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Implementation of a Genetic Algorithm for Jiles-Atherton's Parameters Optimization

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Resumen

Una de las principales herramientas en el análisis de la respuesta magnética de materiales, son las curvas de magnetización en función de campo aplicado; en el caso de curvas de histéresis ferromagnética uno de los modelos más ampliamente utilizados es el de Jiles-Atherton[1]. La solución propuesta como ecuación de magnetización[1,2] es una sumatoria de derivadas recurrentes en la magnetización, con una función de distribución gaussiana para el anclaje; la característica recurrente hace del ajuste de curvas experimentales una tarea complicada. Por tal razón se han propuesto distintas metodologías para la optimización de parámetros al ajustar una curva histerética experimental con el modelo mencionado[3,4]; éste trabajo muestra la implementación de un algoritmo genético para la optimización de parámetros del modelo de Jiles-Atherton sobre el entorno *Mathematica* de *Wolfram Research*. Los parámetros de entrada para este algoritmo son: curva experimental de magnetización en función del campo, valor máximo del campo magnético, probabilidad de mutación aleatoria y probabilidad de mutación exploratoria. Los parámetros de salida son: magnetización de saturación (*Ms*), parámetro de fluctuación térmica (*a*), constante de campo promedio (α), amplitud de la distribución gaussiana de anclaje (k_0), desviación estándar de la distribución gaussiana de anclaje (σ) y el gráfico de la medida experimental junto a la curva ajustada.

***Palabras Clave*:**algoritmo genético, Jiles-Atherton, parámetros.

Abstract

One of the main tools in magnetic materials response analysis, are the magnetization as function of applied field curves; in the case of ferromagnetic hysteresis one of the most widely used is the Jiles-Atherton model[1]. The proposed solution as an equation of magnetization[1,2] is a sum of recurrent in magnetization derivatives, with a Gaussian pinning distribution function; the recurrent characteristic makes the experimental fitting a complicated job. Due to this reason, different methodologies for parameter optimization of an experimental hysteretic curve with the mentioned model have been proposed[3,4]; it is shown in this work the implementation of a genetic algorithm for parameter optimization of the Jiles-Atherton model on *Wolfram Research*'s *Mathematica* environment. The entry parameters for this algorithm are: experimental magnetization as a function of the field curve, maximum magnetic field, random mutation probability and exploratory mutation probability. The output parameters are: saturation magnetization(*Ms*), thermal fluctuation parameter(*a*), mean field constant(α), Gaussian pinning distribution amplitude (k_0), Gaussian pinning distribution standard deviation (σ), and the graphics of experimental and fitted curves.

***Keywords*:** genetic algorithm, Jiles-Atherton, parameters.

1. Introduction

The Jiles-Atherton model[1] represents ferromagnetic hysteresis having into account reversible and irreversible magnetization processes, as magnetic domain reorientation, domain wall bending, pinning in defects, etc. The equation representing the magnetization as a function of the applied magnetic field is a differential equation(1); its solution is a sum of derivatives(2) and these two equations are recurrent in magnetization[1]:

$$M = \mathscr{L}\left(\frac{Be}{a}\right) - \delta k\left(\frac{\partial M}{\partial Be}\right) \qquad (1)$$

$$M = M_s \sum_{n=0}^{\infty} \left[(-1)^n (k\delta)^n \mathscr{L}^n \left(\frac{\mu_0 (H + \alpha M)}{a} \right) \right] + \delta C (B_{max}) \quad (2)$$

$\mathscr{L}$ represents the Langevin Function, $\mathscr{L}^n$ its *n-th* derivative, $Be = \mu_0 (H + \alpha M)$ is the effective or mean field, M_s is the saturation magnetization, *a* is the thermal fluctuation term (given in magnetic field units), α is the mean field constant (dimensionless), *k* stands for pinning (given in permeability units), δ parameter is ± 1 depending on the field direction and $C (B_{max})$ is an integration constant. The solution (2) has a restriction: converges only if the condition $(a > k)$ is fulfilled. Jiles et al. indicate that the solution can be modified by using a function of the *H* field to stand for the pinning and/or the saturation magnetization; taking into account the proposal of Fecioru-Morari et al. the pinning is represented by means of a Gaussian function[2]:

$$k (H) = k_0 \exp \left(- \left(\frac{H - \mu_k}{2\sigma} \right)^2 \right) \quad (3)$$

The solution(2) can be calculated by using an iterative method, in such a way that the entry parameter *M* in the mean field is the calculated magnetization for an early state. When we have a hysteretic experimental curve to fit with this model, the objective is to find a set of parameters that allows the simulation of an optimally fitted curve; the search of this set is an extensive and not always obvious task; due to this reason it has been proposed the use of genetic algorithms[3], neural networks, random and deterministic searches[4] among others. Genetic algorithms are adaptive methods based on the evolutionary process of biological organisms, where the best fitted individuals pass their genes to future generations, beyond the selection and reproduction process each generation contains best fitted individuals than the earlier generations.

2. Designed Algorithm and Results

The algorithm was designed to fit the curves generated by the SMOKE system used by the *Magnetic Materials and Nanostructures Group* of the *Universidad del Quindío*[5], in such a way that it's necessary to indicate the maximum magnetic field value.

- *Search Space*: The intervals creating the search space are defined from characteristic values (saturation magnetization M_S, and coercive field H_C) obtained from the experimental curve ($M_S = [M_S, 1{,}2M_S]$, $a = [0{,}5H_C, 2H_C]$, $\alpha = [1 \times 10^{-4}, 1 \times 10^{-2}]$, $k_0 = [0{,}5H_C, 2H_C]$, $\sigma = [0, H_{Max}]$).
- *Coding*: The algorithm is real coded, due to the search space is real and the numeric mutation mechanisms are more efficient in this case.
- *Fitness Function*: The function used to measure the individuals' fitness is a Least Squares (L.S.) calculation that is realized point by point between the simulated and experimental curves.
- *Chromosome*: The chromosome structure is given by $(M_s, a, \alpha, k_0, \sigma, \mu_k)$.
- *Generation 0*: The first generation is randomly created in the search space; the created individuals fulfill the condition $(a > k_0)$.

The search space is small enough to identify the solution region very quickly, besides the probability for locating a generation 0 individual near the solution is high; due to those reasons, in the early stages of development we had premature convergence and overcompression issues.

- *Reproductive Trials*: The *Fitness Ranking* technique is used in three ranks, the first group inviduals are assigned two reproductive trials, this group contains a quarter of the population (the best fitted individuals); one reproductive trial is assigned to the second group individuals, this group contains a half of the population; in such a way that the least quarter of population (the worst fitted individuals) does not reproduce. This techinique reduces overcompression that was due to an excellent fitted individual in a poor fitness population, promoting the whole's population evolution before some individuals' evolution.
- *Population Size*: The above characteristic makes the population size a multiple of four. To avoid overcompression due to the existence of a superfit individual, the population is totally replaced in each generation.
- *Parents Selection*: The first group's individuals do not mate between them, so each of these individuals mates with a second group's individual, random mating is used. This mechanism used along with *Fitness Ranking* eliminates premature convergence.
- *Crossover*: *Uniform Crossover* is used; a chromosome mask is randomly generated and it is applied to first parent's chromosome, the mask's Boolean Not is applied to the second parent's chromosome; this way an offspring is obtained. Another offspring is obtained by inverting the parent-mask relation. This technique makes unnecessary to consider *epistasis* (strong dependence between genes).
- *Non-Valid Individuals Remapping*: The *Uniform Crossover* method creates individuals who do not complain the convergence condition of (2); due to this

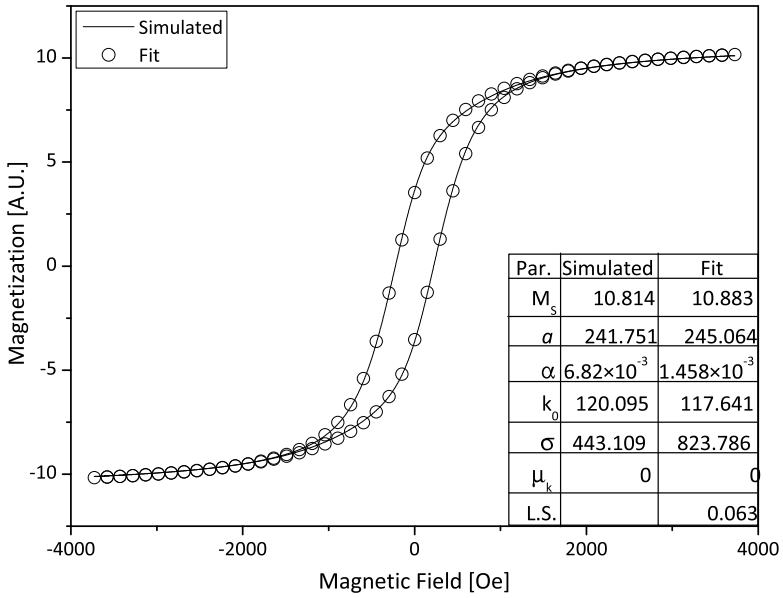

Figura 1. Simulated curve (line) and the fitted one(circles). The inset shows the parameters for both curves and the Least Squares calculation for the solution individual, where the physical units depend on the experimental curve units (M and H).

reason the individuals with (a, k_0) non-valid genes are remapped into valid individuals by using a random mutation of the non-valid genes.

- *Random Mutation*: Along the whole algorithm random mutation is realized, the mutant genes and individuals selection is a random process. The goal of this kind of mutation is the constant exploration of the search space.
- *Exploratory Mutation*: When the population presents a mean deviation equal or less than 5 % the near-to-solution-region is considered as identified; from this point a mutation is applied to the decisive genes(a, k_0) in the individual's fitness, that modifies them randomly in the range $(0{,}9gen, 1{,}1gen)$, a fine search around the convergence region is achieved in this way. If the population's mean deviation gets greater than 5 % in later generations, exploratory mutation is stopped and will be restarted when the population's mean deviation is fewer than 5 %.
- *Ending Criterion*: When the population's mean deviation is equal or less than 1 % the genetic algorithm is considered as finished; the solution individual is the one (among all the calculated ones) that minimizes the fitness function, this is necessary due to the total population replacement mechanism.

The calibration test is as follows[3], the algorithm is fed with an experimental NiZn curve obtained with the SMOKE system[5,6]. This curve is compared to the Algorithm's Fit. The solution was found after 22 generations of 32 individuals each.

Conclusions

The presented genetic algorithm converges around 20 generations giving an excellent fit. The use of *Fitness Ranking*, *Uniform Crossover* and *Exploratory Mutation* eliminate the *Overcompression* and *Premature Convergence* issues.

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