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ABSTRACT

In this paper, we present an Improved Genetic Algorithm (IGA) for solving the problem of sub-optimal convergence as well as over fitting/elitism of the parent selection method. This entails the development of a K-means clustering selection method where chromosomes are clustered into two non overlapping groups with the best group being selected for the reproduction process. This work is geared towards an on-going effort in developing a Vehicle Ad-hoc Network (VANET) route optimization algorithm for road anomaly monitoring. Towards the realization of this goal, the developed improved GA was tested on mathematical test functions as part of the preliminary performance evaluation of the algorithm as reported here. Specifically, it was observed that the IGA converges to a better average solution after 40 iterations when compared to that of the conventional GA with roulette wheel selection technique. Thus, suggesting an improved performance when applied for road anomaly route optimization in a VANET system.

Keywords: *Genetic Algorithm, Optimization, Route, Solution and Test Functions*

1 INTRODUCTION

Genetic Algorithm (GA) is a robust optimization algorithm founded on the basis of natural evolution and genetics (Aibinu, Bello-Salau, Akachukwu, & Nwohu, 2014; Aibinu, Salami, & Farooqi, 2011; Akachukwu, Aibinu, Nwohu, & Bello-Salau, 2014; Bello-Salau, Onwuka, & Aibinu, 2013). The mechanism used by GA in obtaining optimal solutions to a particular problem includes population initialization, objective function evaluation, chromosome selections for reproduction, crossover and mutation (Akachukwu, et al., 2014; Goh, Lim, & Rodrigues, 2003). It has found applications in many areas of engineering research among which includes urban route network bus transit design (Ngamchai & Lovell, 2003; Pattnaik, Mohan, & Tom, 1998), cloud database route scheduling (Latiff, Madni, & Abdullahi, 2016; Yan-hua, Lei, & Zhi, 2011), process route optimization(Bo, Hua, & Yu, 2006), power optimization (Gebraad, Teeuwisse, Wingerden, Fleming, Ruben, Marden, & Pao, 2016) etc. It searches large complex spaces in converging to better solutions (Aggarwal, Rawat, Kumar, & Upadhyay, 2015; Bello-Salau, et al., 2013). GA works on individual chromosomes representing a feasible solution to the problem (Ding, Xu, Su, & Zhu, 2010). However, the major challenge of this algorithm is its convergence to suboptimal solutions when used for route and test function optimization (Aibinu, Bello-Salau, Rahman, Nwohu, & Akachukwu, 2016; Andrade, Errico, Aquino, Assis, & Barbosa, 2008; Chudasama, Shah, & Panchal, 2011).

The selection method used in the GA process greatly determines the success of the algorithm. The search space is more exploited than explored when fitter chromosomes are selected for reproduction, while selecting less fit chromosomes will favor more of exploration. Hence, there is need to ensure a balance between the exploration and exploitation of the search space, in order to avoid convergence to sub-optimal solution. In this regard, we propose a new GA selection method based on a non-probabilistic approach referred to as K-means clustering for the GA process. This variant of GA selection method was incorporated into the GA process and called Improved Genetic Algorithm (IGA). The performance of the developed IGA optimization technique was evaluated by applying it on benchmark mathematical test functions optimization. Results obtained show better performance as compared to the GA with probabilistic (Roulette wheel) selection technique. Thus, suggesting that this IGA has the potential of giving an improved performance when used for route optimization. Hence, the contribution made in this paper is considered to be the development of an improved GA based optimization algorithm for possible applications for benchmark mathematical test functions evaluation. Furthermore, it is envisage that the developed IGA can be used for VANET route optimization in communicating sensed road anomalies among vehicles or to a database. It is note that VANET is a technology that uses moving cars as nodes in a network to create a mobile network.

The rest of the paper is organized as follows: section 2 presents a brief literature review, an overview of the proposed IGA is provided in section 3. Simulation results and discussion is presented in section 4, while section 5 concludes the paper.

2 BRIEF LITERATURE REVIEW

This section presents an overview of some achievements reported in literature that motivated this study. Basically, it is note that a major drawback associated with most GA approaches is the convergence to sub-optimal solution, when used for mathematical test functions or route optimization. As an example, a new GA with a hybrid of roulette wheel and rank selection technique was developed in (Kumar, 2012a). Similar, approach was also presented in (Jebari & Madiafi, 2013) that involved the hybridization of a selection method each from the elitist and probabilistic GA selection class. This developed variant of GA show better performance compared to that of GA with roulette wheel selection when used in evaluation of objective test functions. A new GA selection technique called High Low-Fit (HLF) was developed in (Ali & Elamin, 2006). This entails selecting individual chromosomes in the HLF for mating with another chromosome from the low fit group for reproduction. Similarly, a variant of adaptive GA for global mathematical test functions was also presented in (Mahmoodabadi & Nemati, 2016). Results shows improved performance when used for evaluating mathematical test functions compared to GA with roulette wheel selection method.

A new GA selection technique called 'alternis', where a restriction window is set in selecting weak individual for mating was proposed in (Anand, Afreen, & Yazdani, 2015). Also, the performance of GA roulette wheel and rank selection techniques were investigated alongside the developed GA alternis selection in optimizing an objective test functions. Simulation results shows that the proposed GA with alternis selection technique performs better when compared to that of GA with roulette wheel or rank selection. In addition, the proposed algorithm is flexible, ensures diversity in the population as well as avoids premature convergence of the GA process. However, the algorithm requires a lot of tuning and sometimes converges to suboptimal solution. Similarly, a new variant of GA called fluid genetic algorithm was proposed in (Jafari-Marandi & Smith, 2017). This proposed variant involves replacing the mutation process in conventional GA with a smart population diversity being introduced by the proposed FGA. Experimental results show a better performance in terms of accuracy, speed, and smarter convergences when compared to conventional GA performance. However, the proposed FGA is complex to implement and involves a lot of tunning.

Several GA selection methods viz elitism, roulette wheel and tournament were studied for solving route optimization problem in (Chudasama, et al., 2011; Noraini & Geraghty, 2011). Simulation results show improved performance when used for route optimization. Similarly, a polygamy based GA selection approach was proposed in (Aibinu, et al., 2016; Kumar, 2012b; Sharma & Tyagi, 2013). Results obtained shows better performance compared to that of GA roulette wheel selection technique. Though, a major drawback with these variants of GA selection approach is convergence to sub-optimal solution due to chromosome over fitting (Aibinu, et al., 2016; Jebari & Madiafi, 2013; Jafari-Marandi & Smith, 2017) . Furthermore, the performance of most of these techniques when applied for route optimization drops if it involves higher number of nodes/ cities (more than 10).

3 PROPOSED IMPROVED GENETIC ALGORITHM OPTIMIZATION TECHNIQUE

The proposed IGA is an improved variant of the conventional GA with probabilistic (roulette wheel) selection technique. Decision variables were encoded into binary strings (chromosomes) using equation (2).

$$2^{n_j-1} < \left(ub_j - lb_j\right) \times 10^p \leq 2^{n_j} - 1 \qquad (1)$$

where, n_j is the required number of chromosome bits, p is the required number of precision (decimal points), ub_j ,lb_j are the upper and lower boundary of the domain variable x_j respectively. In computing the required number of chromosome bits to the nearest whole number, equation (2) is used which is a representation of (1).

$$n_j = \frac{\log\left(ub_j - lb_j\right)}{\log 2} + 1 \qquad (2)$$

The variable x_j is decoded back from binary string bs_j to a real number (decimal) using equation (3).

$$x_j = lb_j + bs_j \times \frac{ub_j - lb_j}{2^{n_j} - 1} \qquad (3)$$

Ten random initial populations of individual chromosomes were generated; this serves as the initial solution in the search space. Each of the six benchmark mathematical test functions used for this study namely, Ackley 2, Bohachevsky 1, Bohachevsky 2, Bohachevsky 3 and Zettl Functions presented in Table 1 (Jamil & Yang, 2013) were evaluated. It is noted that the first three optimization test functions used for evaluating the performance of the developed IGA were unimodal functions which imply that they have one local optimal solution. While, other test functions used were multimodal with more than one local optimal solution. The choice of these two classes of test functions was to study and evaluate the performance of the proposed IGA on mathematical functions with different local optimal solution.

Table 1: Benchmark Mathematical Test Functions

Function Name	Mathematical Representations
Ackley 2 Function (Continuous, Differentiable, Non-Separable, Non-Scalable, Unimodal)	$f(x) = -200e^{-0.02\sqrt{x_1^2+x_2^2}}$ Subject to $-32 \le x_j \le 32$ The global minimum is located at origin $x = (0,0)$, $f(x) = -200$
Zettl Function (Continuous, Differentiable, Non-Separable, Non-Scalable, Unimodal)	$f(x) = (x_1^2 + x_2^2 - 2x_1)^2 + 0.25x_1$ Subject to $-5 \le x_j \le 10$ The global minimum is located at $x = (-0.0299, 0)$, $f(x) = -0.003791$
Zirilli or Aluffi-Pentini's Function (Continuous, Differentiable, Separable ,Non-Scalable, Unimodal)	$f(x) = 0.25x_1^4 - 0.5x_1^2 + 0.1x_1 + 0.5x_2^2$ Subject to $-10 \le x_j \le 10$ The global minimum is located at $x = (-1.0465, 0)$, $f(x) \approx -0.3523$
Bohachevsky 1 Function (Continuous, Differentiable, Separable, Non-Scalable, Multimodal)	$f(x) = x_1^2 + 2x_2^2 - 0.3\cos(3\pi x_1) - 0.4\cos(4\pi x_2) + 0.7$ Subject to $-100 \le x_j \le 100$ The global minimum is located at $x = f(0,0)$, $f(x) = 0$
Bohachevsky 2 Function (Continuous, Differentiable, Non-separable, Non-Scalable, Multimodal)	$f(x) = x_1^2 + 2x_2^2 - 0.3\cos(3\pi x_1) \times 0.4\cos(4\pi x_2) + 0.3$ Subject to $-100 \le x_j \le 100$ The global minimum is located at $x = f(0,0)$, $f(x) = 0$
Bohachevsky 3 Function (Continuous, Differentiable, Non-separable, Non-Scalable, Multimodal)	$f(x) = x_1^2 + 2x_2^2 - 0.3\cos(3\pi x_1 + 4\pi x_2) + 0.3$ Subject to $-100 \le x_j \le 100$ The global minimum is located at $x = f(0,0)$, $f(x) = 0$

The evaluated test functions were converted into fitness values. These values were then selected for mating using the proposed non-probabilistic K-means clustering algorithm that clusters the chromosomes into two non-overlapping clusters based on their distance from the centroid. This approach ensures that the Good Group Chromosome Cluster (GGCC) was selected in each generation. Thus, maintaining diversity in the population. Two non-overlapping clusters were created so as to ensure that each individual chromosome in the population belongs to either the GGCC or the Fair Group Chromosome Cluster (FGCC). This approach ensures high selection pressure thereby ensuring convergence to optimal solution. The chromosome in the GGCC with smaller distance is selected for the benchmark test functions minimization operation. The steps involved in the K-means algorithm implementation process is summarized in Table 2.

Table 2: Summary of the K-Means Clustering Process

1. *Two chromosome fitness centroid value C1 and C2 are randomly generated*
2. *Each individual fitness value is grouped into the appropriate cluster based on computed centroid distance.*
3. *Recomputed the two centroid position after assigning the fitness value of the chromosome to a cluster.*
4. *Re-iterate step 2 and 3 until centroid stability is attained and no change is observed in cluster of chromosome fitness value resulting in the GGCC and FGCC*
5. *The two centroid are compared, and the one with the higher numerical centroid value is assigned to the GGCC while the other cluster is assigned to the FGCC*
6. *Terminate the clustering process*

The K-means clustering reduces the size of the initial population of individuals because only one cluster

(GGCC) is selected from the two clusters. This chromosome population in the GGCC are increased back to the initial population size using a selection approach referred to as elitism. This approach entails randomly selecting certain percentage of the fitter individual chromosomes to increase the population size of the GGCC back. New offspring's were produced during reproduction using two-point chromosome inversion. In ensuring diversity in the population, one-point chromosome inversion was used and convergence to global solution was ensured by the introduction of the elitism approach. New population were formed after the entire genetic process and the generational counter increased by 1. This developed IGA process continues until the convergence criterion is met or the predefined number of generations has elapsed. The flowchart in Figure 1 summarizes the entire developed IGA with elitism process.

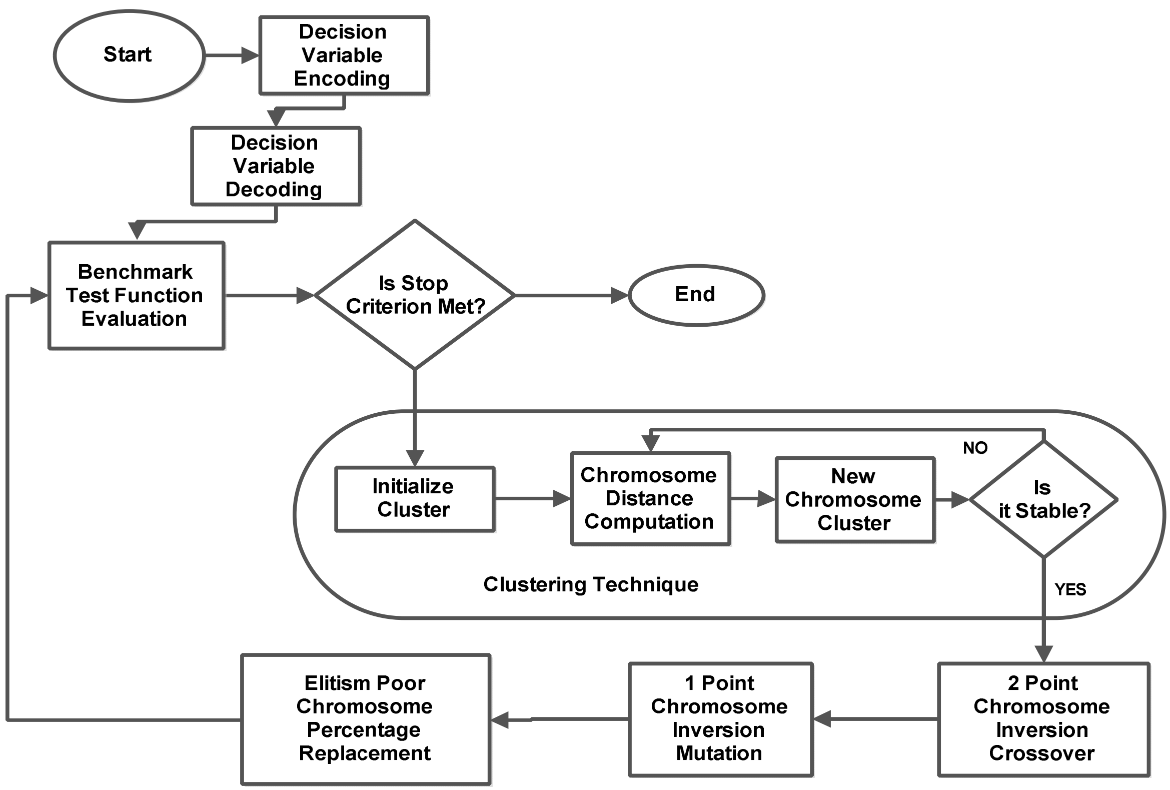

Figure 1: Flowchart of the Developed IGA with Elitism Algorithm

4 SIMULATION RESULTS AND DISCUSSION

We present here our preliminary evaluation of the performance of the developed IGA when applied for the optimization of benchmark mathematical test functions presented in Table 1. This was carried out towards examining the potential of the developed IGA for possible application to VANET route optimization for road anomaly monitoring. The simulation parameters settings for the conventional GA with probabilistic selection technique and the developed IGA are presented in Table 3 and 4 respectively. These parameters value were obtained after tuning each of the GA and IGA algorithms to give optimal performance. The average solutions obtained after 40 iterations in evaluating each of the benchmark test functions using the developed IGA and conventional GA with probabilistic selection technique is presented in Table 5. Observe generally, that the average estimated solutions obtained by the developed IGA is more closer to the expected solutions of the benchmark test functions reported in (Jamil & Yang, 2013) and used in this study compared to that of the average estimated solutions by GA (see Table 5). A possible reason for the improved performance of the proposed IGA can be attributed to the high selection pressure introduced by the GGCC that ensure balancing the exploration and exploitation of the search space, thereby leading to convergence to optimal solution.

Table 3: Simulation Parameter Settings for GA

Parameters	GA
Population Size	60
Number of Generation	250
Crossover Probability	0.5
Mutation Probability	0.2

Table 4: Simulation Parameter Settings for Proposed IGA

Parameters	IGA
Population Size	60
Number of Generation	250
Crossover Probability	0.4
Mutation Probability	0.15
Selection Probability	0.3

It is seen for the Ackley 2 test function that GA converges to a solution of -199.935, which is approximately equal to that of the expected solution of -200 except for the variable x1 and x2 where the solution is obtained as 0.0069, -0.0079 respectively for GA, and 0, 0 for the expected solution. However, the developed IGA converges to the same solution as the expected solution (see Table 5). Similarly, for the Bohachevsky 1 and Bohachevsky 3 test functions, the developed IGA converges to the same solutions of 0 with 0, 0 for the variable x1 and x2 respectively with that of the expected solution. Though, GA converges to a sub-optimal solution of -0.0020 x1 and 0 x2 with 2.9985 f(x) for Bohachevsky 1, -1.8900 x1 and 0.0967 x2 with 5.9833 f(x) for Bohachevsky 3 as seen in Table 5. This convergence to suboptimal solution by GA can be attributed to the use of the probabilistic selection approach (roulette wheel) used in the GA process.

In addition, it is observed for the Bohachevsky 2, Zettl and Zirilli function that the average solution obtained by the IGA are more approximately closer to that of the expected solution than the GA. The closeness of this solutions attained by the IGA when applied to the evaluation of the test functions (see Table 5) can be attributed to the high selection pressure and diversity introduced in the population by K-means elitism selection process in the IGA.

Table 5: Performance Evaluation of the Developed IGA

Functions	Expected Solution			Av Estimated Solution (GA)			AV Estimated Solution (IGA)		
	x1	x2	y	x1	x2	y	x1	x2	y
Ackley 2 function	0	0	-200	0.0069	-0.0079	-199.9359	0	0	-200.0000
Bohachevsky 1 Function	0	0	0	-0.0020	0	2.9985	0	0	0.0000
Bohachevsky 2 Function	0	0	0	-0.0020	0	2.9985	0	0	0.1800
Bohachevsky 3 Function	0	0	0	-1.8900	0.0967	5.9833	0	0	0.0000
Zettl Function	-0.0299	0	−0.003791	-0.0117	0.0390	-0.0088	-0.0243	0.0012	-0.0028
Zirilli Function	−1.0465	0	−0.3523	-1.0154	0.0114	-0.2958	-1.0443	0.0020	-0.3446

5 CONCLUSION

An Improved Genetic Algorithm (IGA) with a non-probabilistic K-means selection approach has been developed to overcome the challenge of sub-optimal convergence of the GA, when used for optimization. The performance of the developed IGA was evaluated by applying it to optimize standard benchmark mathematical test functions. Simulation results show that the developed IGA performs better in terms of convergence to an average better solution after 40 iterations, compared to that of GA. Thus, suggesting the potential of the IGA for VANET route optimization, that serves as the motivation for the study. Future research work will consider the tuning and application of the developed IGA for efficient VANET route optimization in communicating road anomaly information.

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