Research Article

Neurogenetic Algorithm for Solving Combinatorial Engineering Problems

M. Jalali Varnamkhasti[1] and Nasruddin Hassan[2]

[1] *Department of Mathematics, Dolatabad Branch, Islamic Azad University, Isfahan 84318–11111, Iran*
[2] *School of Mathematical Sciences, Faculty of Science and Technology, Universiti Kebangsaan Malaysia,*
43600 UKM Bangi, Selangor DE, Malaysia

Correspondence should be addressed to M. Jalali Varnamkhasti, jalali.m.v@gmail.com

Diversity of the population in a genetic algorithm plays an important role in impeding premature convergence. This paper proposes an adaptive neurofuzzy inference system genetic algorithm based on sexual selection. In this technique, for choosing the female chromosome during sexual selection, a bilinear allocation lifetime approach is used to label the chromosomes based on their fitness value which will then be used to characterize the diversity of the population. The motivation of this algorithm is to maintain the population diversity throughout the search procedure. To promote diversity, the proposed algorithm combines the concept of gender and age of individuals and the fuzzy logic during the selection of parents. In order to appraise the performance of the techniques used in this study, one of the chemistry problems and some nonlinear functions available in literature is used.

1. Introduction

A large scale of design, control, scheduling, or other engineering problems results in solution of optimization problems. Genetic algorithms (GAs) were first considered by Holland [1]. A genetic algorithm is a numerical optimization procedure that is based on evolutionary principles such as selection, recombination, and mutation. In many areas of chemistry, there are problems to which GAs can be used. For example, one of the principal subfield of analytical chemistry is the qualitative and quantitative identification of the main components of unknown mixtures by means of spectroscopic methods that investigate the molecules utilizing electromagnetic radiation. Genetic algorithms have been used here as they are effective at finding patterns in data even when the data contains a large amount of extraneous information. Genetic algorithms have also been used for the generation of regression curves,

protein folding, and structure elucidation and for system optimization [2–4]. Yang et al. [5–8] utilized GA in real applications of various soft-computing techniques in different fields.

Premature convergence is a classical problem in finding optimal solution in GA. The population diversity is a way of avoiding the premature convergence in a GA. In a traditional GA, chromosomes reproduce asexually where any two chromosomes may be parents during crossover. Gender division and sexual selection here inspire a model of gendered GA in which crossover takes place only between chromosomes of opposite sex. The sex of chromosomes is not only accountable for preserving diversity in population and maintaining a victorious genetic pool by means of selection, crossover, and mutation, but it is also accountable for the optimization of the different tasks which are very important for survival.

Jalali Varnamkhasti and Lee [9] introduced a new sexual selection. In their technique, the population is divided into two groups of males and females. During the sexual selection, the female chromosome is selected by the tournament selection while the male chromosome is selected based on the hamming distance from the selected female chromosome, fitness value, or active genes. In another study conducted by Jalali Varnamkhasti and Lee [10], a fuzzy genetic algorithm based on this technique for selection mechanism was suggested. They used some nonlinear numerical functions, and by considering the results from each test function, they showed that the proposed technique of grouping the male and female chromosomes alternately outperforms other grouping techniques of sexual selection mechanisms. Also, the application of this technique for sexual selection is given by Jafari et al. [11] for committee neural networks.

In this study, an obvious characteristic between the two gender groups, with the possibility of embedding different tasks for each one, is considered such as the determination of which partners are suitable for mating and crossover. We believe the relations between age, effectiveness and fitness as in biological systems will affect the selection procedure. A bilinear allocation lifetime approach is used to label the chromosomes based on their fitness value [12]. The obtained chromosomes labels are used to characterize the diversity of the population. The population is then divided into two groups: male and female, so that they are selected in an alternate way. In each generation, the layout of selection for male and female is different.

In short, the aim of this paper is to keep the diversity of population by female preference. The selection of the female chromosome is done through a set of fuzzy rules and a newly developed genetic-neurofuzzy algorithm.

2. Neurofuzzy Inference Systems Genetic Algorithm

In this section, we concentrate on the discussion of the proposed neurofuzzy inference systems genetic algorithm for solving combinatorial optimization problems. In the remainder of this section, we explained the framework of the proposed algorithm as illustrated in Figure 1.

2.1. Initial Population

For the nonlinear functions, a solution can be simply encoded by a string of 0's and 1's. A good initial population makes it easy for a GA to converge to good solutions while a poor initial population can prolong a GA convergence. There are different approaches in generating initial population for a GA. The most common method is by random generation [10]. In this paper, we use the random generation method to achieve better diversity in the population.
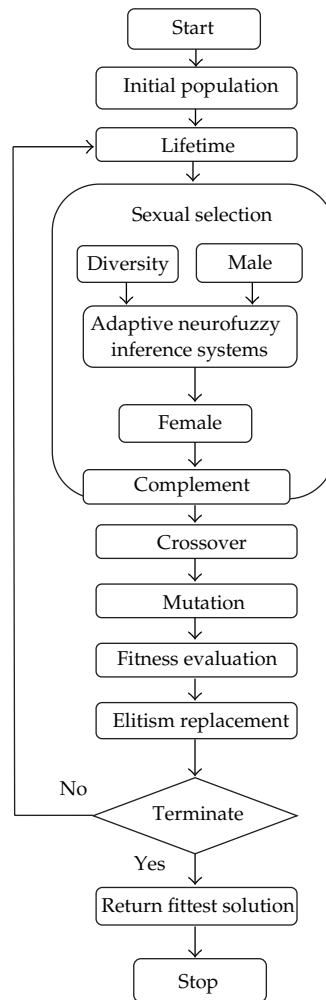
Figure 1: Framework of neurofuzzy inference systems genetic algorithm.

2.2. Lifetime

Three methods are presented for the calculation of chromosomes lifetime in genetic algorithms with varying population size, chromosomes are categorized according to their fitness. The purpose is to use the allowed range of lifetime values in a way which is more suitable to search the optimum than proportional, linear, and bilinear strategies [12]. In this study, a bilinear allocation lifetime approach proposed in [12] is used to label the chromosomes based on their fitness value which will then be used to characterize the diversity of the population. In this case, a linguistic variable "age" is utilized for chromosomes. Figure 2 describes the linguistic variable age where infant, adult and old are the linguistic values. The membership functions for the linguistic terms are called semantic rules.

To find the membership function, we use the fitness value of each chromosome and the minimum, maximum, and average fitness values of the population in each generation. Each chromosome has its own label determined by the age function.
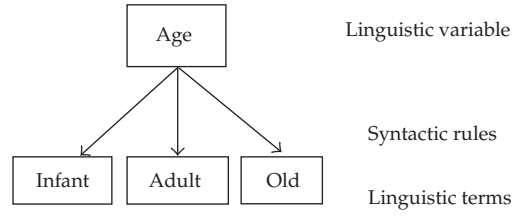
Figure 2: Three linguistic variables for age.

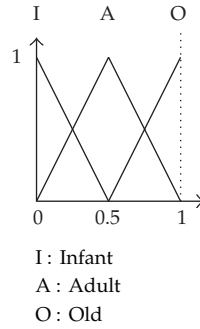

I : Infant
A : Adult
O : Old

Figure 3: The membership function for male and female chromosomes.

Let $\varphi = f_i - f_{\min} / f_{\text{avr}} - f_{\min}$, $\phi = f_i - f_{\text{avr}} / f_{\max} - f_{\text{avr}}$, and $\tau = f_{\text{avr}} - f_i$, where f_i is fitness value of chromosome i; f_{avr} is average fitness value; $f_{\min}$ is minimum fitness value; and $f_{\max}$ is maximum fitness value of population.

The age function can be written as

$$\text{age}(c_i) = \begin{cases} \dfrac{L + \alpha\varphi}{n}; & \tau \geq 0, \\[3mm] \dfrac{\beta + \alpha\phi}{n}; & \tau < 0, \end{cases} \tag{2.1}$$

$$\text{age}(c_i) = \begin{cases} \dfrac{U - (L + \alpha\varphi)}{n}; & \tau \geq 0, \\[3mm] \dfrac{U - (\beta + \alpha\phi)}{n}; & \tau < 0, \end{cases} \tag{2.2}$$

where c_i is chromosome i; n is population size; $\alpha = (U - L)/2$ and $\beta = (U + L)/2$; L and U are minimum and maximum age respectively.

Equation (2.1) is suited for maximization problems which relate to higher fitness values while (2.2) is more suitable for minimization problems which relate to lower fitness values. The fuzzification interface defines for each chromosome the possibilities of the three linguistic values. These values determine the applicability degree for each rule premise. The computation takes into account all chromosomes in each generation and relies on the triangular membership functions shown in Figure 3 with $L = 2$ and $U = 10$.
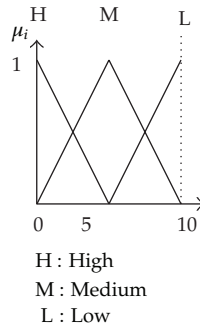
H : High
M : Medium
L : Low

Figure 4: The membership function for diversity.

On the other hand, we can consider linguistic rules and membership function for each rule as follows:

$$\text{age} = \begin{cases} \text{Infant } \mu_1 = -2x + 1 & 0 \leq x \leq 0.50, \\ \text{Adult } \mu_2 \begin{cases} 2x & 0 \leq x \leq 0.50, \\ -2x + 2 & 0.50 < x \leq 1, \end{cases} \\ \text{Old } \mu_3 = 2x - 1 & 0.50 \leq x \leq 1, \end{cases} \quad (2.3)$$

A bilinear allocation lifetime approach proposed in [12] is used to label the chromosomes based on their fitness value which will then be used to characterize the diversity of the population:

$$D(c_i) = \begin{cases} L + \alpha\varphi; & \tau \geq 0, \\ \beta + \alpha\phi; & \tau < 0, \end{cases} \quad (2.4)$$

Let ψ be the label of half of the population, and then the population can be divided into three levels, low, medium and high diversity as follows:

$$\text{population diversity} = \begin{cases} \text{High,} & 0 \leq \psi \leq 2L + t, \\ \text{Medium,} & 0 \leq \psi \leq 4L + 2t, \\ \text{Low,} & 2L + t \leq \psi \leq 4L + 2t, \end{cases} \quad (2.5)$$

where $t = [\lambda(L + U)/n]$ is a parameter that has correlation with the domain of labels in the population and $\lambda = [n/10]$ ($[x]$ means nearest integer number to x, e.g., $[2.3] = 2$ and $[2.8] = 3$). This computation is performed in every generation and relies on the triangular membership functions shown in Figure 4.

We can consider linguistic rules and membership function for each rule as follows:

$$D = \begin{cases} \text{High, } \eta_1 = -\dfrac{1}{5} + 1 & 0 \le x \le 5, \\[2mm] \text{Medium, } \eta_2 = \begin{cases} \dfrac{1}{5}x & 0 \le x \le 5, \\[2mm] \dfrac{1}{4}x - \dfrac{1}{4} & 5 < x \le 10, \end{cases} \\[6mm] \text{Low, } \eta_3 = \dfrac{1}{5}x - 1 & 5 \le x \le 10. \end{cases} \qquad (2.6)$$

2.3. Sexual Selection

Darwin differentiated sexual and natural selections as different types of processes operating on different sorts of traits each in accordance with varying evolutionary dynamics types. From Darwin's perspectives, natural selection enhances the abilities of an organism to survive in a competitory environment whereas sexual selection (SX) pertains more to the capabilities of attracting and selecting mates in an effort to generate an offspring that is viable and attractive.

Indeed, organisms reproducing sexually should refrain from random mating since the genetic quality of a mate will dictate half of the genetic quality of the respective offspring. The clue to successful selection of mates is evolving a mechanism for mate selection that internalizes the long-term fitness reproducing results with various types of possible mates. The gain of mate selection is that passive fitness features which in the past posed threat to survival can be escaped while in the meantime the positive ones can be utilized. Accordingly, choice of mate is well calibrated if the recognized sexual attractiveness of the likely mates is strongly linked with the factual attractiveness, viability, and fertility of those offspring they may produce.

In numerous species, females choose the males for mating and producing offspring. This, on one hand, implies that the males must compete with one and another to make sure they will be selected as mates. On the other hand, females will be concerned in finding those males having high fitness and attractiveness as by mating with them they will guarantee production of offspring having high survival potentials and being attractive well enough to be later selected as mates by females in the succeeding generations.

Inspired by the nongenetic sex determination system prevalent in some reptile species where sex is determined by the temperature at which the egg is incubated, the population is divided such that the male and female would be selected in an alternate way. The layout of the male and female chromosomes in each generation is different [10].

During the sexual selection, the male chromosome is selected randomly from the male category and the selection of the female chromosome is done through a set of fuzzy rules and a newly developed genetic-neurofuzzy algorithm.

2.3.1. Adaptive Neurofuzzy Inference Systems Genetic Algorithm

The Sugeno fuzzy model [13] was proposed for a systematic approach to generate fuzzy rules from a given input-output dataset. A typical Sugeno fuzzy model given in Figure 5
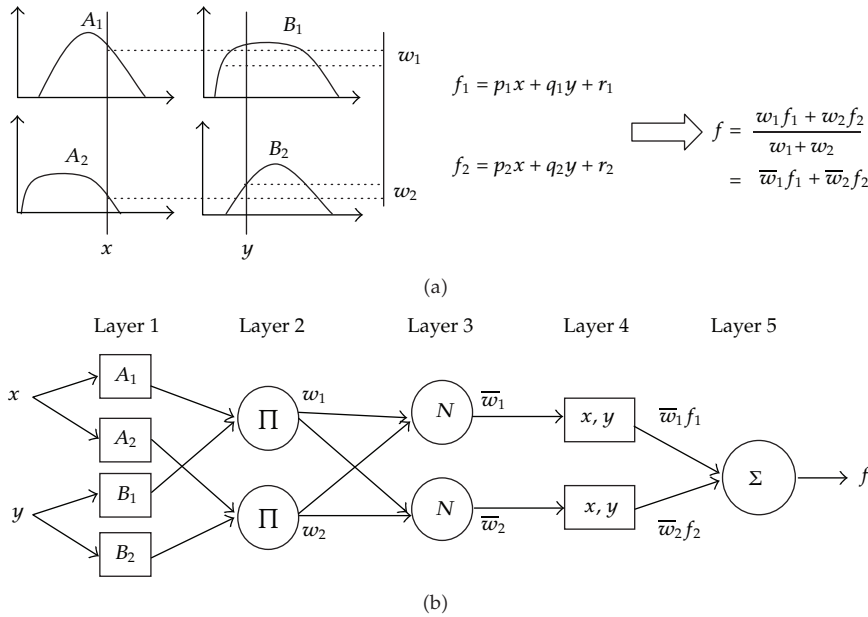
(a)

(b)

Figure 5: Adaptive neurofuzzy inference systems [13].

shows the ANFIS architecture that corresponds to the first-order Sugeno fuzzy model. For simplicity, we assume that the ANFIS has two inputs x_1 and x_2 but only one output y.

In adaptive neurofuzzy inference systems genetic algorithm (ANFISGA), there are two inputs: x_1 = male's age and x_2 = population diversity and one output: y = female's age, F_{age}.

In ANFISGA, we have five layers. Layer 1 is the input layer. Neurons in this layer simply pass external crisp signal to Layer 2. Layer 2 is the fuzzification layer. Neurons in this layer perform fuzzification. Layer 3 is the rule layer. Each neuron in this layer corresponds to signal Sugeno-type fuzzy rule. Layer 4 is the normalization layer. Each neuron in this layer receives inputs from all neurons in the rule layer and calculates the normalized firing strength of given rule. Layer 5 is the defuzzification layer. Each neuron in this layer is connected to the respective normalization neuron, and also receives initial inputs, α and β.

The main difference between ANFISGA and ANFIS is the adaptation. The ANFIS relies on the weights, w_i during adaptation. But in the ANFISGA, the weights are all constant. For adaptation, we use sexual selection based on female choice and population diversity. Figure 6 shows the ANFISGA architecture that corresponds to the first-order Sugeno fuzzy model. The rules for ANFISGA are given in Table 1, where $w_i = i(i = 1,2,3,4)$, $\overline{W}_i = W_i / \sum |w_i|$, α and β are defined in (2.1), μ_i is given in (2.3), η_i is taken from (2.6), and the output of ANFISGA is $D_i = F_{age}$ which refers to the lower bound of the F_{age} during the selection of the female chromosome.

After finding F_{age}, if we are not able to find a chromosome that has a value at least equal to F_{age}, then we select a chromosome having the nearest fitness value to F_{age}. On the other hand, if we are able to find more than one chromosome which satisfies having F_{age} condition, then we choose a chromosome having the highest fitness value among them. This technique is called complement method.
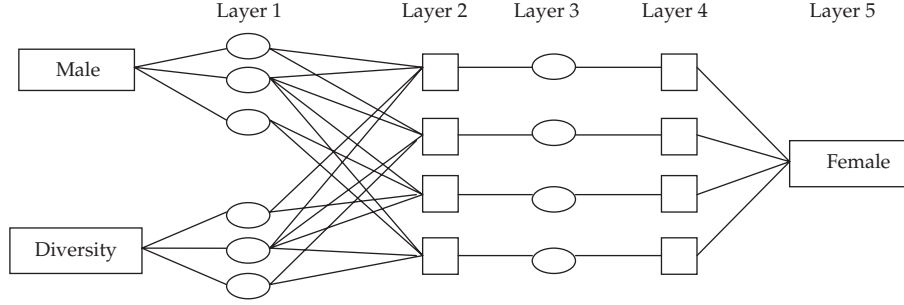
Figure 6: Adaptive neurofuzzy inference systems genetic algorithm (ANFISGA).

Table 1: Rules for ANFISGA.

Layer 3	Layer 5
$W_1 = w_1\mu_1 + w_2\mu_2 + w_3\eta_1 + w_4\eta_2$	$D_1 = \overline{W_1} + \beta/2$
$W_2 = w_1\mu_1 + w_2\mu_2 + w_3\eta_2 + w_4\eta_3$	$D_2 = \overline{W_2} + \beta/3$
$W_3 = w_1\mu_2 + w_2\mu_3 + w_3\eta_1 + w_4\eta_2$	$D_3 = \overline{W_3} + \alpha/2$
$W_4 = w_1\mu_2 + w_2\mu_3 + w_3\eta_2 + w_4\eta_4$	$D_4 = \overline{W_4} + \alpha/3$

3. Computational Experiments

The experiments are conducted to compare the performance of our proposed ANFISGA to other GAs found in [14] (see Table 2) for solving the well-known generalised Rosenbrock's Function introduced in [15] and one of the chemistry problems, namely, multieffect systems.

3.1. Generalized Rosenbrock's Function (f_{Ros})

The generalized Rosenbrock's function is a continuous and unimodal function, with the optimum located in a steep parabolic valley with a flat bottom. This feature will probably cause slow progress in many algorithms since they must continually change their search direction to reach the optimum:

$$f_{\text{Ros}}(x) = \sum_{i=1}^{n-1} \left[100\left(x_{i+1} - x_i^2 \right)^2 + (x_i - 1)^2 \right], \tag{3.1}$$

where $-5.12 \leq x_i \leq 5.12$.

We also included a binary-coded GA (BGA) with 30 genes per variable, multiple crossovers with two points and proportional selection probability into the experiments. Each algorithm is tested for 30 times with a maximum of 5000 generations per each run. The results

Table 2: Real Coded Genetic Algorithms (RGA) [14].

Algorithms	Mutation	Crossover
RGA1	Random	Simple
RGA2	Nonuniform	Simple
RGA3	Random	Uniform $\alpha = 0.35$
RGA4	Nonuniform	Uniform $\alpha = 0.35$
RGA5-α	Nonuniform	BLX (α: 0, 0.15, 0.3, 0.5)
RGA6	Nonuniform	Discrete
RGA7	Nonuniform	Linear
RGA8	Nonuniform	Extended intermediate
RGA9	Nonuniform	Extended line
ANFISGA	$P_m \in [0.001, 0.2]$	$P_c = 0.70$

Table 3: Comparison of GAs with ANFISGA.

Algorithms	Average	Algorithms	Average
BGA	$1.9045e + 00$	RGA5-0.30	$4.8854e - 01$
RGA1	$6.0669e + 00$	RGA5-0.50	$1.7329e + 00$
RGA2	$4.7343e - 01$	RGA6	$3.5106e - 01$
RGA3	$6.3745e + 00$	RGA7	$5.1499e - 01$
RGA4	$8.9244e - 01$	RGA8	$5.3325e - 01$
RGA5-0.0	$9.1602e - 01$	RGA9	$3.8014e - 02$
RGA5-0.15	$7.0929e - 01$	ANFISGA	$2.3240e - 03$

of the test function are listed in Table 3. The entries reported the average over 30 runs of the best fitness value found at the end of each run.

3.2. Multieffect Systems

Multieffect systems have two sequences of integration: forward integration sequence, where the heat integration is in the direction of the mass flow and backward or reverse integration sequence, where the integration is in the opposite direction of the mass flow as shown in Figure 7.

In this study, we considered multieffect distillation that is used in [16]. In this multieffect distillation of methanol/water system comprised of two 16 staged columns. The feed stream contains 0.73 mole percentage of methanol is fed to the column at the rate of 4320 kmol/h.

The objectives are to determine the appropriate configuration, feed locations, reflux, and boilup flows in both columns that minimize the operating cost.

For formulation, Preechakul and Kheawhom [16] used the common assumptions of equi-molar overflow, total condenser, and partial reboiler. This method creates acostly product by using as little energy as possible. The product from both columns must contain at least 99% methanol, and the methanol concentration in bottom stream from the second column must not be larger than 1%. The temperature difference between the condenser of high-pressure column and the reboiler of low-pressure column must be larger than 10°C.

(a) Direct   (b) Indirect
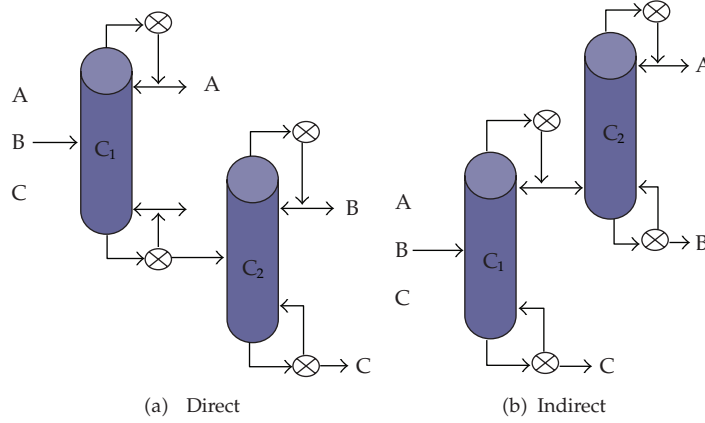
Figure 7: Conventional distillation sequences for the separation of ternary mixtures [17].

The following equations describe the model:

$$0 = (V_{i-1}y_{i-1} + L_{i+1}x_i + 1) - (V_iy_i + L_ix_i) \quad i \neq n_f,$$

$$0 = (V_{i-1}y_{i-1} + L_{i+1}x_i + 1) - (V_iy_i + L_ix_i) + F_z \quad i = n_f,$$

$$0 = L_2x_2 - (V_1y_1 + Bx_1),$$

$$0 = V_{n-1}y_{n-1} - (L + D)x_n,$$

$$0 = L_2h_2 - V_1H_1 + Q_R,$$

$$0 = V_{n-1}H_n - 1 - (L + D)h_n - Q_c,$$

$$y = \frac{\gamma x p^0}{p},$$

$$\ln\frac{p^0}{p} = \frac{\Delta h_{\mathrm{vap}}}{R}\left(\frac{1}{T_b} - \frac{1}{T}\right), \tag{3.2}$$

$$\ln\gamma_1 = -\ln(x_1 + \Lambda_{12}x_2) + x_2\left(\frac{\Lambda_{12}}{x_1 + \Lambda_{12}x_2} - \frac{\Lambda_{21}}{x_2 + \Lambda_{21}x_1}\right),$$

$$\ln\gamma_2 = -\ln(x_2 + \Lambda_{21}x_1) + x_1\left(\frac{\Lambda_{12}}{x_1 + \Lambda_{12}x_2} - \frac{\Lambda_{21}}{x_2 + \Lambda_{21}x_1}\right),$$

$$\Lambda_{12} = \frac{v_2^L}{v_1^L}\exp\left(\frac{-\lambda_{12}}{RT}\right),$$

$$\Lambda_{21} = \frac{v_1^L}{v_2^L}\exp\left(\frac{-\lambda_{21}}{RT}\right),$$

where γ: activity coefficient; λ_{ij}: binary parameter; B: bottom stream flow rate; D: overhead stream flow rate; F: feed stream flow rate; H: enthalpy of vapor; h: enthalpy of liquid;

Table 4: Best results for GA, HSS, and ANFISGA algorithms.

Algorithm	Forward Integration kg mol/h	Backward Integration kg mol/h
GA	1975.95	879.63
HSS	2288.72	1885.24
ANFISGA	2293.07	1891.21

L_i: liquid flow rate at stage i; n: number of equilibrium stages; n_f: feed location; p: pressure; p^0: absolute pressure, Q_c: heat flow rate at condenser; Q_R: heat flow rate at reboiler; R: ideal gas constant; T: temperature; T_b: normal boiling point temperature; v: molar volume; V_i: vapor flow rate at stage i; x_i: mole fraction of liquid phase at stage i.

The objective function is

$$\text{Max} F = D_{\text{HP}} + D_{\text{LP}} - w(Q_{R_{\text{LP}}} + Q_{C_{\text{HP}}}), \tag{3.3}$$

where D_{HP} and D_{LP} are the products (methanol) of the high-pressure and low-pressure column, respectively. Q_R is the heat load to the column, and $w = 0.3244$ mol/MJh is the relative cost of energy [16].

This fuzzy genetic algorithm is used in order to find the suitable configuration and to seek other operating situation.

The performance of our algorithms was compared with the presentation of the classical genetic algorithm and Hammersley sequence sampling (HSS) in [16] these results are shown in Table 4.

For traditional GA and genetic algorithm based on HSS, the population size 500 is considered and probability of crossover and mutation used are 0.8 and 0.1 respectively. In ANFISGA, probability of crossover is considered 1 and probability mutation and population size are the same other algorithms.

4. Conclusion

The principle conclusions derived from the results of experiments carried out are the following.

(i) The procedure presented is the most successful one for controlling diversity as compared with other methods proposed in the GA literature that have been considered for the experiments.

(ii) The adaptation capability of this procedure allows suitable parent to be used for producing a robust operation for test function with different difficulties.
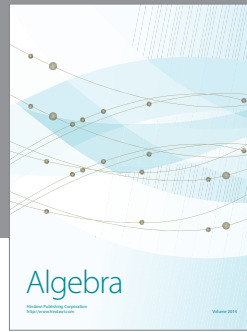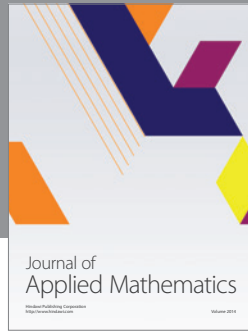
Therefore, we may conclude that the female choice by ANFISGA is a suitable way for improving the performance of GAs in keeping the diversity of the population.

Acknowledgment

References

[1] J. H. Holland, *Adaptation in Natural and Artificial Systems*, University of Michigan Press, Ann Arbor, Mich, USA, 1975.

[2] V. E. Bazterra, M. B. Ferraro, and J. C. Facelli, "Modified genetic algorithm to model crystal structures. I. Benzene, naphthalene and anthracene," *Journal of Chemical Physics*, vol. 116, no. 14, pp. 5984–5991, 2002.

[3] K. D. M. Harris, B. M. Kariuki, M. Tremayne, and R. L. Johnston, "New methodologies for solving crystal structures from powder diffraction data," *Molecular Crystals and Liquid Crystals Science and Technology A*, vol. 313, pp. 1–14, 1998.

[4] S. Hernández, J. Gabriel Segovia-Hernández, and V. Rico-Ramírez, "Thermodynamically equivalent distillation schemes to the Petlyuk column for ternary mixtures," *Energy*, vol. 31, no. 12, pp. 1840–1847, 2006.

[5] X. H. Yang, Y. N. Guo, and Y. Q. Li, "Projection pursuit hierarchy model based on chaos real-code genetic algorithm for river health assessment," *Nonlinear Science Letters C*, vol. 1, no. 1, pp. 1–13, 2011.

[6] X. H. Yang, Z. F. Yang, and Z. Y. Shen, "GHHAGA for environmental systems optimization," *Journal of Environmental Informatics*, vol. 5, no. 1, pp. 36–41, 2005.

[7] X. H. Yang, Z. F. Yang, X. A. Yin, and J. Q. Li, "Chaos gray-coded genetic algorithm and its application for pollution source identifications in convection-diffusion equation," *Communications in Nonlinear Science and Numerical Simulation*, vol. 13, no. 8, pp. 1676–1688, 2008.

[8] X. H. Yang, Z. F. Yang, Z. Y. Shen, and J. Q. Li, "A grey-encoded hybrid accelerating genetic algorithm for parameter optimisation of environmental models," *International Journal of Environment and Pollution*, vol. 28, no. 3-4, pp. 239–252, 2006.

[9] M. Jalali Varnamkhasti and L. S. Lee, "A genetic algorithm based on sexual selection for the multidimensional 0/1 knapsack problems," *International Journal of Modern Physics*, vol. 9, pp. 422–431, 2013.

[10] M. Jalali Varnamkhasti and L. S. Lee, "A fuzzy genetic algorithm based on binary encoding for solving multidimensional knapsack problems," *Journal of Applied Mathematics*, vol. 2012, Article ID 703601, 23 pages, 2012.

[11] S. A. Jafari, S. Mashohor, and M. J. Varnamkhasti, "Committee neural networks with fuzzy genetic algorithm," *Journal of Petroleum Science and Engineering*, vol. 76, no. 3-4, pp. 217–223, 2011.

[12] J. Arabas, Z. Michalewicz, and J. Mulawka, "GAVaPS—a genetic algorithm with varying population size," in *Proceedings of the 1st IEEE Conference on Evolutionary Computation*, pp. 73–78, June 1994.

[13] T. Takagi and M. Sugeno, "Fuzzy identification of systems and its applications to modeling and control," *IEEE Transactions on Systems, Man and Cybernetics*, vol. 15, no. 1, pp. 116–132, 1985.

[14] F. Herrera, E. Herrera-Viedma, M. Lozano, and J. L. Verdegay, "Fuzzy tools to improve genetic algorithms," in *Proceedings of the European Congress on Intelligent Techniques and soft Computing*, pp. 1532–1539, Granada, Spain, 1994.

[15] K. A. DeJong, *An analysis of the behavior of a class of genetic adaptive systems [Ph.D. thesis]*, Department of Computer Science, University of Michigan, 1975.

[16] C. Preechakul and S. Kheawhom, "Modified genetic algorithm with sampling techniques for chemical engineering optimization," *Journal of Industrial and Engineering Chemistry*, vol. 15, no. 1, pp. 110–118, 2009.

[17] D. Ozdemir, M. Mosley, and R. Williams, "Hybrid calibration models: an alternative to calibration transfer," *Applied Spectroscopy*, vol. 52, no. 4, pp. 599–603, 1998.