

De Jong's Sphere Model Test for a Human Community Based Genetic Algorithm Model (HCBGA)

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Abstract—A new structured population approach for genetic algorithm, based on the custom, behavior and pattern of human community is provided. This model is named the Human Community Based Genetic Algorithm (HCBGA) model. It includes gender, age, generation, marriage, birth and death. Using the De Jong's first function 1, "The Sphere Model" comparisons between values and results concerning the averages and best fits of both, the Simple Standard Genetic Algorithm (SGA), and the Human Community Based Genetic Algorithm (HCBGA) model are obtained. These results are encouraging in that the Human Community Based Genetic Algorithm (HCBGA) model performs better in finding best fit solutions of generations in different populations than the Simple Standard Genetic Algorithm. The HCBGA model is an evolution of the simple Genetic Algorithm (SGA).

The result of this paper is an extended of the result concerning algorithm in [6].

Keywords—Genetic Algorithms (GAs); Evolutionary Algorithms (EA); Simple Standard Genetic Algorithms (SGA), Human Community Based Genetic Algorithm (HCBGA) model; De Jongs' functions, the Sphere model

I. INTRODUCTION

Genetic Algorithms (GAs) were early proposed in the 1960s and 1970s. These search algorithms were initially proposed by Holland, his colleagues and his students at the University of Michigan. GA's are based on nature and mimic the mechanism of natural selection [1, 3, 5, 6, 7, 8, 9].

In his book "Adaptation in Natural and Artificial Systems" [1] Holland initiated GA's as a new area of study. Theoretical foundations besides exploring applications were also presented.

The solution to the problem is represented as a genome (or chromosome) [1, 3, 4, 5, 6] in GAs. The operators such as the crossover and mutation of GA are applied to initialize the population [1, 3, 4, 5, 6]. And with their natural selection they have an iterative procedure usually used to optimize and select the best chromosome (solution) in the population. This population consists of various solutions to hard complex problems and is usually generated randomly [5, 14]. Fig. 1 below represents the Simple Standard GA evolution flow.

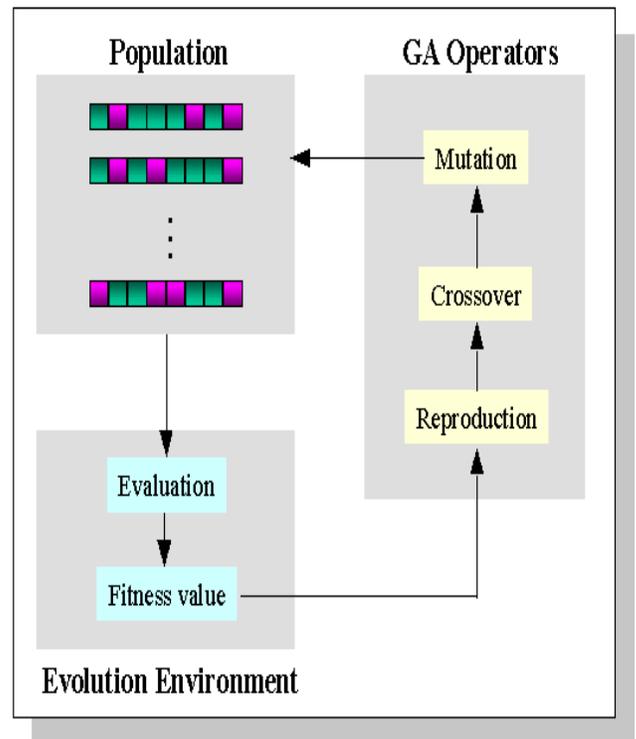


Fig. 1. Evolution flow of genetic algorithm [5]

GAs attracted many researchers to search and optimize complex problems. In addition, they proved to be efficient in solving different combinatorial optimization problems. They are considered heuristic search algorithms that solve unconstrained and constrained problems [3]. GAs plays a main role in designing complex devices such as aircraft turbines, integrated circuits and many others [3].

GAs has many advantages in terms of global optimization. On the other hand, from these advantages; potential disadvantages appear [3].

II. RELATED WORK

John Holland, his colleagues and his students have designed some kind of artificial system software to explain adaptive processes of natural systems [3, 6].

In a certain problem, GA is unaware of the problem itself. It only needs the input parameters. After that, GA represents these inputs in a chromosome format. It differs from other search algorithms in that it has this unique characteristic [3]. This is the reason why GAs can be applied to many types of complex problems [1, 3].

Researches began using GAs to solve some academic problems such as the traveling salesman problem and the 8 Queens problem [3, 5, 6, 9]. Years later, GAs grew rapidly. Applications of GAs were increased to optimize complex scheduling problems and many other types of problems that are hard to efficiently maximize [7].

In the Simple Standard Genetic algorithm parents are selected randomly. There are no constraints in choosing two individuals to mate together [36]. Researchers in this field tried to tackle this problem. They tried to design structured population and control the interaction of the individuals in this population [36].

From many researches on GAs different types and models of GAs appeared such as Cellular GA [36], Island GA [37], Patchwork GA [38, 39], Terrain-Based GA [40], and religion-Based GA [41]. Below we will discuss some of them briefly.

A. Cellular GAs (CGA)

By Gorges-Schleuter, 1989 [36]. It is called a diffusion model. A two-dimensional Grid world is used here to arrange the individuals where these individuals interact with each other by the direct neighborhood of each individual [42]. These individuals will be distributed on a graph which is connected together; each individual connects with its neighborhood by a genetic operator. This type of GAs is designed as a probabilistic cellular automation. A self-organizing schedule is added to reproduce an operator [43]. The individual which can interact with its immediate neighbors can only be held in the cell.

B. Terrain-based GA (TBGA)

TBGA showed better performance than the CGA with less parameter tuning [40]. This was discussed in a previous study [36]. At every generation each individual should be processed, and the mating will be selected from the best of four strings, located above, below, left, right.

It is a more self-tuning model compared to cellular genetic algorithm [40]. In which many combination parameter values will be located in different physical locations.

C. Island Models (IGA)

According to the increasing complex problems which appear in evolutionary computation, more advanced models of evolutionary algorithms (EAs) appear. Island models are considered a family of such models [45]. Here the individuals are divided into sections. We call each section a subpopulation which is referred to as an island. These island models are able to solve problems in a better performance than standard models [46, 43]. There is a specific relation between islands through some exchange of some individuals between islands. This process is called migration; this is what island models are famous of, and without these migrations, each

island is considered as a set of separate run. Therefore migration is very important [47, 45].

D. Patchwork Model

This type was introduced by Krink et al., (1999). A combination of ideas from cellular evolutionary algorithms, island models, and traditional evolutionary algorithms were used in this model [38, 39]. Here the grid is a two dimensional grid of fields, each field can have a fixed number of individuals. The patchwork model is considered a self-organized, spatial population structure [44]. In a GA population, in order to allow self-adaptation, patchwork model is used as a base. It contains a grid world and some interesting agents. In modeling biological systems the patchwork model is considered as a general approach.

E. Religion-Based EA Model (RBEA)

It was introduced by Rene Thomsen et al. [44]. The religion-based EA model is based on a part of religious concept which is attracting believers. It attracts new believers to a religion which puts more control than other models such as cellular EA and the patchwork models [41].

III. HUMAN COMMUNITY BASED GENETIC ALGORITHM (HCBGA) MODEL

AL-Madi and Khader [6] presented a new approach for structured population of GAs so-called Social-Based Genetic Algorithm (SBGA). They applied some constraints on the Simple Standard Genetic Algorithm (SGA) in order to control its randomness in selecting parents. This paper provides a new structured population approach for genetic algorithm, based on the custom, behavior and pattern of human community. This includes gender, age, generation, marriage, birth and death. As such, this model is named the Human Community Based Genetic Algorithm (HCBGA) model. This model is an evolution of the simple Genetic Algorithm (SGA). It is considered an extension to results given in [6].

A. HCBGA Chromosome Representation

In the HCBGA, the chromosome represents the genome information and additional attributes that would help in simulating human community behavior. In addition, being in the same society- as the population is divided into subgroups or islands- is a dependable constraint for recombination. The problem of age is considered also by adding an attribute for the age. The age attribute takes three values: youth, parent, and grandparent. This chromosome representation (the presence of father and mother pointers) will keep all family relations which divides the subgroups into a Directed Acyclic Graph (DAG).

All the standard operations in the SGA will be changed in order to add restrictions on each operation including: Social constraints such as the Male/Female '*operator*', this will be added in the selection part which will restrict choosing two different couples. In addition the Birth *operator* which is generating a new population, and the Death *operator* which will discard the worse individuals.

The development of this new model was carried out in a series of steps. This was done in gradual steps to enable the

measurement of the enhancements to be carried out. The major steps are as illustrated in Fig. 2.

B. HCBGA Method

Initially, the first individual is selected randomly from the population - this will be the first parent. Based on the first parent's type (whether a male or a female), the second parent will be chosen such that it is the opposite type of the first parent. This process is repeated for a number of individuals creating the initial population. Next come the stages of selection and crossover, bringing up two new children or *offspring's*. Repeating this for a number of couples a second population will be generated.

Again, the previous process is repeated until the maximum number of generations is reached. (The next main important thing is that the *two individuals* must *not* share the same parents).

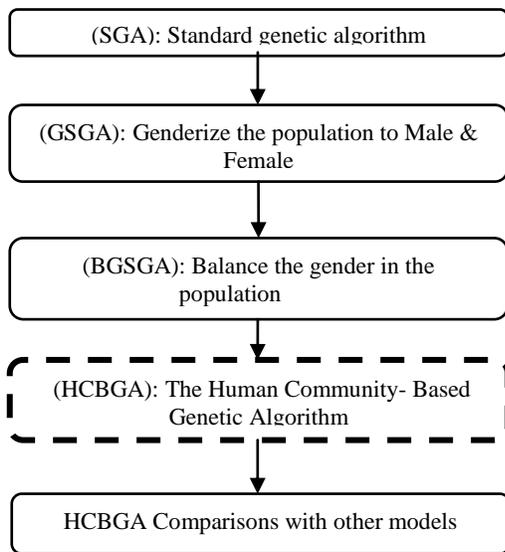


Fig. 2. Development of the HCBGA model

IV. DE JONG'S FUNCTIONS

De Jong's functions were initially introduced in his thesis entitled "An analysis of the behavior of a class of genetic adaptive systems" [8, 11]. These different functions were used as evaluation functions for the genetic algorithm structure. Many different optimization problems were explained in a novel way using these kinds of functions. This made them the most widely used functions for experimenting Genetic Algorithms functionality and allowing direct comparisons with existing available results [8, 12].

A. De Jong's function (1): (The Sphere Model)

De Jong's function no. (1) is considered the easiest and simplest test function among De Jong's other functions [10]. It is also called "The Sphere Model". It is a good example of a continuous, strong convex, unimodal function [9, 10].

The structure of the first functions of De Jong functions is defined as follows:

Function definition:

$$f_1(x) = \sum_{i=1}^n x_i^2 \quad -5.12 \leq x_i \leq 5.12$$

$$f_1(x) = \text{sum}(x(i)^2), i=1:n, 5.12 \leq x(i) \leq 5.12.$$

Global minimum:

$$f(x)=0, x(i)=0, i=1:n.$$

The Sphere model serves as a test case for convergence velocity and is well known and widely used in all fields of evolutionary algorithms occurring in the test sets of Schwefel, De Jong, and Fogel [9, 10]. The three-dimensional topology of the Sphere model which shows the Visualization of De Jong's function (1) is shown in Fig. 3 below.

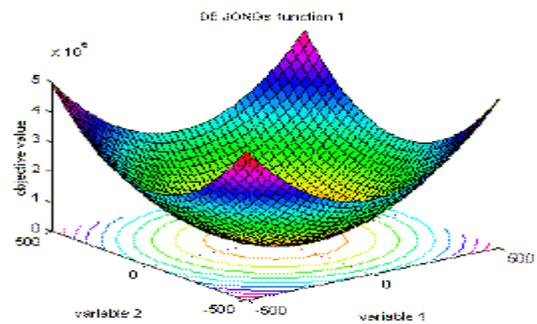


Fig. 3. The Sphere model in a very large area from -500 to 500, [10]

V. EXPERIMENTAL RESULTS

In this paper we have used the first of De Jong's functions - "The Sphere model" to test the Human Community Based Genetic Algorithm (HCBGA) model. We also used it as a test on the Simple Standard Genetic Algorithm (SGA) in order to compare between both algorithms.

A population size of 350 and a randomly selected one-point crossover are used in a process that is both standard and simple [34]. A random integer (crossover point) and a crossover rate of 50% are chosen according to the maximum length of the chromosome in the model. This is the place in the chromosome at which, with probability, the crossover will occur. If the crossover does occur, then the bits up to the random integer of the two chromosomes are swapped. The mutation of a solution is a random change to a gene value [34, 35]. After several experiments of different mutation rates, the most suitable mutation rate is 0.04. The selection method used is the roulette wheel. The number of generations is 100. The implementation part was programmed in C# (C Sharp) Language Version (5.0) on a Pentium 4, HP-Compaq laptop. This function generates values randomly, whereby the value is restricted to between (-5.12 and 5.12). As mentioned earlier, this was defined in the De Jong's first function.

By applying the Sphere model on both the Simple Standard Genetic Algorithm (SGA) and on the Human Community Based Genetic Algorithm (HCBGA) model we can compare the performance of both algorithms. The comparisons in Figures 4 and 5 below show that the constraints put on the new Human Community Based Genetic Algorithm (HCBGA) model has results in better performance to HCBGA than the Simple Standard Genetic Algorithm (SGA) which depends mainly on its randomness in finding the best fit solution.

It is shown that in the Human Community Based Genetic Algorithm (HCBGA) model the average converge toward the optimal solution better than the Simple Standard Genetic Algorithm (SGA), and the best fit values in the Human Community Based Genetic Algorithm (HCBGA) model also show better findings of best fit values in comparison to the Simple Standard Genetic Algorithm (SGA).

1) Diversity measurement

A pair-wise Hamming distance is used in this paper as a measurement to the diversity of the six models SGA, GSGA, BGSGA, HCBGA, CGA and IGA using the Dejong's first test function (f1) problem. This is shown in Figures (4) and (5) respectively.

Fig. 4 illustrates a convergence which occurred in the SGA model, where the curve go down towards the zero x-axis at the second generation. This occurrence is considered a fast convergence. This fast convergence indicates a loss of diversity. As a reason this happened due to the existence of similar or identical individuals as all individuals are of same gender in the SGA, in addition there is no constraints when selecting partners to mate any individual could mate with any individual as long as they have high fitness values. This causes a wide possibility of identical individuals to mate producing similar individuals in the next generation and by repeating this process over the generations it leads the search to get stuck around the same solution which causes the algorithm to find a local optimum and fall in a premature convergence.

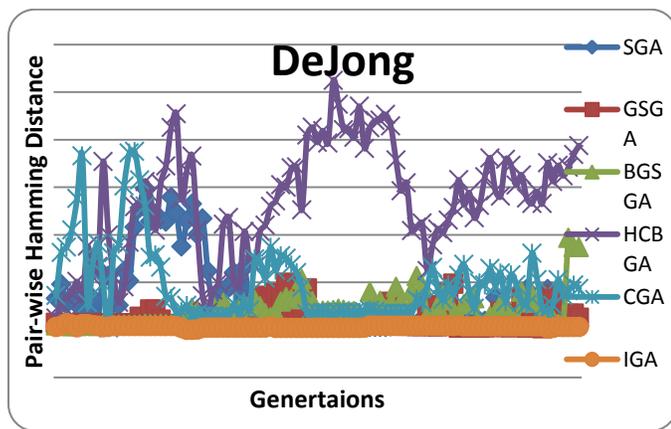


Fig. 4. Pair-wise Hamming Distance for six models SGA, GSGA, BGSGA, HCBGA, CGA and IGA over the 100th generations.

In the GSGA model, it is seen that the curve converges at the 15th generation, then a small improvement in the pair-wise Hamming distance which gave higher values is indicated from the 16th through the 100th generations. But still the GSGA's

Pair-wise hamming distance has a low value which is near to the zero x-axis. On the other hand, GSGA shows a slower convergence towards the zero compared to the SGA model. This slower convergence occurred due to the division to male and females between individuals giving a better opportunity to the GSGA model to search the search space for better solutions than in the SGA. This division applied a better diversity in the GSGA population better than the SGA. But until now there are no restrictions when choosing partners to mate and there is no balance between the number of males and females in the GSGA population which indicates a loss of diversity as shown in Fig. 4.

The BGSGA model with both the division to male and female and the balance of the individuals in the population to 50% males and 50% females caused a much slower convergence towards the zero x-axis as the values of the pair-wise Hamming distance are getting higher over the generations denoting by this a better diversity in the BGSGA population against the GSGA and the SGA models.

Similarly to the SGA model the CGA and the IGA models have a fast convergence towards the zero x-axis. This is due to both CGA and IGA have common features as in the SGA model whereas there is no existence of sexual gender between the CGA and IGA's population. By this a loss of diversity exists due to the random selection between mates to mate which could be similar or identical and they produce new similar or identical individuals in the next generations.

Relating to the pair-wise hamming distance the HCBGA model shows no convergence towards the zero x-axis over the generations and gives higher pair-wise hamming distance than the other models which indicates that this model has a better diversity. This is due to the different constraints put on the individuals as the existence of the balanced gendered population made a kind of balanced diverse population. Besides that the human community rules raised in the rules of marriage which restricts mating to a prohibited female gave the HCBGA a humanizing population with a balanced diversity in the population. All together gave the HCBGA algorithm the opportunity to search for better solutions in the space of potential solutions maintaining by this the diversity and avoiding falling into a premature convergence.

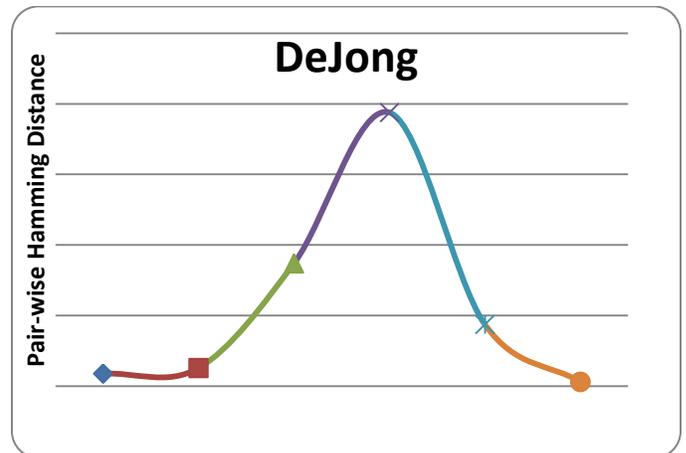


Fig. 5. Pair-wise Hamming Distance for six models SGA, GSGA, BGSGA, HCBGA, CGA and IGA at the 100th generation.

From Fig. 5, the HCBGA’s population diversifies better than the other models whereas, the later shows that the individuals are centralized near zero of x axis due to their low pair-wise Hamming distance. This means that the distance between the individuals is very short. It indicates that the individuals are almost similar or identical which leads to premature convergence. However, in the HCBGA model, the individuals spread over the search space in a tuning way far away from the x axis as such there are differences between individuals which gives a more divers population and avoids the model to fall in a premature convergence. This is indicated from the high pair-wise Hamming distance between individuals of the HCBGA model as in Fig. 5.

2) Statistical Analysis for the models

A statistical analysis has been conducted on the results of the experiments of the paper using the SPSS version 5.0. Table (I) summarizes the results of 20 experiments which compares between 6 models SGA, GSGA, BGSGA, HCBGA, CGA and IGA using the DeJong’s first function test problem. In a minimization problem the lower the mean value is the best the model is. Table (I) shows that the HCBGA is the best model based on the lowest mean, standard deviation and variance where its mean value = 1.06 and its standard deviation value = 0.089. If the standard deviation is a high value it means that the individuals don’t spread towards the minimum, else the low value of the standard deviation explains the spread of individuals towards the minimization. It is found in Table (I) that the HCBGA model has the lowest standard deviation. This indicates that individuals in the population are spreading around the mean in a balanced distribution. In addition, the variance value of the HCBGA = .008 which is also lower compared to the other models, this indicates a variation in the data, so the HCBGA model has achieved more diversity between its individuals than the other models. By this, the HCBGA model could achieve a better fitness value which means better performance than other models.

TABLE I. MEAN, STANDARD DEVIATION AND VARIANCE OF THE POPULATION FOR SGA, GSGA, BGSGA, HCBGA, CGA AND IGA MODELS USING THE DEJONG’S FIRST FUNCTION (F1) PROBLEM AFTER 100 GENERATIONS

Models	No. Generations	Mean		Std. Deviation	Variance
	Statistic	Statistic	Std. Error	Statistic	Statistic
SGA	100	3.354	.0617	.6167	.380
GSGA	100	2.03	.035	.354	.126
BGSGA	100	1.371	.0269	.2687	.072
HCBGA	100	1.06	.009	.089	.008
CGA	100	3.975	.0605	.6053	.366
IGA	100	3.630	.0637	.6370	.406

TABLE II. FRIEDMAN TEST SHOWS RANKS BETWEEN SGA, GSGA, BGSGA, HCBGA, CGA AND IGA MODELS

Models	Mean Rank
CGA	5.35
IGA	5.20
SGA	4.45
GSGA	2.94
BGSGA	1.92
HCBGA	1.15

The lowest rank in a minimization problem is considered the best. Table (II) shows the mean ranks of the six models; HCBGA model clearly outperforms the other models as it achieved the lowest rank. Since HCBGA yields the best rank against the other models this means that this model has achieved better fitness values in its populations along the 100 generations towards the optimal minimum.

TABLE III. KENDALL’S W TEST SHOWS SIGNIFICANT DIFFERENCES BETWEEN SGA, GSGA, BGSGA, HCBGA, CGA AND IGA MODELS

N	100
Kendall's W(a)	.898
Chi-Square	448.932
Df	5
Asymp. Sig.	.000
Monte Carlo Sig.	.000

In Table (III), N is the number of generations the chi-square indicates a test of independence, whereas its value is very high in Table (III) meaning that the HCBGA model is independent from other models. The Df is the degree of freedom its value is k-1 where k is the number of models tested where in this test there is 6 models so the Df value is 5. In addition, the Kendall’s W value is .898 which is a high value near to 1, this indicates a full agreement that the HCBGA model performs significantly better in exploring the search space for best solutions than other models. Finally, in Table (III) it shows a Monte Carlo significant value of .000 which means the HCBGA model has a 100% effect and it has a high significant difference over the other models with a level of confidence of 99% due to .000 is less than 5%.

VI. CONCLUSION

In this paper, a test function of the De Jong’s function 1 which is also called “The Sphere Model” is used to evaluate and compare results between the Simple Standard Genetic Algorithm (SGA) and a new approach for structured population of GA called the Human Community Based Genetic Algorithm (HCBGA) model.

It is concluded based on the analysis results that the Human Community Based Genetic Algorithm (HCBGA) model is better in terms of best finding as shown in our given results than the Simple Standard Genetic Algorithm (SGA) and other enhanced models (CGA and IGA).

The Average of the Human Community Based Genetic Algorithm (HCBGA) model is trying to converge towards the minimum despite its restricted constraints to the best values. In addition, the findings of the best solutions of best fit values are better in the Human Community Based Genetic Algorithm (HCBGA) model than in the Simple Standard Genetic Algorithm (SGA).

This model could be considered as a new enhanced model of the SGA. The HCBGA performed better and produced better results in terms of the average of the individuals' fitness as well as the best fit value of individuals in the population, which lead to global optima.

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