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A novel Clustering based Genetic Algorithm for route optimization

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ABSTRACT

Genetic Algorithm (GA), a random universal evolutionary search technique that imitates the principle of biological evolution has been applied in solving various problems in different fields of human endeavor. Despite its strength and wide range of applications, optimal solution may not be feasible in situations where reproduction processes which involve chromosomes selection for mating and regeneration are not properly done. In addition, difficulty is often encountered when there are significant differences in the fitness values of chromosomes while using probabilistic based selection approach.

In this work, clustering based GA with polygamy and dynamic population control mechanism have been proposed. Fitness value obtained from chromosomes in each generation were clustered into two non-overlapping clusters. The surviving chromosomes in the selected cluster were subjected to polygamy crossover mating process while the population of the offsprings which would form the next generation were subjected to dynamic population control mechanisms. The process was repeated until convergence to global solution was achieved or number of generation elapsed. The proposed algorithm has been applied to route optimization problem. Results obtained showed that the proposed algorithm outperforms some of the existing techniques. Furthermore, the proposed algorithm converged to global solution within few iterations (generations) thus favoring its acceptability for online-realtime applications. It was also observed that the introduction of clustering based selection algorithm guaranteed the selection of cluster with the optimal solution in every generation. In addition, the introduction of dynamic population control with polygamy selection processes enabled fast convergence to optimal solution and diversity in the population respectively.

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1. Introduction

Genetic Algorithm (GA) is a random universal search technique that imitates the principle of natural biological evolution [1–8]. John Holland pioneered the examination of the dynamics of GAs and the formulation of initial associated theories, thus leading to innovation and growth of GAs in the 1960s [7–9]. In accordance with Darwin's evolution process shown in Fig. 1, GA operates on the principle of survival of the fittest in a population of possible solutions to generate an approximate better or best solution. At each generation, a new set of solution is generated by selecting likely solutions (individuals) with respect to its fitness value within the problem area [7–9]. This is achieved by the application of

reproduction operators borrowed from natural genetics. The result of this process is the evolution of populations of offspring that are more adapted to their environment than their parents and are better off in terms of performance [10–12,15]. A probabilistic rule is used by GA to guide its search and selection process thereby reducing the risk of convergence to local solution. In addition, this allows for exploration of most promising areas in search space. This is achieved by considering numerous points in the search space simultaneously, thus, favoring the mating of the fitter individuals [15]. Thus, making GA to be an effective and robust search algorithm that allows the quick location of high quality solution areas in a large and complex search space [15,16,20].

GA stands out among other search algorithms and distinguishes itself by working on a population of individuals, each representing a possible solution to a problem. The fitness function evaluation, population solution encoding and decoding, selection, reproduction and convergence are the basic principles of GA [7,8,20,16].

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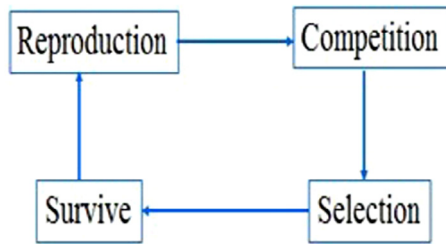


Fig. 1. Darwin's Evolution principle.

Other advantages of GA over other traditional optimization techniques include:

1. The ease of understanding of concepts; robust for usage in noisy environments [7];
2. Ease of running in parallel;
3. Capability of altering or changing the fitness function from iteration to iteration hence facilitating the incorporation of new data if available in the model;
4. Ability to support multi-objective optimization. Furthermore, GA has been shown in various works to sometimes lead to optimal and global solutions [1,2,7,8].

GA has been widely applied to various areas of human endeavor notable among these are: Electronic voltage oscillator designs [1,2], Digital Signal Processing [10,12,13], Welding [14], Communications [17,18], Agriculture [19], Power Generation [20], Finance [21], Robotics [22], Immune System [23], Examination Time Table [24,25], Digital Image Processing [26–28], Time Series Analysis [29], Environmental Planning [30,31], Prediction [32,9], Machining [33,34], Functions optimization [40,41], just to mention but a few. Detailed review of application of GA in power optimization is contained in [11].

The rest of this paper is organized as follows: Review of GA selection process is discussed in Section 2; Mathematical derivation of the proposed methodology is presented in Section 3 while performance analysis and discussions are contained in Section 4. Conclusions and recommendations are presented in the last section of this paper.

2. Review of Genetic Algorithm selection process

In this section, review of GA reproduction process is presented with emphasis on the selection mechanism. Performance comparison table showing the shortcomings and benefits of some of the existing GA Selection processes is also presented in this section. One of the critical processes in GA reproduction process is the chromosome selection approach. It has been argued that the process determines the success or otherwise of the algorithm since it entails determining and choosing which solutions are good and desirable to be preserved and for reproduction purposes. It ensures that only the fittest survives in each generation while the unfit are discarded within a constant population [3–7]. Numerous GA selection methods exists in literature among which are:

1. Tournament selection
2. Roulette wheel selection
3. Rank selection
4. Steady state selection

- **Roulette wheel selection (RWS) method:** Is one of the most popular GA selection methods and upon which some other selection techniques are based [7–9]. Parents chromosomes are chosen based on their fitness values. In implementing this, the

roulette-wheel circumference is marked for each string proportionate to the string's fitness. The roulette-wheel is spun n times and choosing an instance of the string selected by the roulette-wheel pointer each time. The better chromosomes stand a greater chance to be selected since the circumference of the wheel is marked based on a string proportionate to the strings fitness functions. However difficulty is encountered when there is significant difference in the fitness values [7,3–5]. In addition, there is no absolute guarantee that good individuals will be selected though selection is based on fitness value [3].

- **Rank selection methods:** The Rank selection technique was developed to cater for the problem encountered in the Roulette-wheel selection method. In RWS, chromosomes with low fitness values have minimal chances of being selected and large difference in fitness value leads to situation where only the fittest chromosome may be selected. Hence, the ranking selection method was introduced to solve these problems [3,4]. In this approach, individual chromosomes are ranked based on their fitness value and probabilistic approach is then introduced for selection. This ranking approach introduce slow convergence speed and sometimes converge to sub-optimal solution as less fit chromosomes may be preserved from one generation to another.
- **Tournament selection Methods:** In this approach, different tournaments are played among few individuals who are randomly selected from the population. The individual that emerges as the winner of each tournament is chosen for next generation. The tournament size can be changed so as to ease the adjustment of the selection pressure. However, chances abound for selection of weak individuals when the tournament size is large [3,5,4].
- **Steady state selection method:** Steady state selection method involves creation of new offspring by few good chromosomes in each generation. Some bad chromosomes are removed and new offsprings are used to replace the bad ones. Hence, the rest of the population migrates to the next generation without going through selection process.

Summary of the performance evaluation showing strength and weakness of the widely known GA selection processes are presented in Table 1.

3. Development of Clustering based Genetic Algorithm with polygamy reproduction and population control technique

In overcoming the aforementioned shortcomings in the existing GA reproduction processes presented in Table 1, this work presents Clustering based Genetic Algorithm (CGA) with polygamy selection and dynamic population control technique.

The main contribution of this paper is in the development of the proposed technique which overcomes the short comings associated with roulette wheel, rank and elitism approach in GA selection process by minimizing the distance between centroid and individual chromosomes in improving the search space instead of the use of probabilistic approach associated with some of the known selection techniques. The introduction of polygamy mating system, dynamic population control and birth control mechanism introduces greater diversity in the population thus offering better solution with fast convergence speed.

Detailed discussions of each of the steps in the proposed CGA are shown in methodology flow diagram in Fig. 2.

1. Parameters settings

The proposed CGA technique mimics the natural evolution process that experiences increase or decrease in population over

Table 1

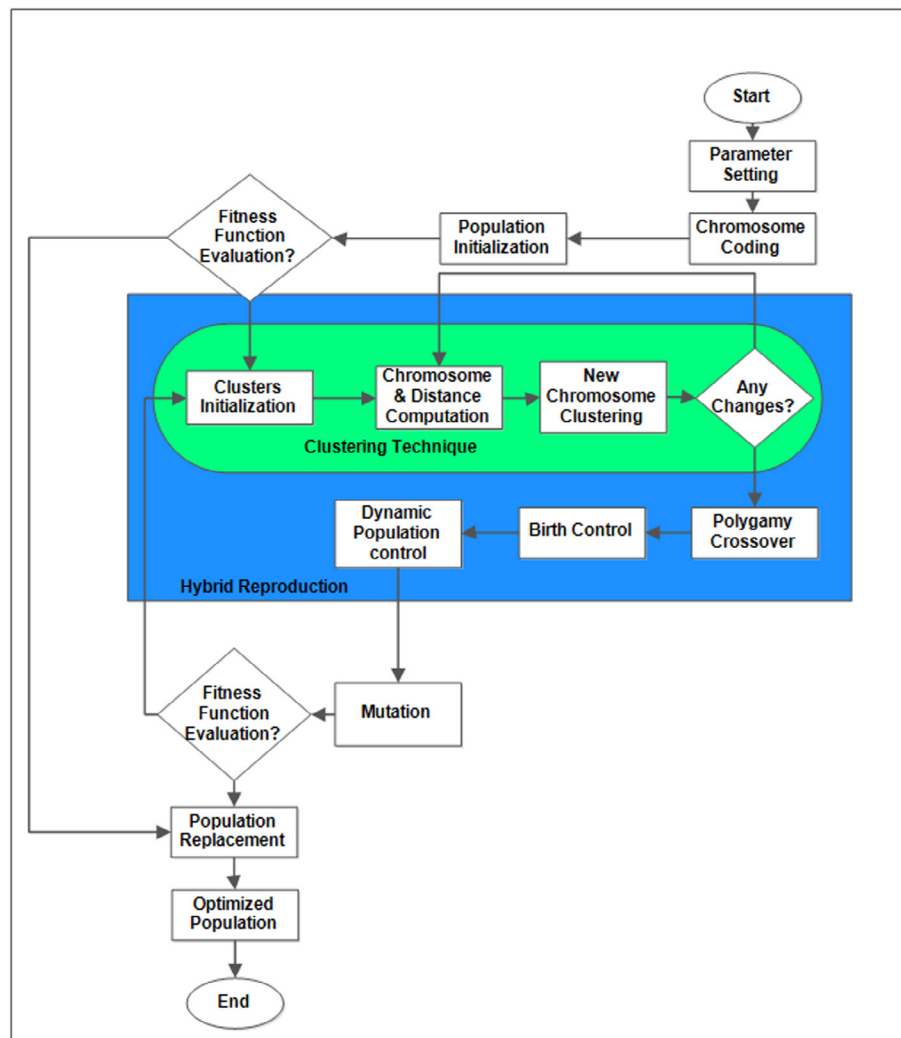
Comparison Table for GA Selection process.

No	Types	Strength	Weakness
1	Roulette wheel selection	There is a high probability for the better chromosome to be chosen; Simple and Easier to implement	Difficulty is encountered when there is significant difference in the fitness values; No guarantee in selecting fittest chromosomes; Probabilistic in nature; High stochastic variability.
2	Rank selection	All the chromosomes have a fair chance of being selected; High selection pressure; Better performance compared to RWS	Can lead to slower convergence, because the best chromosomes do not differ so much from other ones; Probabilistic in nature
3	Tournament selection	Tournament size can be changed so as to ease the adjustment of the selection pressure; preserve diversity; no susceptibility of marginalizing weak chromosomes; suitable for cases without objective function	There is a chance for weak individuals to be elected if the tournament size is large; Probabilistic in nature thus subject to stochastic effect; Need preference ordering; no guarantee that each chromosome will appear in a given cycle
4	Steady state selection	It always lead to the production new offsprings by few good chromosomes	It requires a large number of iterations

generations. In addition, it is devoid of constant population associated with the existing and widely known GA techniques and requires setting of only four parameters as compared to setting of six different parameters in the conventional GA techniques. The required parameters are:

- (a) Initial population size (N)
- (b) Maximum population growth rate (r)
- (c) Mutation rate (α)
- (c) Number of generations (Ω)

Unlike most of the existing variants of GA, this algorithm can start with low initial population size (N). The maximum population growth rate (r) allows for dynamic increase or decrease in population size from generation to generation till the maximum generation (Ω) is reached, hence evolving like a normal human evolution process. The population growth rate is achieved using a random number generator to generate the growth rate from generation to generation, and its value varies from $-r$ to $+r$.

**Fig. 2.** Proposed CGA with polygamy and population control mechanism.

Justification for increase or decrease in population size hinge on available data on human population as reported in [35]. The data shows that evolution from one generation to the other, involves population variation, hence no country experienced static population growth over generations.

2. Initialization, genes coding and decoding

The initial population size, N , of candidate solutions (chromosomes) are generated based on the problem definition. A chromosome being an abstract representation of candidate solutions are products of concatenation of the variables (genes). For route optimization related problems, the use of string may be applicable for gene or chromosomes representation while for other optimization problems the use of binary chromosomes may be appropriate. Uniform distribution approaches have been adopted for initial chromosomes generation. In MATLAB, this can be achieved using `rand()` in-built function.

The use of binary chromosome representation approach involves encoding and decoding operations. Likely solution of the variables (genes) are converted to binary form. A three stage encoding operation has been adopted in this work.

(a) Genes/chromosomes encoding

The first stage involves determination of appropriate number of bits required for optimal encoding while the second stage involves determination of bit step size for the encoding operation. The third stage involves conversion from integer to binary strings. Explanation and mathematical notation for the three stages are presented herewith.

- i. *Determination of number of bits*: The first stage in the binary encoding scheme is the determination of required number of bits based on expected resolution for each gene. If the domain of the variables (genes) x_i are $[a_i, b_i]$ and the required precision are p_i decimal points, the required number of bits m_i for encoding the solution value are calculated using

$$2^{m_i-1} < (b_i - a_i) \times 10^{p_i} < 2^{m_i} - 1 \quad (1)$$

- ii. *Step size and location determination*: Once the required number of bits, m_i , have been determined for the genes using (1), the second stage involve the determination of the appropriate step size. The step size Δ_i is obtained using

$$\Delta_i = \frac{b_i - a_i}{2^{m_i} - 1} \quad (2)$$

Upon determination of appropriate Δ_i using (2), the appropriate integer equivalent or location determination (L_i) is computed using

$$L_i = \left\lfloor \frac{x_i - a_i}{\Delta_i} \right\rfloor \quad (3)$$

- iii. *Integer location to binary conversion*: The last stage involves conversion from Integer location L_i to binary using m_i number of bits. The appropriate function used for achieving this in MATLAB is `dec2bin` (L_i, m_i), thus

$$bs = \text{dec2bin}(L_i, m_i) \quad (4)$$

The resulting binary string bs representing the gene can be represented as

$$bs_i = d_{im}d_{im-1}d_{im-2} \dots d_{i2}d_{i1} \quad (5)$$

where d_{im} are binary integers.

(b) Genes/chromosomes decoding

The corresponding decoding operation involves mapping from binary string to real number. The decoding of variable x_i is given as

$$x_i = a_i + \text{bin2dec}(bs_i) \times \Delta_i \quad (6)$$

where bs_i denotes the encoded binary chromosomes string to be decoded into decimal within the domain $[a_i, b_i]$, Δ_i is governed by (2) and `bin2dec` is a binary to decimal converter given as

$$\text{bin2dec}(bs_i) = \sum_{k=1}^{m_i} d_{ik} \times 2^i \quad (7)$$

3. Fitness function evaluation

The desirability of a solution is quantified by a fitness function, which is closely related to the objective of the optimization process. The fitness level is used in evaluating the resulting chromosomes, thus the values obtained from evaluation of the chromosomes using the fitness function characterized the suitability performance of candidate solutions [16]. Evaluation of the fitness of the chromosomes in the population involve computations governed by the objective function subject to available constraints. The objective function is usually expressed as a function of the variables or genes encoded in the chromosomes. Most optimization related problems involve either minimization or maximization of the objective function, thus reason for using two centroids clustering approach (i.e $K = 2$). In this work, minimization has been assigned cluster number, $K = 1$ while maximization is assigned cluster number $K = 2$ which will be subsequently used in the chromosomes selection stage.

4. Reproduction operations

A three-stage approach involving clustering, polygamy mating and population control process has been proposed in this work. The clustering approach adopted is similar to K-Means technique and is a non-probabilistic approach that ensures selection of the fittest chromosomes for reproduction purposes in each generation and enhance diversity in the population. The clustering approach introduces high selection pressure in the reproduction process thus increasing the average generation fitness value and increasing speed of convergence without susceptibility of domination by particular chromosome as cluster of fittest chromosomes are selected. Polygamy mating ensures that the fittest chromosomes emanating from the selection enjoys polygamy reproduction process so as to transfer some of its characteristics to the offsprings. The last stage ensures that the population in that generation does not exceed the accepted population growth rate by using birth control or population control technique. Detailed discussion of each stage is presented subsequently.

(a) GA clustering selection technique

The choice of two centroids clustering ensures that each chromosome in the population belongs to either the Fitter Chromosomes Cluster (FCC) or Less Fit Chromosomes Cluster (LFCC) in every population. This binary approach of chromosomes selections for mating employs an iterative algorithm that minimizes the sum of distances from every chromosome to its cluster centroid, over the two clusters. Chromosomes are moved between clusters until the sum can no longer be reduced further. This results to a set of clusters that are as dense and well-spaced as possible for the solution. The chromosomes in the cluster with the smaller distance is selected for minimization operation while chromosomes in the cluster with the bigger distance are selected in a typical maximization operation.

Mathematically, let the total point scatter T for a set of N chromosomes in the i th generation given as

$$T = \frac{1}{2} \sum_{i=1}^N \sum_{j=1}^N d(x_i, x_j) \quad (8)$$

where $d(x_i, x_j)$ is the distance between 2 chromosomes, hence (8) can be written as

$$T = \frac{1}{2} \sum_{k=1}^K \sum_{C_i=k} \left(\sum_{C_j=k} d(x_i, x_j) + \sum_{C_j \neq k} d(x_i, x_j) \right) \quad (9)$$

Therefore, (9) can be generalized as

$$T = W(C) + B(C) \quad (10)$$

where $W(C)$ is within class scattered distance, $B(C)$ is between cluster distance and C_i denotes cluster number for the i^{th} observation [39].

If $d(x_i, x_j)$ is considered as the Euclidean distance, then

$$W(C) = \sum_{k=1}^K N_k \sum_{C_i=k} \|x_i - m_k\|^2 \quad (11)$$

The implementation for the CGA selection can be summarized with the following steps:

- i. *Step-1:* Randomly generate 2 initial chromosomes fitness value centroids, i.e initialize C_1, C_2 .
 - ii. *Step-2:* Assign each fitness value of the chromosome to the group that has the closer centroid using 11.
 - iii. *Step-3:* When the fitness value of the chromosomes have been assigned, recalculate the position of the 2-centroids.
 - iv. *Step-4:* Repeat step 2 and 3 until the centroids no longer move and chromosomes fitness values does not change cluster. This produces a separation of chromosomes fitness values into groups, namely FCC and LFCC.
 - v. *Step-5:* Compare the two centroids.
 - vi. *Step-6:* If the objective function is maximization based, then the class centroid with the higher numerical value is assigned to FCC while the other cluster is assigned to LFCC. Similarly, if the objective function is minimization based, the class centroid with the lower value is assigned to FCC while the other is assigned to LFCC.
 - vii. *Step-7:* End
- (b) Polygamy Mating Process: The clustering selection technique reduces the population of the fitter chromosomes from N to N_1 as a result of the selection operation. The resulting population N_1 is usually less than or equal to the original population, i.e $N_1 \leq N$. In ensuring that a sizeable number of chromosomes are available for evaluation in the subsequent generation, a polygamy selection process for mating has been introduced in this work. Selection for mating among the cluster of fitter chromosomes and the resulting new population N'_1 is governed by combinational operation defined as

$$N'_1 = \frac{N_1}{2!(N_1 - 2)!} \quad (12)$$

where N_1 is the population of the chromosomes in the FCC and N'_1 is the new population produced as a result of polygamy operation. Crossover operations such as 1-point crossover, 2-points crossover, partially mapped Crossover etc can be performed on the resulting combinational pairing of chromosomes to obtain the new generation of feasible solutions.

- (c) Population Control Process: Application of (12) usually leads to the multiplying effect on the resulting population of chromosomes produced after crossover operation. Therefore, further simplification of (12) reveals the relationship between N_1 and N'_1 as

$$N'_1 = N_1 \times \frac{N_1 - 1}{2} \quad (13)$$

Mathematically, high value of N_1 will ultimately lead to over-population with attendant increase in algorithm computation time, hence, population control inline with natural evolution has been suggested. Two types of population control have been proposed in this work, these are Birth Control (BC) and Population Growth Rate Control (PGRC).

i. Birth Control (BC)

In BC approach, two techniques have been proposed namely, single offspring and double offspring. In a Single Offspring BC (SOBC), two parents are only allowed to produce a single offspring after crossover operation whereas in the double offspring BC (DOBC) approach, two parents are allowed to produce two offsprings from the crossover operations.

ii. Population Growth Rate Control (PGRC)

Despite the introduction of BC, sometimes the resulting population of offsprings is still higher than the expected or estimated population hence reduction in population is achieved either by randomly selecting N'_1 from $\frac{N'_1}{2}$ children i.e chromosomes, or by selecting the best N'_1 children based on result obtained from fitness value evaluation. In this paper, the latter type of population control is called Population Growth Rate Control with Evaluation (PGRC-E) while the former is referred to Population Growth Rate Control Using Random Selection (PGRC-R). The new population can thus be computed as

$$N'_1 = r \times N'_1 \quad (14)$$

where r is the population growth rate.

5. Mutation: Mutation locally but arbitrarily alters the offspring. The genes of the offsprings are randomly modified to allow for variation in the population. Mutation usually involves one or more changes being made to an individual's trait or traits. In a binary chromosome representation approach, mutation may involve bit reversal while in string chromosomes representation this may involve re-ordering of the string. Furthermore, mutation alters one or more genes with a probability equal to the mutation rate, (α). As an example, when given a mutation rate, (α) = 0.03. The expectation is that 3% of the genes in the population will mutate, thus if there are 100 genes, 3 mutations per generation is expected.
6. Replacement: The original parental population is replaced by the created offspring population (solution). Thus the mutated genes or chromosomes are now the new population for the next generation.
7. Repeat: Reiterate steps 2 – 7 pending convergence or a predefined ending condition is met.

4. Results and discussion

The developed algorithm has been applied to Robot route navigation problem. The first problem presented in subSection 4.1 has been specifically selected in order to evaluate the applicability of the proposed algorithm in solving engineering related problems. Emphasis has been placed on results obtained from Robot route planning, due to numerous applications associated with route optimization and existence of abundance literature and work in this area. It is important to note that the simulation time or time of completion (in seconds) depends on the properties of the computer used, hence in this case a HP Laptop Computer running on Windows 8, Processor Intel(R) Core(TM) i7-3630QM CPU @ 2.40 GHz 2.4 GHz, 8.00 GB RAM, 64-bit Operating System, x64-based processor was used.

4.1. Robot Route Navigation Planning

The robot route navigation problem is a variant of the popular Traveling Salesman Problem (TSP). The TSP problem and its variants have found favorable mentioning in the literature [36–38]. Similar to some of the aforementioned work, the proposed algorithms have been applied to solving Robot movement and route pattern. The challenge involves determining the shortest route to 5 different locations shown in Fig. 3. The robot is to travel between 5 locations not far apart along the earth surface. The order in which it travels is of no importance, however it must visit each location only once during its trip and finishes the trip at the starting location. The distance between any two points are symmetrical and are connected by visible line of sight. The problem is to determine which route gives minimal cost distance (i.e route distance). The locations as shown in Fig. 3 are designated as D_1, D_2, D_3, D_4 , and D_5 , a typical optimal (Best) route path is as shown in Fig. 4b while a typical non-optimal (Worst) route is as shown in Fig. 4c. In the challenge, D_0 is the origin where the robot docked after the challenge while Fig. 4b shows a typical robot optimal path in the Maze. It is assumed that the distance between any two points is symmetrical and are on a flat plane considering the shortness of the distances relative to the earth's circumference. It is also assumed that there are no changes in the elevation value of the points in consideration. Hence, the distance between point D_k and point, D_n can be computed using

$$S_{kn} = \sqrt{(x_k - x_n)^2 + (y_k - y_n)^2} \quad (15)$$

where S_{kn} is the distance between point D_k with coordinate (x_k, y_k) and point D_n with coordinates (x_n, y_n) . The total symmetrical distance matrix computed using 15 is as shown in Table 2.

The definition of terms used in this paper are as contained in Table 3.

1. Developed algorithm performance analysis

The effects of each of the newly introduced parameters will be evaluated in this subsection. Furthermore, optimal values or range for these parameters will also be suggested as applicable to the robot route optimization. Necessary inferences and conclusions will be drawn based on the results obtained. Parameters settings used to obtain the results will firstly be stated in a table while average results obtained from 20 iterations will

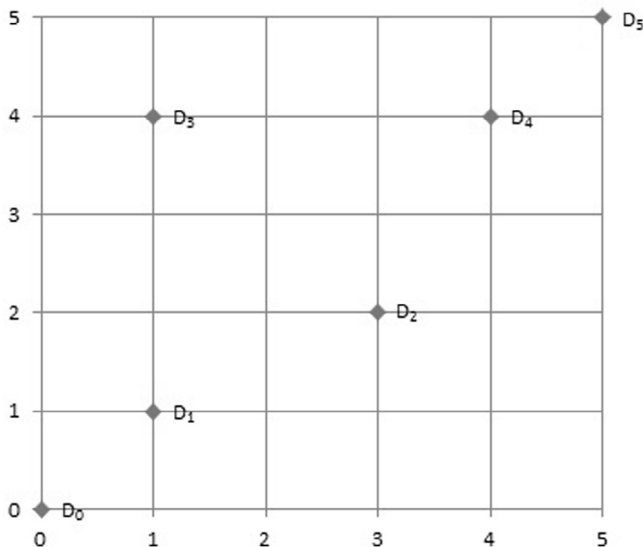


Fig. 3. Robot route optimization (a) robot route maze.

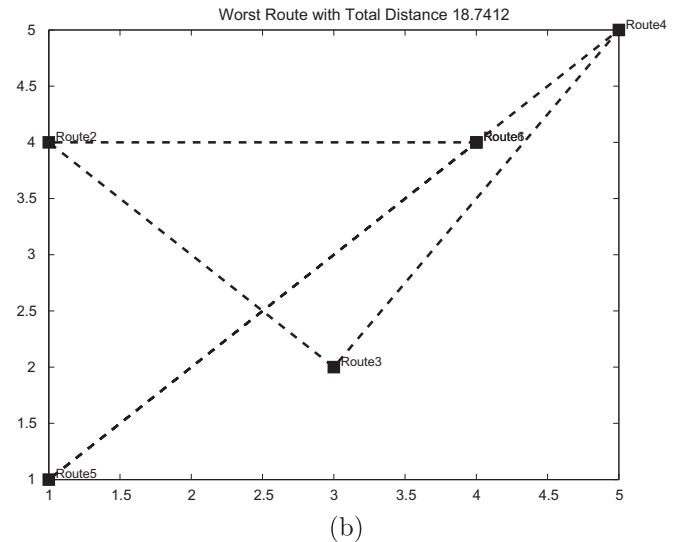
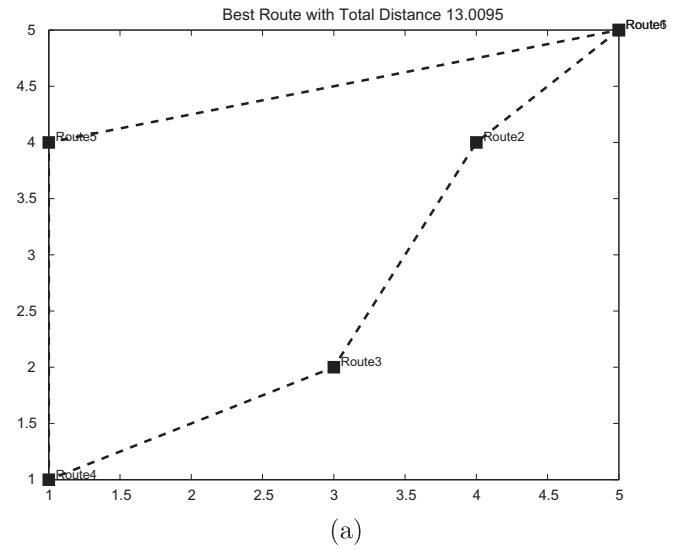


Fig. 4. Robot route optimization (a) robot route maze (b) typical optimal route robot movement (c) typical non-optimal route robot movement.

Table 2

Robot distance matrix.

	D_1	D_2	D_3	D_4	D_5
D_1	0	2.2361	3.0000	4.2426	5.6569
D_2	2.2361	0	2.2361	2.2361	3.6056
D_3	3.0000	2.2361	0	3.0000	4.1231
D_4	4.2426	2.2361	3.0000	0	1.4142
D_5	5.6569	3.6056	4.1231	1.4142	0

be reported using either figures or tables. Little or no mention was made about the standard deviation and variance as the values obtained during each run were almost similar.

(a) Effect of mutation rate

In evaluating the performance of the proposed algorithm, the effects of mutation rate at constant MPGR on the two types of birth control (i.e SOBC and DOBC) and population control (i.e. PGRC-E and PGRC-R) have been evaluated in this subsection. The parameter setting used for the algorithm is stated in Table 4 while results obtained are shown in Table 5.

i. Observation:

As observed from Table 5, high mutation rate has little or no effect on SOBC/PGRC-R technique, as there is little or no improvement on both the BR and APR values obtained. The reason for this may be primarily due to the introduction of polygamy mating technique which naturally introduced diversity into the population. Hence, mutating the chromosomes does not really give additional new chromosomes to the population. Similar trend was observed from results obtained using SOBC/PGRC-E technique though the APR values obtained for this technique consistently shows better performance as compared to the SOBC/PGRC-R technique. Furthermore, the general observation in both the DOBC/PGRC-R and DOBC/PGRC-E techniques, increase in mutation rate partially shows corresponding increase in the APR value away from the BR and showing more divergent from the BR. Hence, lower value of MR rate shows better

Table 3

Definition of terms

Acronyms	Full meaning
BR	Best Route
WR	Worst Route
APR	Average Population Route
SOBC	Single Off-Spring Birth Control
DOBC	Double Off-Spring Birth Control
PGRC-R	Population Growth Rate Control with Random Selection
PGRC-E	Population Growth Rate Control with Evaluation Selection
FPS	Final Population Size
TOC	Time of Completion
MPGR	Maximum Population Growth Rate
Gen	Generation

Table 4

Parameters setting for Robot Route Path Planning.

Parameters	Values
Mutation Rate (MR)	$0.01 \leq \alpha \leq 0.25$
Max. Population Growth Rate (MPGR)	$r = 0.25$
Initial Population at start	$N = 60$
Max number of Generations	$\Omega = 10$

Table 5

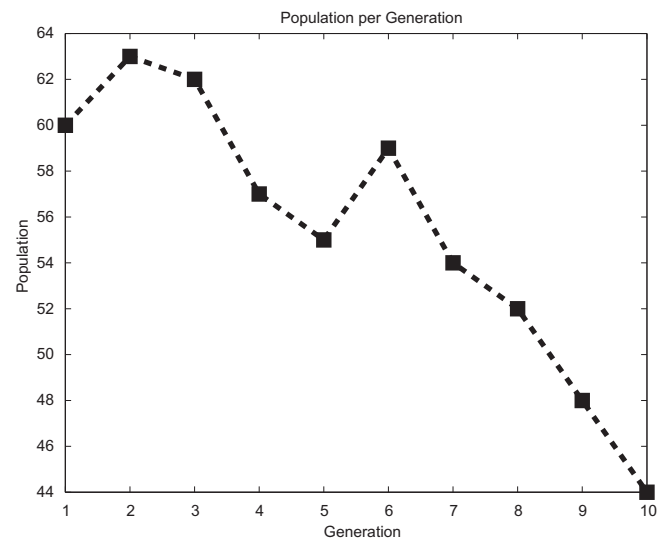
Results from effect of mutation rate.

Mutation Rate	SOBC/PGRC-R		SOBC/PGRC-E		DOBC/PGRC-R		DOBC/PGRC-E	
	BR	APR	BR	APR	BR	APR	BR	APR
0.0100	14.2007	14.6800	13.0095	13.9248	13.0095	13.3012	13.0095	13.3208
0.0200	14.0518	14.8744	13.0095	13.7116	13.0095	13.3306	13.0095	13.3102
0.0300	13.0588	13.6698	13.0341	13.6749	13.0095	13.3042	13.0095	13.3415
0.0400	13.0341	13.7239	13.0341	13.7483	13.0095	13.4295	13.0095	13.3494
0.0500	13.1081	13.8154	13.0095	13.7051	13.0095	13.3731	13.0095	13.3541
0.0600	13.1081	13.8319	13.0834	13.8760	13.0095	13.3605	13.0095	13.3558
0.0700	13.2077	14.4588	13.0095	13.6356	13.0095	13.3724	13.0095	13.3895
0.0800	13.0834	14.8314	13.0095	13.6707	13.0095	13.4336	13.0095	13.4858
0.0900	13.1573	13.9398	13.0095	13.7327	13.0095	13.4141	13.0095	13.4350
0.1000	13.0095	13.8719	13.0095	14.3374	13.0095	13.5275	13.0095	13.4590
0.1100	13.0095	13.7108	13.0095	13.8755	13.0095	13.4125	13.0095	13.5482
0.1200	13.2580	14.6512	13.0095	13.9912	13.0095	13.5530	13.0095	13.5097
0.1300	13.0095	13.7758	13.0095	13.6599	13.0095	13.5745	13.0095	13.5290
0.1400	13.0588	13.9489	13.0095	13.9435	13.0095	13.5550	13.0095	13.5519
0.1500	13.0095	14.5788	13.0095	14.1506	13.0095	13.4222	13.0095	13.5253
0.1600	13.0341	14.4746	13.0095	14.2322	13.0095	13.6674	13.0095	13.5299
0.1700	13.0095	13.8322	13.0095	13.9233	13.0095	13.5760	13.0095	13.6316
0.1800	13.0588	14.2029	13.0588	13.9563	13.0095	13.5387	13.0095	13.5440
0.1900	13.0834	14.4514	13.0095	14.2288	13.0095	13.6367	13.0095	13.6201
0.2000	13.0095	14.2659	13.0588	14.8094	13.0095	13.7182	13.0095	13.6566

Table 6

Parameters setting for evaluating MPGR.

Parameters	Values
Mutation Rate (MR)	0.05
Maximum Population Growth Rate (MPGR)	$0.01 \leq r \leq 0.25$
Initial Population at Start	$N = 60$
Max number of Generation	$\Omega = 10$
GA Type	DOBC/PGRC-E

**Fig. 5.** Typical population per generation.**Table 7**

Results obtained from evaluating MPGR.

Generation	BR	WR	APR	Population
1	13.0095	18.7412	15.6668	60
2	13.0095	13.0095	13.0095	63
3	13.0095	13.0095	13.0095	62
4	13.0095	13.0095	13.0095	57
5	13.0095	13.0095	13.0095	55
6	13.0095	13.0095	13.0095	59
7	13.0095	13.0095	13.0095	54
8	13.0095	13.0095	13.0095	52
9	13.0095	13.0095	13.0095	48
10	13.0095	13.0095	13.0095	44

Table 8

Effect of population: constant population against dynamic population for SOBC/PGRC-R scheme.

Gen	Constant Pop		MPGR = 1.0		MPGR = 2.0		MPGR = 2.5	
	FPS	TOC	FPS	TOC	FPS	TOC	FPS	TOC
1	60	0.2135	60	0.2172	60	0.2304	60	0.2090
2	60	0.4867	59	0.4358	59	0.4567	49	0.1833
3	60	0.6295	55	0.5496	64	0.4421	58	0.4912
4	60	0.7074	56	0.8175	52	0.6381	73	1.2676
5	60	0.8598	52	0.6125	62	0.0434	57	0.0052
6	60	0.8652	49	0.5634	74	0.0484	57	0.7423
7	60	0.8633	53	0.6648	76	1.4062	69	1.1512
8	60	0.8517	52	0.6732	74	1.3812	82	1.6510
9	60	0.8544	51	0.6073	64	0.9817	94	2.1949
10	60	0.8553	50	0.5779	74	1.4086	112	3.1471
Average	60.00	0.7187	53.70	0.5719	65.90	0.7037	71.10	1.1043

Table 9

Effect of population: constant population against dynamic population for SOBC/PGRC-E scheme.

Gen	Constant Pop		MPGR = 1.0		MPGR = 2.0		MOGR = 2.5	
	FPS	TOC	FPS	TOC	FPS	TOC	FPS	TOC
1	60	0.4006	60	0.4483	60	0.6836	60	0.4570
2	60	0.2960	59	1.1795	51	0.8979	60	0.8513
3	60	1.4567	58	0.1806	60	0.2643	58	0.3357
4	60	1.6630	58	1.4884	51	0.9949	68	2.1529
5	60	1.6458	64	1.8038	59	1.5958	58	1.5174
6	60	1.5357	61	1.6915	62	1.7093	61	1.7105
7	60	1.5857	67	2.0239	69	2.2275	56	1.4080
8	60	0.4439	68	2.1363	65	1.8868	53	1.2579
9	60	1.5234	75	2.8308	74	2.4249	58	1.5219
10	60	1.6080	82	3.1500	82	3.1219	71	2.3683
Average	60.00	1.2159	65.20	1.6933	63.30	1.5807	60.30	1.3581

Table 10

Effect of population: constant population against dynamic population for DOBC/PGRC-R scheme.

Gen	Constant Pop		MPGR = 1.0		MPGR = 2.0		MOGR = 2.5	
	FPS	TOC	FPS	TOC	FPS	TOC	FPS	TOC
1	60	0.2647	60	0.3510	60	0.1367	60	0.1268
2	60	0.8688	57	0.8191	55	0.4266	64	0.6245
3	60	0.8462	58	0.8154	65	0.9988	76	1.5339
4	60	0.8724	57	0.8087	78	1.5019	58	0.8289
5	60	0.8277	58	0.8189	92	2.1077	51	0.6862
6	60	0.8494	53	0.6842	79	1.5686	56	0.8011
7	60	0.8455	56	0.7611	95	2.2504	56	0.7425
8	60	0.8481	54	0.6813	101	2.5917	64	0.9788
9	60	0.9219	49	0.5818	95	2.1935	71	1.2296
10	60	0.8169	46	0.4834	107	2.8674	65	1.0033
Average	60.00	0.7962	54.80	0.6805	82.70	1.6643	62.10	0.8556

Table 11

Effect of population: constant population against dynamic population for DOBC/PGRC-E scheme.

Gen	Constant Pop		MPGR = 1.0		MPGR = 2.0		MOGR = 2.5	
	FPS	TOC	FPS	TOC	FPS	TOC	FPS	TOC
1	60	0.3795	60	0.4689	60	0.3318	60	0.3920
2	60	1.8333	65	2.0827	58	0.9426	58	1.5931
3	60	1.6574	68	2.1538	63	1.8790	72	2.4376
4	60	1.6936	69	2.1365	58	1.5186	59	1.5669
5	60	1.6902	64	1.8169	59	1.5760	59	1.5814
6	60	1.5741	63	1.8916	58	1.5853	74	2.7154
7	60	1.6359	66	2.0164	66	2.0160	62	1.7525
8	60	1.6811	72	2.5000	60	1.6287	58	1.5211
9	60	1.7119	71	2.2783	70	2.3797	45	0.9412
10	60	1.6858	75	2.8106	59	1.7225	51	1.1988
Average	60.00	1.5543	67.30	2.0156	61.10	1.5580	59.80	1.5700

Table 12

Parameters setting for CGA in Robot Route Path Algorithm.

Parameters	Values
Mutation Rate (MR)	$0.01 \leq \alpha \leq 0.20$
Population Growth Rate (MPGR)	$0.01 \leq r \leq 0.25$
Initial Population at Start	$N = 60$
Max number of Generation	$\Omega = 10$
GA Type	DOBC/PGRC-E

performance as compare to higher value. Similarly, comparing SOBC technique with DOBC, results obtained shows better performance with respect to BR and APR value for all different iterations.

ii. Conclusion:

Based on the deductions from the results obtained, it can be inferred that low mutation rate shows better perfor-

mance compare to high mutation rate value and better performance is recorded using DOBC as compare to SOBC technique.

(b) Effect of dynamic growth rate

The effect of introduction of MPGR has been evaluated in this work. The system parameters for evaluating this effect is as contained in Table 6 and observation and conclusion are presented herewith.

i. Observation and discussion

Results obtained from introducing MPGR in the proposed algorithm as against the use of the static population per generation is firstly reported. A typical result obtained in a single run of maximum generation of 10 is as shown in Fig. 5b. Similarly, as can be observed from Table 7, the population in each generation varies based on the proposed population control mechanism, a value which is between $\pm r$ in this work. Various values of r have been

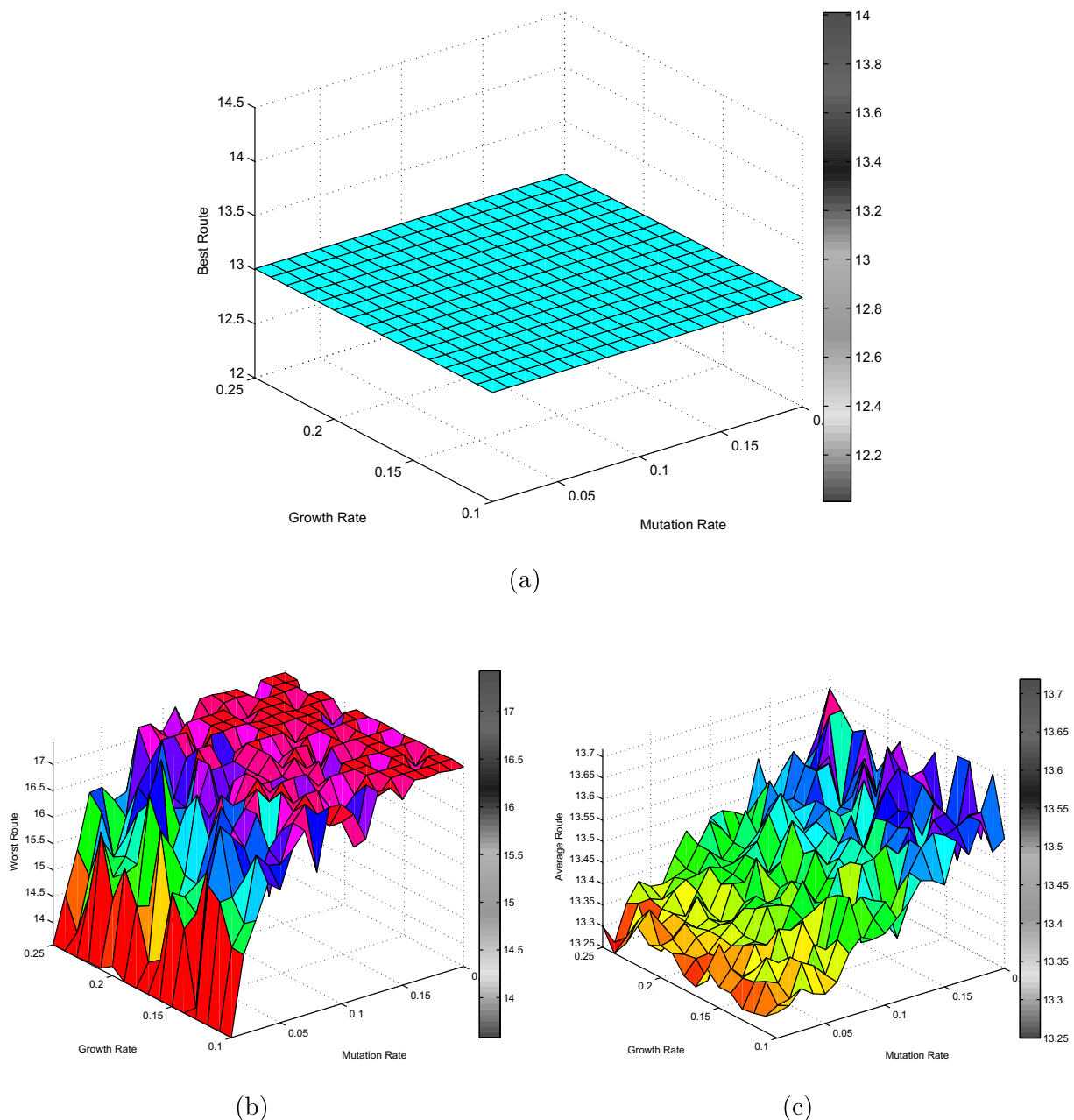


Fig. 6. Combine effect of mutation and MPGR on (a) Best Route (b) Worst Route (c) average population route.

Table 13

Parameters setting for Robot Route Path Planning.

Parameters	Values
Mutation Rate (MR)	0.05
Max. Population Growth Rate (MPGR)	$r = 0.25$
Initial Population at Start	$N = 60$
Max number of Generation	$\Omega = 10$

evaluated and as evident from Table 6, the corresponding APR, BR and WR obtained shows that the introduction of MPGR with polygamy and birth control mechanism can lead to earlier convergence of the system to optimal solution.

Similarly, the algorithm was also compared with the case of constant population under four different conditions proposed in this work, namely: SOBC/PGRC-R shown in Table 8; SOBC/PGRC-R shown in Table 9; DOBC/PGRC-R shown in 10 and DOBC/PGRC-E shown in Table 11. No significant difference between constant GA population and the proposed MPGR in terms of time of completion (toc) under the various proposed techniques, however there are probably chances that the MPGR uses shorter toc compared to the constant population technique under certain conditions. Typical case is as observed in Table 8 where the toc for MPGR technique is less than that of constant population technique. Similarly, the BR, APR and WR for both approaches shows almost similar trend from one generation to another with the MPGR showing better performance in certain cases.

- ii. Conclusion: Results obtained from this evaluation shows that the introduction of MPGR technique offers better performance in term of computation time, convergence speed and accuracy in this work.

(c) Effect of dynamic growth and mutation rate

The combined effects of MR and MPGR have also been evaluated in this work. The system parameters for evaluating the effects of these are stated in Table 12. The MR rate was varied from 0.01 to 0.20 so as to sufficiently evaluate

the effect of this on the algorithm under varying growth rate condition. Similarly, the MPGR varies from 0.05 to 0.25 and the results obtained are presented using a 3D plots under varying conditions.

i. Observation and discussion

The effect of sweeping the mutation rate and MPGR over certain range of values in SOBC/PGRC-R, SOBC/PGRC-R, DOBC/PGRC-R shown and DOBC/PGRC-E mode have also been evaluated in this work. Though, only the result for DOBC/PGRC-E mode has been reported in this section, this is due to the fact that almost similar trend was observed in all techniques evaluated. The 3D plot for the BR, WR and APR using the parameters in Table 12 are shown in Fig. 6a-c respectively. The BR for all the parameters used was firstly evaluated and results obtained is shown in Fig. 6a. Significant difference was noticed regarding the WR and APR shown in Fig. 6b-c respectively.

- ii. Conclusion Results obtained shows that low MR and high MPGR favors the proposed algorithm. This confirm earlier and effect of mutation rate earlier deduced in this work.

2. Performance comparison test

The proposed algorithm has been compared with the popular Roulette wheel selection algorithm. Parameters setting for the proposed algorithm is as shown in Table 13 while results and conclusion are subsequently presented in this subsection.

(a) Observation

Table 14 shows results obtained by comparing the performance of the proposed CGA selection with Roulette Wheel selection Technique (RWST) in terms of APR, BR, WR and TOC. As can be observed from the table, TOC for RWST is consistently lower than that of the proposed hybrid algorithm under almost all scenarios reported in this work. Reason for this might be due to various steps involved in the proposed hybrid algorithm as compared to little number of steps involve in RWST. Thus the proposed Hybrid algorithm

Table 14

Parameters setting for Robot Route Path Planning.

Population size	Roulette wheel				DOBC/PGRC-E			
	BR	WR	APR	TOC	BR	WR	APR	TOC
80	13.0095	18.7412	16.2417	0.5320	13.0095	15.9750	13.3760	1.7378
	13.0095	18.7412	16.1188	0.5370	13.0095	17.3832	13.3764	1.6651
	13.0095	18.7412	16.2659	0.5287	13.0095	16.5369	13.3732	1.6754
	13.0095	18.7412	16.1407	0.5339	13.0095	16.4015	13.3680	1.9575
	13.0095	18.7412	16.3666	0.5331	13.0095	16.4373	13.3600	1.8462
60	13.0095	18.7412	16.3349	0.4104	13.0095	16.1507	13.3708	1.3257
	13.0095	18.7412	15.9745	0.4135	13.0095	16.4462	13.3634	1.3241
	13.0095	18.7412	16.0964	0.4097	13.0095	15.7925	13.3966	1.5384
	13.0095	18.7412	16.1380	0.4142	13.0095	16.2839	13.3885	1.5102
	13.0341	18.7412	16.1801	0.4112	13.0095	16.5593	13.4180	1.5037
40	13.0341	18.7412	16.1447	0.2983	13.0095	15.9548	13.3175	1.4926
	13.0095	18.7412	16.2760	0.2988	13.0095	14.9888	13.2869	1.13249
	13.0095	18.7412	16.0964	0.2977	13.0095	15.2317	13.2955	1.3170
	13.0218	18.7412	16.5466	0.2977	13.0095	15.8709	13.3352	1.3186
	13.0095	18.7412	16.1801	0.3011	13.0095	15.5048	13.3274	1.3136
20	13.1338	18.7412	16.4963	0.1837	13.0095	13.6073	13.3047	1.1693
	13.1081	18.7412	15.7025	0.1818	13.0095	13.6823	13.2655	1.1968
	13.0588	18.7166	15.6778	0.1844	13.0095	13.7361	13.3576	1.1796
	13.0095	18.7412	16.5466	0.1836	13.0095	14.0517	13.2884	1.1158
	13.0095	18.6919	15.2579	0.1840	13.0095	14.7424	13.2238	1.1660
10	13.0095	18.3438	16.1195	0.1130	13.0095	14.0607	13.2215	1.0292
	14.4469	18.3695	16.9071	0.1139	13.0095	14.0025	13.5530	1.0569
	14.0518	18.7166	16.5476	0.1115	13.0095	13.7361	13.4876	1.0213
	14.2858	18.6673	16.0990	0.1120	13.0095	14.0025	13.5021	1.0538
	13.3309	18.6180	15.9597	0.1119	13.1830	14.1066	13.5244	1.0513

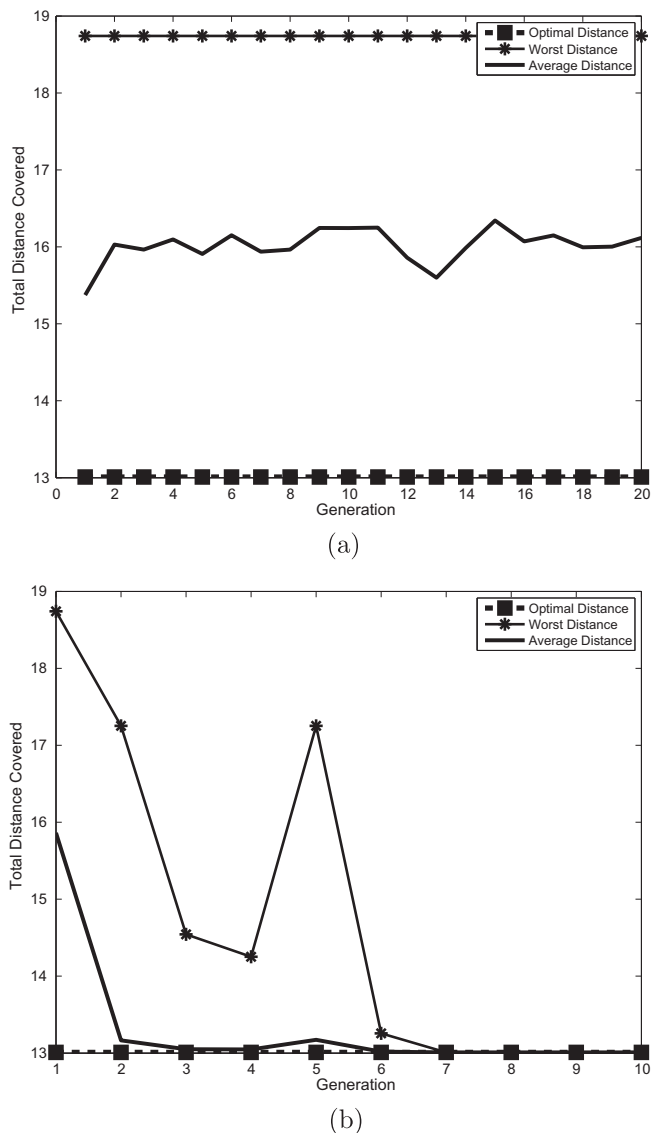


Fig. 7. Performance comparison-total distance: roulette wheel (b) CGA technique.

Table 15
Parameters setting for Robot Route Path Planning.

Generation	Roulette Wheel				DOBC/PGRC-E			
	BR	WR	APR	TOC	BR	WR	APR	TOC
5	13.0095	18.7412	16.1819	0.2413	13.0095	16.9321	13.6724	0.3507
	13.0588	18.7412	16.0382	0.2416	13.0095	16.7507	13.6071	0.4449
	13.0095	18.7412	16.2007	0.2401	13.0095	16.9321	13.6290	0.5650
	13.0095	18.7412	15.9007	0.2388	13.0095	16.6925	13.5915	0.4644
	13.0095	18.7412	16.1317	0.2408	13.0095	16.7418	13.6866	0.5917
10	13.0095	18.7412	15.9182	0.4171	13.0095	16.9925	13.3537	1.1278
	13.0095	18.7412	15.9745	0.4135	13.0095	15.8417	13.3205	1.1422
	13.0095	18.7412	16.0964	0.4097	13.0095	16.1350	13.4072	1.1403
	13.0095	18.7412	16.1380	0.4142	13.0095	15.7332	13.3258	1.1396
	13.0341	18.7412	16.1801	0.4112	13.0095	15.3224	13.3451	1.2982
15	13.0095	18.7412	16.1456	0.5941	13.0095	16.3000	13.2569	1.3202
	13.0259	18.7412	16.0411	0.5844	13.0095	17.1365	13.2886	1.3989
	13.0588	18.7412	16.4205	0.5854	13.0095	16.2865	1.2803	17.1909
	13.0752	18.7412	16.2435	0.5905	13.0095	16.1433	13.2878	1.3427
	13.0095	18.7083	16.0272	0.5876	13.0095	15.4708	13.2365	1.3425
20	13.0095	18.7289	16.0442	0.7609	13.0095	16.9024	13.2639	1.9145
	13.0218	18.7412	16.4650	0.7726	13.0095	16.0438	13.2197	1.8757
	13.0095	18.6673	16.3744	0.8285	13.0095	15.4164	13.1919	1.7349
	13.0341	18.7412	16.2987	0.7619	13.0095	15.9565	13.2034	1.8523
	13.0218	18.7412	16.0975	0.7588	13.0095	15.0811	13.2314	1.7087

spent longer time in selection and clustering than the use of RWS. Despite having lower TOC, a great difference between APR and BR per generation in RWST was observed compared to that CGA selection technique over all instances. Typical results obtained are as shown in Fig. 7a-b. The differences between the BR and APR for RWST shown in Fig. 7a is far greater than the differences noticed between APR and BR shown in Fig. 7b hence convergence in RWST may occur at longer generation while the APR and BR in the clustering approach converges to optimal values easily after short iterations. Thus, the proposed technique shows that most of the chromosomes in the proposed technique tends to converge to the same optimal BR solution better than the RWST, thus reason for the small difference in APR and BR and may therefore be regarded as an elitist approach for selection proposed.

Furthermore, it was observed that RWST works best with large population of chromosomes in the solution pool when compared to the CGA approach that shows no significant difference between few population and large population size. The number of chromosomes per generation was varied from 80 till 10, results obtained shows that global route optimal value was hardly reached at lower population of chromosomes in the population with RWST whereas at even low population the proposed hybrid CGA selection technique still converges to the optimal BR of 13.0095.

The effect of generations on accuracy and convergence capability of the two techniques have also been evaluated. Table 15 shows results obtained from the algorithms at various generation setting. The proposed CGA shows better performance over different generation settings when compared with results obtained from using RWST. When set to lower generation value, Roulette wheel technique hardly converges to optimal solution whereas the proposed technique do converge to optimal solution.

Reason for early convergence to the optimal solution in the proposed algorithm has been observed to be due to the use of Clustering and Polygamy technique in the reproduction stage, this favors selection of the fitter chromosomes only and the polygamy effect allows for breeding of the fitter off-spring. Other reason responsible for this better performance

include the use of dynamic population growth, does the population is not limited to the initial number only rather increases as the number of generations increases.

(b) Conclusion

It has been observed that the proposed techniques show better performance compared to RWST: when the population of chromosomes was small; when the number of generation was low, convergence between APR, BR and WR sometimes occurred. However, the RWST technique appeared to be faster than that of the Proposed technique.

5. Conclusion

In this work, novel clustering based GA with Polygamy and population control algorithms have been presented. The proposed technique involves clustering, polygamy mating and population control processes have been proposed in this work. The clustering approach introduces high selection pressure in the reproduction process thus increasing the average.

In the proposed CGA, unlike the traditional GA, mutating the chromosomes does not really give additional new chromosomes to the population as the introduction of polygamy and birth control has taken care of this variation. Though, low mutation rates show better performance compared to high mutation rate values and better performance was recorded using DOBC as compared to SOBC technique.

Furthermore, results obtained show that the introduction of maximum population growth rate technique offer better performances in terms of computation time, convergence speed and accuracy in the proposed CGA.

It was also observed that the proposed techniques show better performance compared to probability based selection techniques such as Roulette Wheel. Clustering based Genetic Algorithm (CGA) better performance was obvious when the population of chromosomes was small and when the number of generation was low. However, the RWST appears to be faster than the proposed technique.

Results obtained also show that the proposed algorithm converges to global solution within few generations and with little population of chromosomes in the solution pool. It has also been shown that the introduction of dynamic control with polygamy selection process in the reproduction stage enables fast convergence to optimal solution. Future work will explore the application of this algorithm to other areas of human endeavor.

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