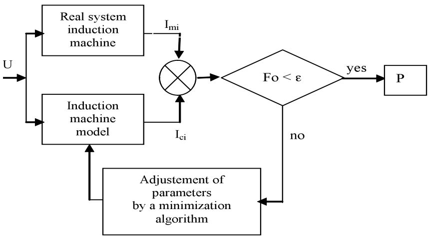
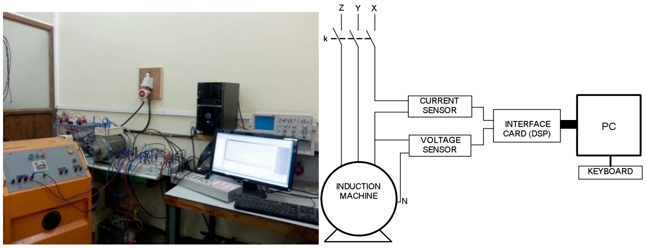


Fig. 7 — Identification process.

5. EXPERIMENTAL RESULTS

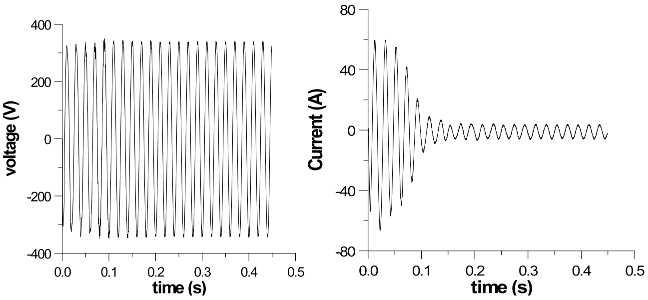
The experimental data is obtained from transient test on a three-phase induction motor.



(a) (b)

Fig. 8 — (a) View of the experimental setup (b) Measurement setup.

The start-up current and the corresponding phase voltage are simultaneously measured by a DSpace card. The experimental setup is shown in Fig. 8. Test is carried out on a three-phase induction machine with the following characteristics: Motor M: 4 poles, 220/380V, 1.5 kW. The curves in Fig. 9 represent respectively the measured voltage and the current of no-load starting of the IM.



(a) (b)

Fig. 9 — (a) Voltage measured; (b) current measured.

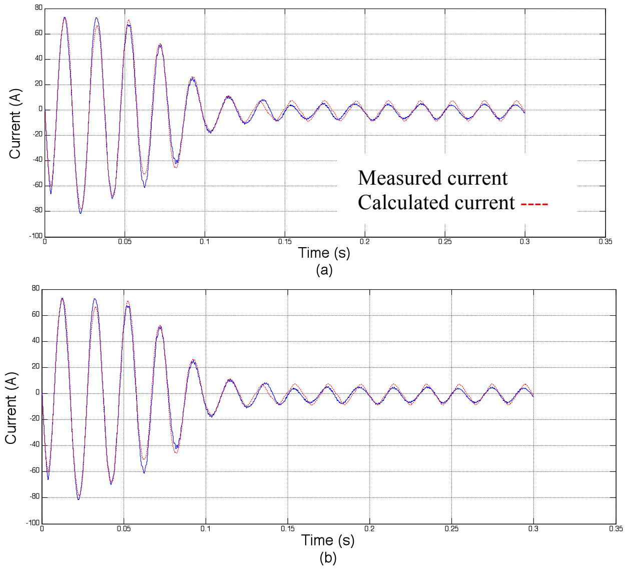
The estimated parameters obtained using the measured data are given by Table 2. It can be noticed that the experimental results confirm well the fast convergence about the GAP compared to the other GAs.

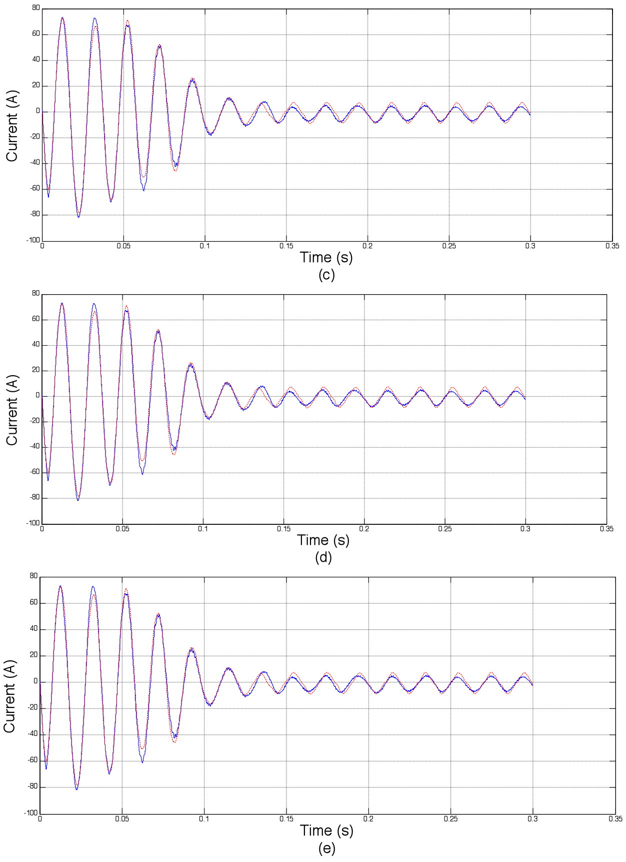
Table 2

Results of estimated parameters

Parameters	GAP	GAL	GANL	GAU	GAT
σ	0.069	0.0689	0.0691	0.069	0.069
Tr (ms)	135.43	135.9	135.4	135.61	135.57
Ls (mH)	190	190.6	190	190.02	190.17
Ts (ms)	87.35	87.6	87.4	87.45	87.4
J (Kg.m^2)	0.035	0.0353	0.0353	0.0353	0.0353
B (Nm.s/rad)	0.009	0.0099	0.0099	0.0099	0.0099
Number of iterations	227	1211	406	1027	548
Computing time (s)	3474.9	55459.45	18820.63	16604.03	10012.44

The computed current is obtained by estimated parameters. Figure 10 shows the superposition of the calculated current with the measured one both in transient and steady state.





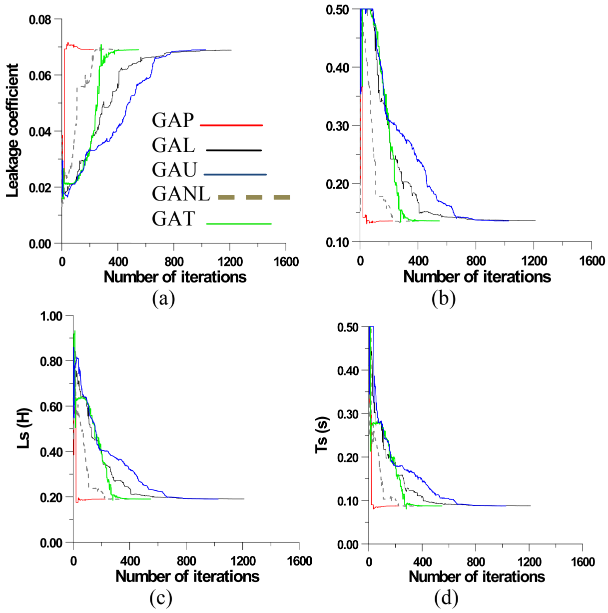
(c)

(d)

(e)

Fig. 10 — Superposition of the measured current and calculated one with the estimated parameters to motor M (a) by GAP (b) by GAL (c) by GANL (d) by GAU (e) GAT.

In order to show the convergence process related on GAP, GAL, GANL, GAU and GAT, Fig. 11 illustrates the evolution of each parameter versus number of iterations for motor M. It can be observed in the evolution of parameters that the faster convergence of GAP over the other GAs.

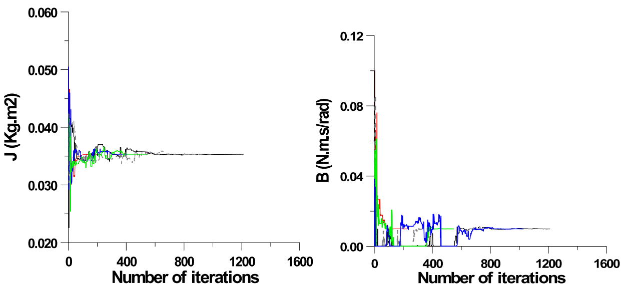


(a)

(b)

(c)

(d)



(e) (f)

Fig. 11 — Parameters evolution of M: (a) leakage coefficient, (b) T_r, (c) L_s, (d) T_s, (e) J, and (f) B.

6. CONCLUSION

The proposed dynamic selection based on power ranking is presented and compared to the linear-nonlinear-uniform ranking and binary tournament selections in genetic algorithms. Using only the starting current and the corresponding phase voltage, the electrical and mechanical parameters are estimated simultaneously by GAs. The parameters are estimated by the method of output error based on the minimization of the quadratic error between the current acquired experimentally from the induction machine and the computed values from the adopted model. The matching in the transient and in steady state of computed currents with the measured ones confirms the accuracy of the identified parameters. The experimental results indicate that the superiority of the GAP versus GAL, GANL, GAU, and GAT in terms of computing time and convergence speed. Therefore, the proposed method can be used as a more efficient and reliable alternative algorithm for parameter identification problems.

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