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An Integrated Neurogenetic Algorithm for Combinatorial Engineering Optimization

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Introduction

Optimization issues arise from the need to solve design, management, timing, and other technical problems on a grand scale. Holland _1_ was the first to examine genetic lgorithms _GAs_. Ased on evolutionary principles like election, recombination, and mutation, a genetic algorithm is a numerical optimization process. GAs can be applied to a wide variety of chemistry-related challenges. For instance, spectroscopy techniques that study molecules using electromagnetic radiation constitute a major branch of analytical chemistry that allows for the qualitative and quantitative determination of the primary componants of unfamiliar combinations. In this case, genetic algorithms were used because of their ability to effectively discover patterns in data, even when that data also includes a great deal of noise.

In addition to their use in system optimization (_2-4_), enetic algorithms have found application in the creation of regression curves (Journal of Applied Mathematics), protein folding (Journal of Applied Mathematics), and structure analysis. GA was used by Yang et al. _5-8_ in practical uses of several commonplace computing methods across disciplines. One of the traditional difficulties in using GA to discover the best answer is premature convergence. Premature convergence can be prevented in a GA by increasing the population's genetic variety. During crossing in a conventional GA, any pair of chromosomes can act as parents. In this context, gender segregation and sexual selection motivate a concept of gendered GAin which chromosome crossing occurs only between those of different sexes. The sex of chromosomes is not only responsible for optimizing the various duties that are crucial to life, but it is also responsible for keeping population variety and sustaining a successful genetic pool through selection, crossover, and mutation. There was a change in sexual preference after the work of Jalali Varnamkhasti and Lee _9_. Their method involves separating the populace into male and female subsets.. The female chromosome is chosen through tournament selection, and the male chromosome is chosen either by its hamming distance from the chosen female chromosome, its itness value, or its active genes. A flexible genetic algorithm using this method as its selection echanism was proposed in a different research by Jalali Varnamkhasti and Lee _10_. By analyzing the outcomes of various test functions and employing some nonlinear numerical functions, they were able to prove thatThe method of arranging male and female chromosomes interchangeably that has been suggested works better than other methods used in reproductive selection processes. In addition, Jafari et al. _11_ provide an example of using this method in the context of committee neural networks for sexual selection. This research takes into account a salient difference between the sexes, along with the potential of encoding distinct objectives for each, such as the identification of compatible breeding and crossing companions. We anticipate that the selection process will be influenced by the age-effectiveness-fitness relationships observed in biological systems. The chromosomes are assigned labels according to their fitness levels using a bilinear allocation lifespan method. The discovered genome names are utilized in describing the population's heterogeneity. Separating the populace into males and females allows for a more fair selection of candidates. The order in which males and females are chosen varies from generation to generation. The primary goal of this article is to preserve demographic variety from a feminine perspective. A genetic-neurofuzzy method and a collection of fuzzy criteria are used in the choosing of the female chromosome.

A Genetic Algorithm for Neuro-Fuzzy Inference Systems

To that end, we'll devote the rest of this article to a detailed analysis of the suggested neurofuzzy inference systems evolutionary method for addressing combinatorial optimization roblems. Following this, we detail the components of the suggested method, shown in Figure 1, and explain how they function together. 2.1.

A answer to a problem involving nonlinear functions can be represented by a series of binary digits. Convergence in a GA is sped up by starting with a decent original population and slowed down by starting with a bad one. The original populace for a GA can be generated using a variety of methods. Random number creation is the most widely used approach. This work employs the random number generator in order to better diversity in the population.

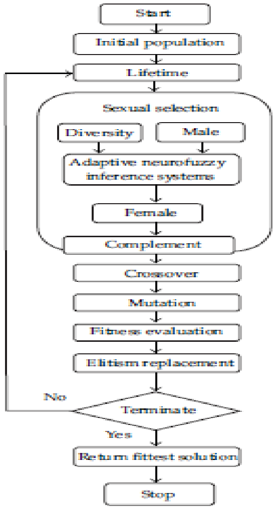


Figure 1: Framework of neurofuzzy inference systems genetic algorithm.

Permanent function.

There are three approaches presented for calculating the fitness-based lifespan of chromosomes in genetic algorithms with different population sizes. The goal here is to find an approach to using the permitted range of lifespan values that is better suited to searching the optimal than proportionate, linear, and bilinear methods _12_. Labeling the chromosomes according to their fitness value, the research will then use this information to describe the population's variety using a bilinear allocation lifespan method oposed in _12_. In this context, the word "age" stands in for chromosomes as a language variable. Age is a language variable depicted in Figure 2 with the possible values "infant," "adult," and "old." Semantic norms refer to the language word membership functions. The membership function is calculated from the population's lowest, maximum, and average fitness levels over time, as well as from the fitness values of individual chromosomes. A unique name is assigned to each chromosome based on the age

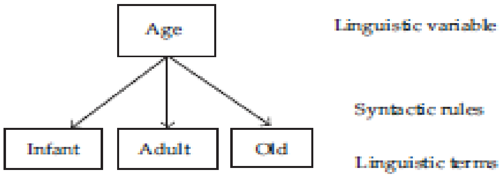
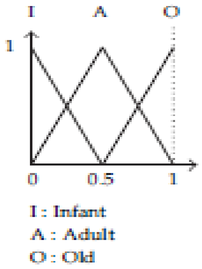


Figure 2: Three linguistic variables for age.



Membership function for male and female chromosomes, shown in Fig. 3.

Let fi be the fitness value of chromosome i, favr the average fitness value of the community, fmin the lowest fitness value, and fmax the maximum fitness value. An expression for aging is

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

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

where ci is the i-th chromosome, n is the total number of people, L is the youngest age, U the oldest, and L and U the minimum and maximum ages, respectively. Maximization problems, which involve greater fitness values, are best represented by Equation _2.1_, while reduction issues, which involve lower fitness values, values, which are most accurately described by Equation _2.2_. The Fuzzification protocol specifies the three possible language values for each gene. Each assumption of the rules has a relevance level that is established by these numbers. All chromosomes in each generation are considered, and the omputation makes use of the L_2 and U_10 triangle membership functions shown in Figure 3.

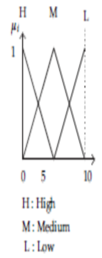


Figure 4: The membership function for diversity.

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

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

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:

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

Let φ 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:

$$\text{population diversity} = \begin{cases} \text{High}, & 0 \le \varphi \le 2L + t, \\ \text{Medium}, & 0 \le \varphi \le 4L + 2t, \\ \text{Low}, & 2L + t \le \varphi \le 4L + 2t, \end{cases} \tag{2.5}$$

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.

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

$$D = \begin{cases} \text{High}, \eta_1 = -\frac{1}{5} + 1 & 0 \le x \le 5, \\ \text{Medium}, \eta_2 = \begin{cases} \frac{1}{5}x & 0 \le x \le 5, \\ \frac{1}{4}x - \frac{1}{4} & 5 < x \le 10, \end{cases} \\ \text{Low}, \eta_3 = \frac{1}{5}x - 1 & 5 \le x \le 10. \end{cases} \tag{2.6}$$

Sexual Selection

Darwin distinguished between sexual and natural choices as two distinct processes acting on distinct characteristics in line with distinct patterns of evolutionary dynamics. According to Darwin, while sexual selection _SX_ is more about enticing and choosing partners in an attempt to produce healthy and beautiful progeny, natural selection improves an organism's ability to live in a competitive environment. Because the genetic quality of a partner determines half of the genetic quality of the corresponding progeny, sexually reproducing creatures should avoid coupling at random. The key to partner selection success lies in the evolution of a system that internalizes the outcomes of long-term optimal reproduction with different kinds of potential companions.

The benefit of partner selection is that it allows individuals to avoid negative inactive fitness traits while capitalizing on positive ones. Mate selection is well-calibrated if the perceived beauty of potential partners is highly correlated with the real appeal, survival, and fecundity of their progeny. Females of many species actively select men to mate with and have children with. On the one hand, this means that men are in a constant state of competition to ensure they are the ones chosen as partners. On the other hand, women are motivated to find physically and sexually attractive men because they know that having children with such fathers will increase their chances of *survival and make them more desirable partners in future generations. The population is split so that the males and females are chosen for in different ways, a strategy inspired by the non genetic sex determination method revalent in some reptilian species, in which sex is decided by the temperature at which the egg is kept. Each new generation brings a new set of genetic arrangements for both sexes. The male chromosome is chosen at random from the male group and the female chromosome is chosen from the female category during reproductive selection chromosome through the use of a genetic-neurofuzzy program and a collection of fuzzy principles. 2.3.1.*

The Use of a Genetic Algorithm to Optimize Neurofuzzy Inference Systems

In order to create fuzzy rules systematically from an input-output collection, the Sugeno fuzzy model _13_ was suggested. In Figure, we see an example of a standard Sugeno fuzzy model.

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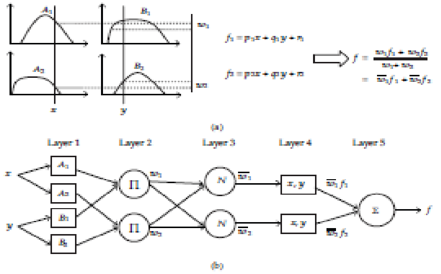

Figure 5: Adaptive neurofuzzy inference systems [13].

shows the ANFIS structure for the Sugeno flexible first order model. Given that x1 and x2 are assumed to be inputs and y to be the unique output of the ANFIS. The adaptive Neurofuzzy inference systems genetic algorithm _ANFISGA_ takes in two inputs (x1 _ male's age and x2 _ population variety) and produces a single output (y _ female's age). Fage ANFISGA has five distinct levels. Layer 1 is responsible for processing input data. Here, neurons' only job is to transmit information clearly received from the outside environment to the next layer. The information is made more vague at the next tier.

The generation of fuzziness occurs in these neurons. The third level is a collection of guidelines. Each neuron in this layer stands for a movable code, like that used by the Sugeno signal detector. Layer 4 is the adjusting layer. Each neuron in this layer uses input from its neighbors to determine the rule's standard discharge intensity. Fifth in the series is the Defuzzification layer. Each neuron in this layer is coupled to its appropriate normalizing neuron and receives initialization signals. The main difference between NFISGA and ANFIS is the adjustment. When making adjustments, the ANFIS takes into account the wi weights. In contrast, ANFISGA weights are consistent throughout all sections. Adaptive evolution is driven by sexual selection, which is influenced by female choice and genetic variety. Figure 6 depicts the ANFISGA architecture for a first-order Sugeno fuzzy model. The ANFISGA principles are summarized in Table 1: wi _ i_i _1, 2, 3, 4_, Wi _ Wi/ |wi|, and are described in _2.1_, i is provided in _2.3_, i is obtained from _2.6_, and Di _ Fage, the lower limit of the resultant fractal dimension, is the outcome of ANFISGA. If, after determining Fage, no chromosome is found to have a value at least as high as Fage, the chromosome with the fitness value closest to Fage is selected. If, If, however, we find that more than one chromosome satisfies the Fage criteria, we choose the one that provides the largest improvement in health. The complement technique is the name given to this strategy.

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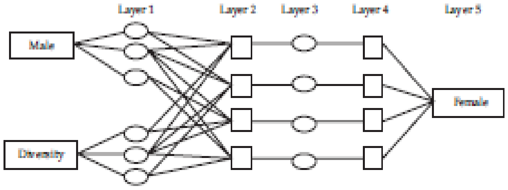
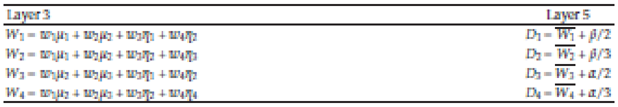
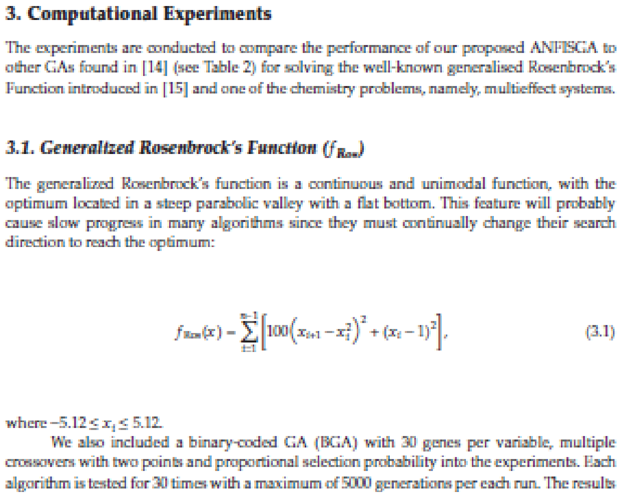


Figure 6: Adaptive neurofuzzy inference systems genetic algorithm (ANFISGA).

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})

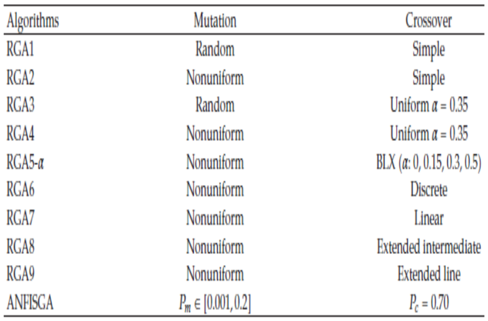
The generalized Rosenbrock's function is a continuous and unimodal function, with the optimum located in a steep parabolic valley with a flat bottom. This feature will probably cause slow progress in many algorithms since they must continually change their search direction to reach the optimum:

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

where $-5.12 \le x_i \le 5.12$.

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	$P_m \in [0.001, 0.2]$	$P_c = 0.70$

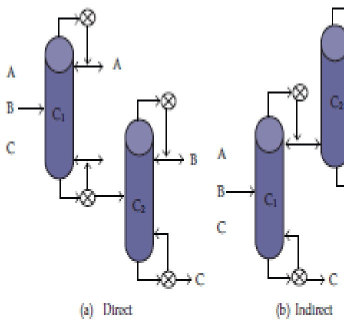
Table 3: Comparison of GAs with ANFISGA.

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

The outcomes of the tests are shown in Table 3. The highest fitness grade at the end of each run and the average over 30 rounds were included in the entries.

Action Sequences, Third Revision

As shown in Figure 7, there are two possible ways of integration in multi effect systems: forward, where heat is integrated along the path of the mass flow, and backward, where integration happens along the path of the opposite mass flow. In this case, we considered multi effect distillation techniques similar to those employed in _16_. This distillation apparatus for methanol/water uses two 16-stage columns to achieve many effects simultaneously. At a rate of 4320 k mol/h, methanol makes up 0.73 of the input stream and is pumped into the column. The objectives are to discover the best cost-effective configuration for both columns with respect to design, input locations, reflux, and boil up fluxes. The system utilized by Preechakul and Kheawhom _16_ included an equi-molar overflow, a full ondenser, and a partial reboiler. This method yields a high-priced product with little input. The output of both columns should contain at least 99% methanol, and the bottom stream methanol concentration from the second column should be less than 1%. The high-pressure temperature difference between the condenser and evaporator column and the low-pressure column reboiler must be above 10 degrees Celsius..



(a) Direct (b) Indirect

Figure 7: Conventional distillation sequences for the separation of ternary mixtures _17_. The following equations

$$
\begin{aligned}
0 &= (V_{i-1}y_{i-1} + L_{i+1}x_i + 1) - (V_iy_i + L_ix_i) \quad i \neq n_f,\\
0 &= (V_{i-1}y_{i-1} + L_{i+1}x_i + 1) - (V_iy_i + L_ix_i) + F_2 \quad i = n_f,\\
0 &= L_2x_2 - (V_1y_1 + Bx_1),\\
0 &= V_{n-1}y_{n-1} - (L + D)x_n,\\
0 &= L_2h_2 - V_1H_1 + Q_R,\\
0 &= V_{n-1}H_n - 1 - (L + D)h_n - Q_c,\\
y &= \frac{\gamma x p^0}{p},\\
\ln\frac{p^0}{p} &= \frac{\Delta h_{\mathrm{vap}}}{R}\left(\frac{1}{T_b} - \frac{1}{T}\right),\\
\ln\gamma_1 &= -\ln(x_1 + \Lambda_{12}x_2) + x_2\left(\frac{\Lambda_{12}}{x_1 + \Lambda_{12}x_2} - \frac{\Lambda_{21}}{x_2 + \Lambda_{21}x_1}\right),\\
\ln\gamma_2 &= -\ln(x_2 + \Lambda_{21}x_1) + x_1\left(\frac{\Lambda_{12}}{x_1 + \Lambda_{12}x_2} - \frac{\Lambda_{21}}{x_2 + \Lambda_{21}x_1}\right),\\
\Lambda_{12} &= \frac{v_2^L}{v_1^L}\exp\left(\frac{-\lambda_{12}}{RT}\right),\\
\Lambda_{21} &= \frac{v_1^L}{v_2^L}\exp\left(\frac{-\lambda_{21}}{RT}\right),
\end{aligned}
\tag{3.2}
$$

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;

Describe the model:

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

Qc = heat flow rate at condenser; Li = liquid flow rate at stage i; n = number of equilibrium stages; nf = feed location; p = pressure; p0 = absolute pressure; Molecular volume (v), vapor flow rate (Vi), mole fraction of liquid phase (xi), temperature (T), normal boiling point temperature (Tb), heat flow rate (QR), ideal gas constant (R), temperature (T), and normal boiling point temperature (Tb). There is an aim function Is where DHP and DLP are the methanol byproducts of the high- and low-pressure columns. The heat load on the column is denoted by QR, and the relative cost of energy is denoted by w_ 0.3244 mol/MJh. This fuzzy genetic method is used in configuration exploration and the search for other operating conditions. Table 4 displays the results of a comparison between the performance of our methods and that presented in _16_, where the traditional genetic algorithm and Hammers ley sequence sampling _HSS_ were both presented. Both classical GA and HSS-based genetic algorithms employ a population size of 500, with a crossover probability of 0.8 and a mutation probability of 0.1. In ANFISGA, the crossover probability is set to 1, and the mutation and population sizes are kept constant..

Conclusion

Some important conclusions from the research are listed below. The suggested strategy is the most effective one for managing diversity when compared to other strategies published in the GA literature that were examined for the experiments. This method is flexible enough to use a suitable parent to build a strong operation for a test function of any complexity. This leads us to believe that ANFISGA's preference for females is a good way to improve GA performance while still preserving population variety.

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