Novel Algorithm for Hand Gesture Modeling Using Genetic Algorithm with Variable Length Chromosome

Noor Adnan Ibraheem
Computer Science Department, College of Science for Women
University of Baghdad, Baghdad, Iraq
e-mail:naibraheem@csw.uobaghdad.edu.iq
Computer Science Department, Faculty of Science
Aligarh Muslim University, Aligarh, India
e-mail:naibraheem@gmail.com

Rafiqul Zaman Khan
Computer Science Department
Faculty of Science
Aligarh Muslim University
Aligarh, India
e-mail: rzk32@yahoo.co.in

***Abstract*—**Many languages the people can exploit for them in order to communicate among them and get the message delivered, but, these languages should be known by those people in order to understand and speak, contrarily, gesture system is the common language that can be adopted for this objective and need less knowledge as compared with spoken languages that need the grammatically and semantically rules, in this paper we applied a novel algorithm for capturing hand gesture shape using one of the evolutionary algorithms in order to fit the hand segment. Previous techniques in the literature that fully captured hand shape applied some artificial intelligent methods [1] or some statistical methods [2]. Genetic Algorithms (GAs) with variable length of chromosomes is used to model the hand structure. The most effective GA parameters used for this purpose are; the generation of initial population, tournament selection, crossover with variable position of the cutting points in the parents, artificial mutation operator, deleting of the repetitive genes in same individual, and elitism strategy. Experimental results shows the robust and efficiency of applying the proposed algorithm.

Keywords- *gesture; feature extraction; genetic algorithms; initial population; variable chromosome length*

*****

I. INTRODUCTION

Recently the world is directed towards the natural visual communications for interacting with available environment tackles [3] [4], gestures considered as the most effective tool in this field, since the appealing merits that gestural interfaces provide to simplify the communication between human and computers and replace the need for utilizing external hardware devices such as mouse and keyboard [5][18]. However, robots recently utilized as human-friendly life-support applications [6][7] and as an intermediate interface between real and cyber world as well [7].

II. GLIMPSE ON GENETIC ALGORITHMS

Genetic algorithms (GAs) are randomized [8] and directed search techniques [9] which depends on the natural evolution and genetics principles [8][10][11]. The nature of searching in GA is probabilistic [4] so that in the problem solutions search space it can produce different solutions [8][4].

GA individuals or chromosomes "agent" [16] consists of a set of discrete elements named genes which can be represented as a string of variables [16][11][8], a set of chromosomes forming the population. The major factor in GAs is the encoding process that transforms problem's variable form phenotype domain into genotype domain and produce a binary, or real encoding chromosome [12][8][11] such that the number of alleles (chromosome length) represents the amount of problem information described in genotype space [12]. Each chromosome assign a fitness value which is used as an indicator for the level of efficiency for representing the problem solution [11] and how the fitter chromosome can be obtained under available ambiance [13]. The fitness value is used to evaluate each chromosome, so that the chromosome with higher fitness value has better chance to survive [13][11][8].

The conventional GA has several operators that guide the algorithm towards optimal or neat optimal solution in the search space, which are; selection (reproduction), crossover, and mutation mechanism. Selection is the process of copying the individuals into the mating pool based on their fitness value [8][13]. Crossover operator which plays an important role which recombine the structure of the selected chromosomes by choosing a random number as the cut point (in case of one point crossover) and the genes after the cut point of both individuals are swapped [13] according to some probability. While mutation is a minor operator and not always performed, change the value of chromosome's gene in random locus (position) according to mutation probability [13]. In this work, we formulate a single chromosome as one possible hand shape by distributed pixels over the hand using proposed technique. Goldberg [8] provides adequate description of GAs approaches. Traditional genetic algorithm can be defined in the following steps [14]:

1) Set up the initialization of the control parameters (population size, crossover rate, mutation rate, etc.).
2) Set GA characteristics, such as translating the real problem into mathematical form by encoding the parameters, specify the proper fitness function, type of selection, crossover, and mutation, and stopping condition as well.
3) Generate initial population.
4) Calculate fitness value for the current population and update the best solution found.
5) If the stop condition is satisfied, exit, else, continue with the following steps.
6) Perform selection.
7) Perform recombination.

8) Perform mutation, replace current population and back to step 4.
9) Encode the genotype into the phenotype problem domain, end.

III. Related Work

Limited research work in the literatures that utilize GA with variable length chromosomes since it depends on the characteristics of the optimization problem and the available facts. However, Kim and Kwak [12] proposed two structural topology problems: a short cantilever problem and a bridge problem using variable chromosome length genetic algorithm (VCL-GA). The suggested system is refined in a multi stage process in the search space [12], in which the solution domain grows up through various generations. Binary encoding is used with zero for void and one for solid of cell density. The convergence for the inner stage is represented by the average fitness of the entire population, and for the outer stages the final mass and maximum length of chromosomes. The system design starts with small initial chromosomes and the optimal result of the inner stage transformed into the outer stage in which the chromosome is refined and size increased. A population size of 50 chromosomes is used and the population size of the last stage is 150 with mutation probability 0.01, crossover probability 1, and 30 % for elitism strategy [12].

Frenzel [15] reported that the GA is constructed on two thoughts; 1) the fitness for each chromosome should represent the precise evaluation criteria to solve the problem, and 2) the solution or chromosome over GA generations will be enhanced by the effect of performing recombination and mutation operations.

Horia and Morignot [16] proposed planning model of STRIPS domains using GA with variable length chromosomes method. The algorithm initialed with variable length of chromosomes around 15-20 genes (the system starts even with a fixed length of initial genes) and 1500 chromosomes , tournament selection has been used for selecting chromosomes based on the minimum fitness between the competing chromosomes, and one-point crossover for recombination them. Six kinds of mutation have been tested and the probability of implementing each kind has been determined individually [16], elitism scheme were used as well. The algorithm stops after a predefined number of generations, and implemented on a Linux workstation [16]. The time required for the algorithm evolution process has uneven time lengths, and period of time needed for one generation varies between0.5 and 2.0 sec.

Riquelme J. et al. [17] detected motion plans coordinates of two manipulator robots using GA with variable length chromosomes, where each individual represents an incremented path that form the sequence of generated coordinates [17]. Uniform distribution of the number of genes was used for generating random lengths of initial population. Fitness function has been evaluated for both valid and non-valid individual. For valid individual, the total time robots required to finish the path and for non-valid individual, calculate far distance from valid individual [17]. Crossover operator applied in a way that the path always is in an increasing state, and two mutation operations proposed; slight mutation for slight changes in the local or neighbor regions, and strong mutation for significant change to explorer more regions in the search space, elitism strategy has been used as well. The individuals are coded in an integer variable with 20 individuals initially, 100 individuals per population and 300 generations. Few researches in the literature applied genetic algorithm for hand gesture recognition problem,

Kaufmann et al. [4] present a hand posture recognition system using steady state genetic algorithm, after preprocessing the image and convert into lab color space. Three hand models are used in the system where the contour of hands shape is extracted and encoded into a list of points. each chromosome represent a hand with a gene consists of five parameters (model of hand, horizontal translation, vertical translation, scale of the model, rotation of the hand). The fitness function computed as the similarity criteria between a particular hand model and input image. Selection, immigration, mutation, and crossover are the three operators used, immigration used for random generation of chromosomes and other operators run as traditional GA. tournament selection size two are used and chromosome with low fitness value are chosen. Fixed and small population size is used for real time performance and time consuming purposes [4]. In the real time application, between each two frames, the genetic engine generates variable number of generation based on the load of system computation in the environment and the fitness value is recalculated at each new video frame, however, the applied algorithm is asynchronous since its work depends at the time the video information being available [4].

IV. Hand Shape Morphology Algorithm Description

In this section, we describe the hand shape morphology algorithm using proposed variable length chromosome genetic algorithm, with the representation of the adopted encoding problem, as well as various GA operators utilized. We will call it Genetic Shape Fitting using Variable Length Chromosome or for simplicity GSF_VLC, the overall procedure for hand gesture shape modeling using the variable chromosome length genetic algorithm is demonstrated in Figure 1.

A. Genetic Domain Representation

The chromosome in traditional GA has a fixed length which is setup a priori at the encoding stage when mapping between phenotype-genotype search space [8][12]. Kim and weck [12] reported two disadvantages when using this method especially at complex design problem. 1) The fitness value is restricted to chromosome length and surely it will not attain the best result, 2) in the context of design freedom concept [12] there is no a priori knowledge about how much freedom variable are demanded for efficient design and hence the how long the chromosome supposed to fit [12]. For solving such problems using traditional GA two choices are available as explained by Kim and weck [12]: 1) if the chromosome length is short, the algorithm may not achieve the desired solution since there is a deficiency in the variable design problems [12], 2) if the chromosome length is long (use extra variables than the required), the algorithm will become computational consuming with no guarantee for promising performance results [12]. In this work we adopted an efficient genetic algorithm that increases the chromosome length gradually in order to capture full hand morphological representation using variable chromosome length. The proposed algorithm will decide the fitted length of chromosome.

B. Chromosome Structure

In most GAs, the chromosome length is fixed and decided in a priori, however, designing the problem with variable length

 ISSN: 2321-8169
2175 – 2183

of chromosome appears more accurate [16] and fitted on problem domain parameters besides we do not know the exact chromosome length required to fully represent the ultimate figure of hand shape. In our problem, the chromosome represents the segmented hand gesture image shape so that the final shape of the hand would be recognized through GA by filling up the segmented hand with points and hence matching hand configuration.

The gene is named by Basic Element Circle (BEC) which is formed by two elements; the position and the image intensity value of x, and y coordinates. Unique individual is represented by a list of BEC. Since we are dealing with a segmented hand, the values of image intensity is either one (white) which indicates the foreground hand object or zero for the background uninterested objects, as we are interesting in capturing the shape of the hand, the chromosome's genes are generated only in the hand object and thus the intensity value equal to one is the solely considered issue in gene representation.

C. *Gene Structure*

For each generated BEC genes, checking for the imposed conditions is performed:

1) The value of each BEC gene should equal to one, to ensure the randomly generated gene lies in the segmented hand area.
2) Checking the overlapping status of the randomly generated BEC points with the already available points to ensure not infiltrate the area of another gene.
3) Checking the repetition status of the BEC points to avoid the generation of points that are already generated.

Chromosome and BEC gene is depicted in Figure 2.

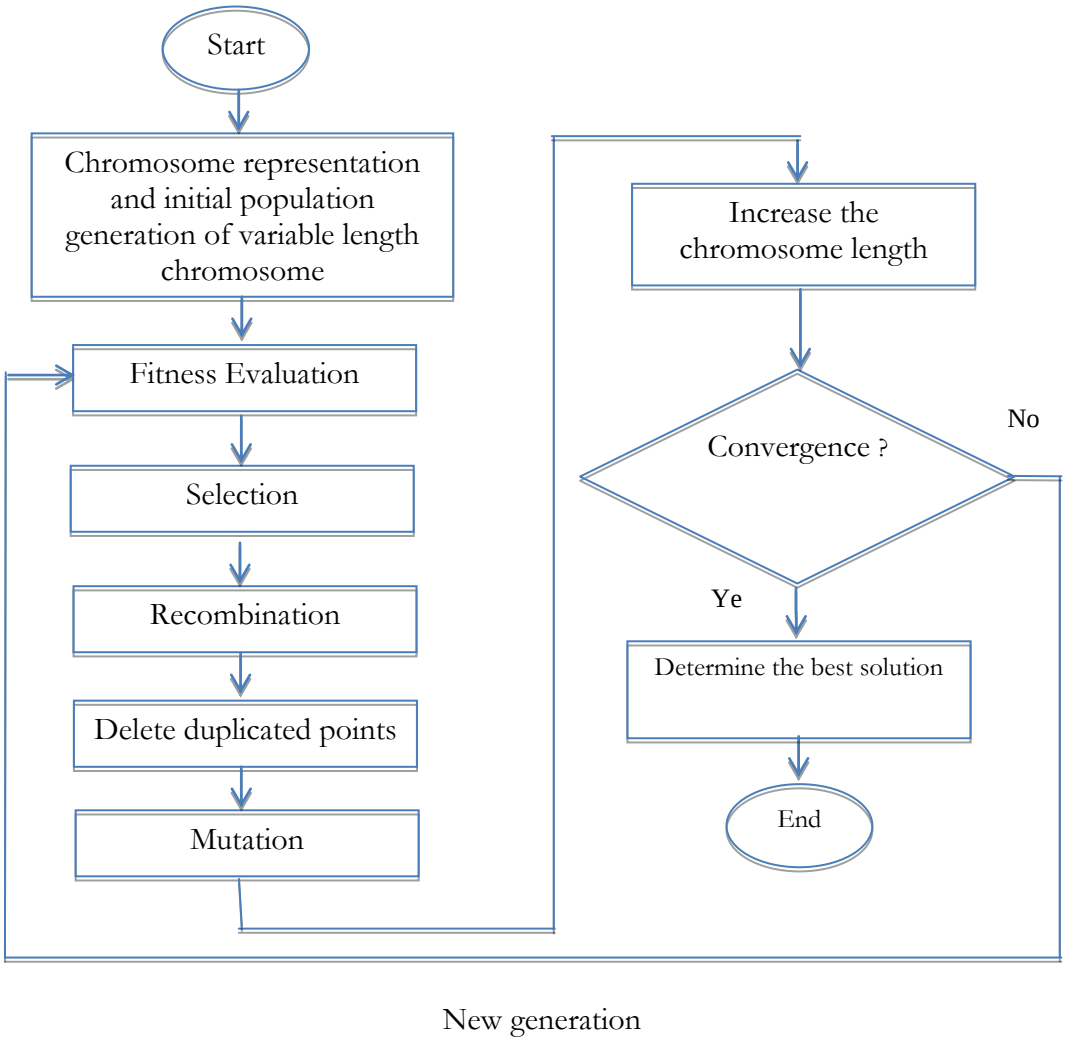

Figure 1: Flow diagram of the proposed variable length chromosome genetic

 ISSN: 2321-8169
2175 – 2183

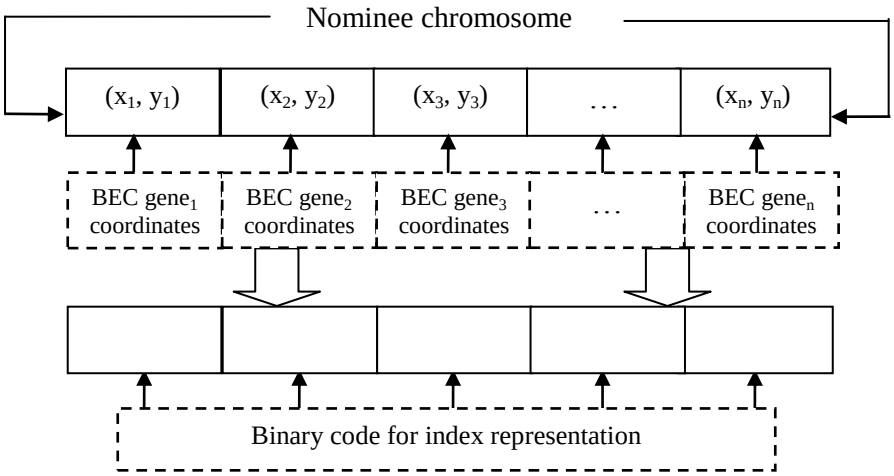

Figure 2: Chromosome and gene structure for GSF_VLC algorithm.

D. Fitness function

The essential component of GA is the fitness function which integrates several parameter variables and user-defined assumptions [16] to produce a probabilistic costing function [13]. In our problem domain, although during the generating of initial population, a checking for non-overlapping situation among the generated BEC genes are performed. This sound feasible for the generating of the initial population, the system will face an overlapping problem with the implementation of successive GA operators in which multiple BEC gene areas might conflicted. To assess the convenient of the generated individual, we should consider two issues: the overlapping factor of BEC gene, and individual length. The motivation behind considering these two factors to form the function fitness is demonstrated by the following two reasons:

1) We have to calculate the number of BEC gene that overlapping with other BEC gene areas. In other word, the individual with a higher degree of overlapping BEC genes unable to represent the correct shape which can lead to incorrect structure. The increment of individual overlapping factor agrees inversely with the fitness function.

2) An individual length has an impact factor on the efficacy of fitness function. Since we are trying to fit and match the exact shape of the hand, the individual length growth at the implementation of iterative GA generations using variable length chromosome model. Individual length represents how much the individual is close to capture the hand shape. The increment of individual length agrees directly with the fitness function.

The objective function can be modeled using the following mathematical representation [19] [13]. Let Len_i be the individual length in function m and let ov_i be its overlapping percentage for an individual i in function n.

The function m is used to represent is a monotonically increasing function [19] defined as:

$$objective\ function_i = F\ (m(L_i), n(o_i)) \quad (1)$$

$$m(x) = \begin{cases} \frac{x - min}{max - min} & if\ x \leq \frac{(max - min)}{2} \\ 1 - \left(\frac{max - x}{max - min}\right) & otherwise \end{cases} \quad (2)$$

Where max and min represent the maximum and minimum length achieved in a specific population respectively.

The function n is selected is a decreasing function [19][13]represent by:

$$n(x) = \begin{cases} 1.0 & if\ x < c_1 \\ 1 - \frac{x}{Ovp} & if\ c_1 \leq x < c_2 \\ 0.0 & otherwise \end{cases} \quad (3)$$

Where c is the overlapping BEC percentage and the range [c1, c2] restricted the overlapped genes. c1 is the fitted individual length at that iteration [19].

Then, the objective function for an individual i can be expressed by the following function:

Where the functions $F, m, \text{and } n$ are normalized to lie within the range [0, 1].

By combining $m(x)$ and $n(x)$, we can be form the function F:

$$F(g_i, s_i) = ((g_i \times \gamma) + (s_i \times \alpha)) \quad (4)$$

Where γ and α are constant values within the range [0, 1], the g_i equal $m(x)$ and s_i equal $n(x)$.

E. Initial Population with Variable chromosome length

Problem domain that require an increasing string length which can spread out in problem solution to warp all the dominate object structure [13] considered an urgent issue to think in the variable chromosome length as an alternative method for dynamically increasing the chromosome's length [13]. In the initial population step, chromosomes are generated

 ISSN: 2321-8169
2175 – 2183

randomly with a length determined by a particular range of [n, m] in which n considered as the lower bound and m considered as the upper bound of uniform distributed random number [20][17]. We should not forget to examine the conditions assumed on the recently generated BEC gene in each chromosome. The following steps explain the proposed scheme:

Step 1. Determine the radius of the BEC gene.
Step 2. Repeat for all the population size.
Step 3. Generated randomly n and m values that represent the range of recently generated chromosome' length.
Step 4. Generated randomly x and y coordinates which define the value of BEC gene.
Step 5. Check the constraints (mentioned in subsection B and here to clarify the definition), if the constraints satisfied, the generated BEC gene considered as a member of the current chromosome, otherwise repeat step 4 and 5 until it satisfy the constraints.
Step 5.1. Overlapping BEC gene.
Step 5.2. Repetition BEC gene.
Step 5.3. x, y coordinates value.
Step 6. Repeat until generated the upper bound of chromosome length m.

The range of the uniform distributed random number [20][17] was empirically set for the initial lengths of the initial population. Experimentally discovered a uniform distribution number of genes between 1 and upper bound m [1, m] is unreliable to form initial chromosomes length [17] since minimum number generated might be one or less more and this will lead to a long execution time of GA generations in order to capture the full demanded shape, furthermore stagnation status can probably arise from the few generated points [17] in other optimization problem, however the number of genes in the initial population empirical limits based on the characteristics of a particular problem [16].

The initial population lengths play an important role in chromosome's length increasing process during proposed mutation operator where the longer genes length the wider spreading of genes over the solution space and hence increase the speed of GA evolution procedure [16] as we will explain in mutation subsection. Figure 3 illustrates an example of two different initial populations with two different ranges initial length sets in different two experiments.

F. Selection Model

The process of selection can be summarized by randomly selected the chromosome with higher fitness function when competing with other chromosome selected randomly [8][16]. The number of the competing chromosomes each time relies on the nature and type of the application [16]. Various types of selection strategies are exists, the most popular selection type is tournament selection [16][14] and roulette wheel selection [8][13][11][6][10]. The selection operation preserves the diversity in the solution space and provides the opportunity to explore the search space [16]. The diversity factor is affected with the number of chromosomes in the tournament which in turn effects on the convergence rate [16]. In this work we adopted tournament selection strategy by selecting two chromosomes randomly each time, and the resulted new population is stored in the mating pool.

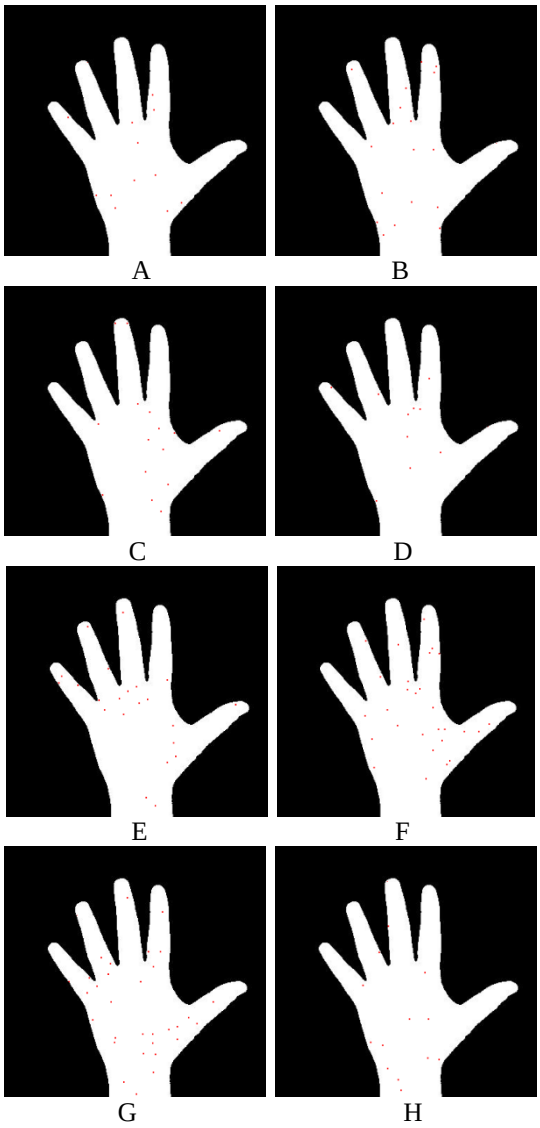

Figure 3: Generation of two groups of random initial population with range [5, 20], and [10, 40] respectively. First group: A. 12 genes, B. 18 genes, C. 14 genes, and D. 9 genes. Second group: E. 22 genes, F. 28 genes, G. 31 genes, and H. 13 genes.

G. Crossover Operation

The proposed system uses one-point uniform crossover for individual's recombination, although we implemented two more complex types of crossover such as two point crossover and uniform crossover [16], we experimentally discovered the same inference concluded by Horia and Morignot [16] in which the system achieved better performance using one cutting point crossover rather than the mentioned two methods, as a result of applying GA with variable length chromosome features besides and the nature of the problem to be solved has great impact on the choice of crossover type operator [16]. In our problem the chromosome fitness function depends on the number of overlapping process among genes where the recombination of the genes after more than one cutting point can increase the overlapping factor and hence decrease fitness for the entire population [16].

ISSN: 2321-8169
2175 – 2183

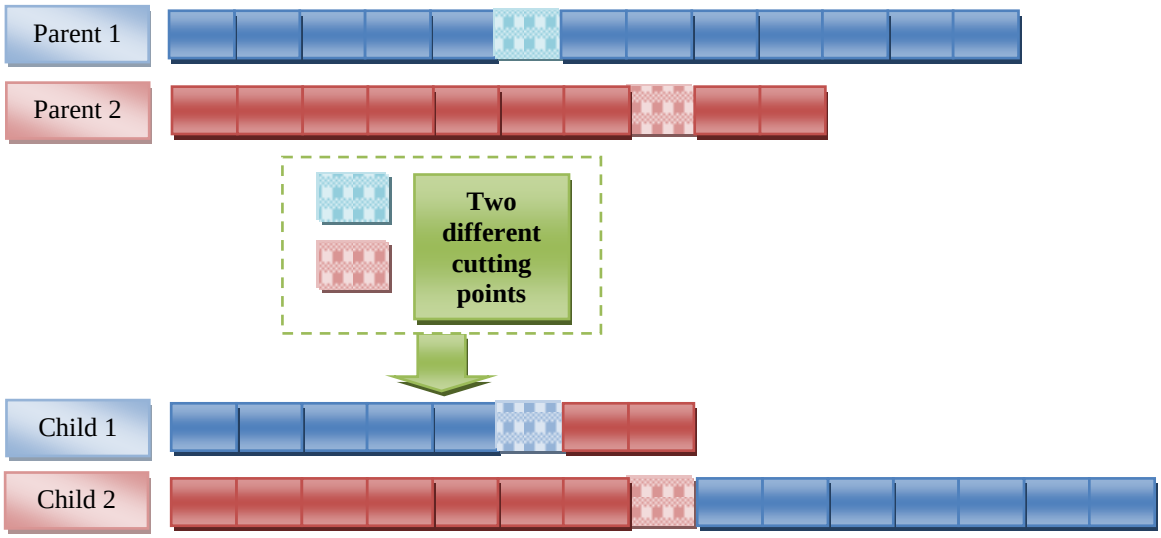

Figure 4: Crossover operation representation.

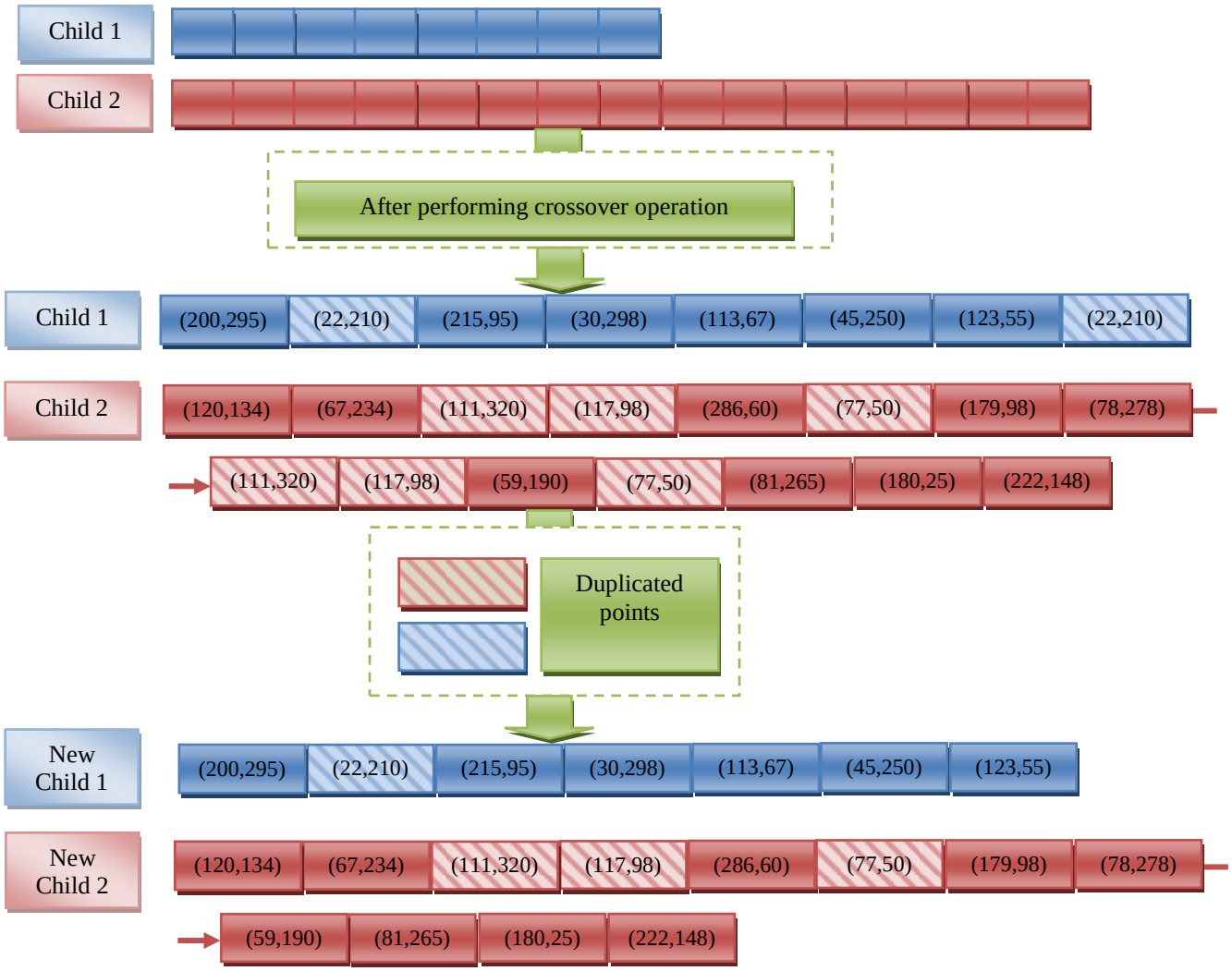

Figure 5: the representation of deleting duplicated points after crossover operation. The length of the chromosomes effected with this process.

In crossover process, after selecting two parent chromosomes randomly from the mating pool, two different cutting points are selected randomly from both parent chromosomes with range from [1, Length-1]. Afterwards two offspring are formed by merging the beginning of one chromosome with the end of the other and vice versa [16].

Although the number of genes will be increased in one offspring and decreased in the other offspring, but there is no creation for new genes besides the repetition of some genes too (i.e. especially if they have an identical parents). Figure 4 depicts the representation of crossover operation.

H. Delete DuplicatedPpoints

Although the crossover operation can increase the length of the generated offsprings, this increment might cause gene's replication in the new generated offspring chromosomes; these repeated genes are not useful since it will only refer to a false indication of an increasing chromosome length besides the extra computation cost at later operations such as mutation and adding new points schema, the optimal solution for this problem is to delete the duplicated points in each offspring in the population in order to prepare the population for the mutation operation. Figure 5 depicts the representation of this process. For explanation purposes the output children of crossover operation are extended in the figure to clearly represent genes of each child and the duplication of some genes as a result of performing parent's recombination. The duplicated genes are shaded in each child and the result of implemented this process is a new child with no repeated in chromosome genes.

I. Proposed Artificial Mutation

Goldberg's simple genetic algorithm considered as the base for many GA research works [13]. The proposed artificial mutation operator tries to explore solution search space by generating new genes based on the currently existed genes besides make benefit from the random criteria of conventional GA. the idea of generating new genes were inspired from Riquelme J. et al. [17] in which they applied two different types of mutation for generating a coordinates of motion plans in multi-robots systems. In their work, they add a fixed number to the existed coordinates to direct the synchronization point's sequence of robots path. The proposed mutation operator adds four genes in four directions that surrounded the selected gene coordinates according to Pm probability. In this technique the genes will exploit the search space wisely and to avoid reaching into local minima [17]. The detailed procedure steps are illustrated as follows.

Step 1. Step 1. For each gene in a particular chromosome in the population, apply mutation operator according to the mutation probability Pm.

Step 2. Step 2. For the current gene, generate four genes in four directions adjacent to positive x-axis, negative x- axis, positive y-axis, and negative y-axis restricted with the circle radius r previously defined r = R where R is an integer number with plausible size.

Step 3. Step 3. Check the recently four generated genes if satisfy predefined conditions, explained in subsection C, Step 5.

Step 4. Step 4. From the generated four genes, if one gene satisfied these conditions, preserve it so that to be joined later with current chromosome length. The reason behind choosing one gene to be added in the preserved gene list is to give a chance for other genes to create gene from their side in order to maintain diversity in the search solution and spread out on large area of problem search space. Besides not all the created genes in the list are joined to the current chromosome length, a predefined joining percent were used to determine the number of genes every time attached to current chromosome length. The following subsection explained the joining strategy.

Step 5. Step 5. This process will continue for all genes in the current chromosome and in all population's chromosomes.

J. Increase Chromosome Length / adding new (point) genes

After preparing the list of genes to be attached with each chromosome in the population, a proportion of the chromosome length is specified. According to that percent, a number of genes from the gene list are joined with the length of that chromosome, this process continues for all the chromosomes in the population, and the new population with new chromosome's length is generated.

K. Elitism

For preserving the best solution over GA iterations, elitism strategy has been used in order to inherit [14] the best chromosome solution among generations, in this literature elitism strategy has been performed with 30%. This elitism percent has been widely used for fair preserving of the best solution over GA evolution [12].

L. Termination Criteria

Before staring GA iterations, an estimation of the number of pixels that should distributed over the segmented area is calculated. This estimated number is calculated by dividing the number of pixels in the white intensity of the segmented area by the circle circumference which explained in the following:

$$C_{cir} = 2 \times r \times \pi \quad (5)$$

C_{cir} is the circle circumference and π represent the constant 3.14285.

$$P_x = \frac{Pi_w}{C_{cir}} \quad (6)$$

P_x represents predicated number of pixels Pi_w is the number of whites intensity pixels. Actually this estimation number will be the tool that defined the stopping condition for GA termination. Since along the evolution of GA, individuals' length are growth increasingly until the length of best solution is less than or equal to the estimated number of pixels. However, the estimated number of pixels is mostly perfect and the GA will not generate a solution near this number, for two reasons; firstly, GA generated solution or optimal solution of the problem, and secondly, because of the repeated recombination and mutation operations besides the insertion of the new generated points and neglecting the overlapped ones through enormous GA generations. These reasons pushed us to check for the another issue which is the length of individuals through the evolution of GA, since after some amount of iterations stagnation status might arise when there is stability situation and no improvement in the number of individual points along the generations. The remedy for this problem can be performed by checking for the increment of best solution length between current generation and last few generations, if the difference of best individuals lengths between these two

generations equals zero (an indication for stagnation case) then the GA iteration breaking down and exit with the best solution, otherwise continue in GA generations. The checking for differences between individuals' lengths is done each ten generations, in this way two methods are performed to ensure correct and normal termination of GA iterations [4].

M. GSF_VLC Algorithm Steps

The previously discussed GSF_VLC algorithm can be summarized by the following steps:

Step 6. Encoding the problem.
Step 7. Generate initial population.
Step 8. Fitness function evaluation.
Step 9. If termination criteria achieved, go to step 12, otherwise continue step 5.
Step 10. Perform Selection.
Step 11. Recombination of population chromosomes.
Step 12. Delete duplicated points from the generated offsprings.
Step 13. Perform artificial mutation.
Step 14. Add new artificially generated genes into each chromosome's length.
Step 15. Performa elitism schema.
Step 16. Go back to Step 4.
Step 17. End.

It is worth to indicate that the output result of applying GSF_VLC algorithm is an array of pixels coordinates which will serve the determination of the initial palm center and the extraction of finger feature.

V. EXPERIMENTAL RESULTS

This section presents an experimental result of applying the proposed GSH_VLC algorithm on a set of different segmented hand gesture images. The hand gestures database used contains 100 different hand images with different gesture classes from two volunteers. Although additional parameters need to be specified in the setting step, such as the percentage of how many pixels are decided to be joined for chromosome extended length, Figure 6 shows the results our applying our suggested algorithm.

For the resultant images obtained in Figure 6, some statistical issues necessary to be considered, the population size applied was 10, the percentage for elitism and for increasing individual length was 30%, other factors are mentioned in Table 1.

VI. CONCLUSION

For any hand gesture recognition system, modeling the hand is one of the important earlier steps that is necessary for the latter stages depending on it. In this paper we proposed a new method to model the hand gesture so that the structure of the hand shape is fully captured. The suggested schema have the following steps; firstly we developed a variable length of chromosomes as the most powerful property for the increasing of chromosomes length during the successive GA generations, crossover operator also with dynamic cutting point in the selected parents helps to generate individual length and to increase the speed of achieving the appropriate length of optimal individual, and then the artificial mutation is applied in a way that can generate new genes in various positions the surrounding the selected mutated gene. These are the most effective GA parameters that can be augmented the individual length gradually besides applying other GA operators. Output results of the suggested approach have been implemented on different gesture shapes with various directions and it shows the robustness and effectiveness of our proposed technique. Traditional GA have been utilized in this method, in the future work micro genetic algorithm can be applied for modeling the hand gesture, besides applied different GA operators to attain better results.

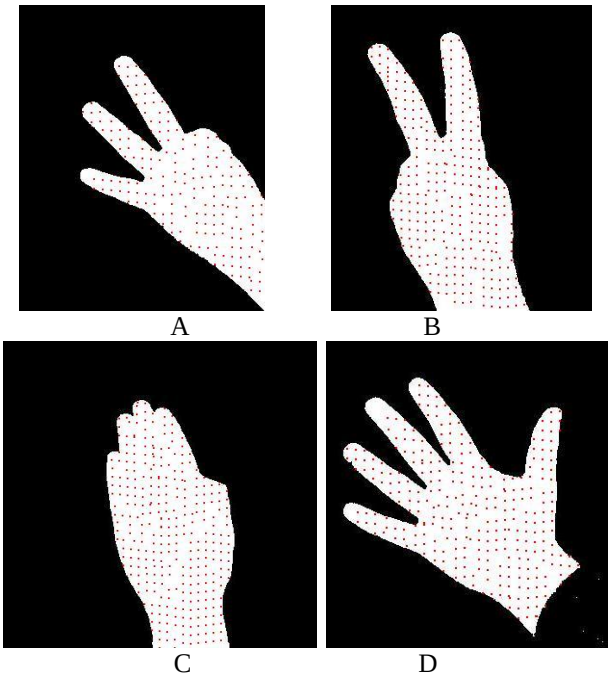

Figure 6: Demonstration of GSH_VLC algorithm implementation.

Table1: Statistics related to images explained in Figure 6.

Picture name	initial range	Diameter size	# Predicted pixels
Figure 6 (A)	[10, 20]	20	409
Figure 6 (B)	[5, 20]	18	510
Figure 6 (C)	[5, 20]	18	557
Figure 6 (D)	[5, 20]	18	538

Picture name	Best length achieved	# Generations
Figure 6 (A)	193	54
Figure 6 (B)	298	82
Figure 6 (C)	314	62
Figure 6 (D)	299	50

REFERENCES

[1] Stergiopoulou, E. and Papamarkos, N. ,"Hand Gesture Recognition using a Neural Network Shape Fitting Technique", Elsevier Journal of Engineering

Applications of Artificial Intelligence, vol. 22, pp.1141–1158, 2009. Doi: 10.1016/J.ENGAPPAI.2009.03.008.

[2] Mokhtar M. Hasan, and Pramod K. Mishra, "Novel Algorithm for Multi Hand Detection and Geometric Features Extraction and Recognition", International Journal of Scientific and Engineering Research, Vol. 3 (5), pp. 1- 11, 2012.

[3] M.K. Bhuyan, Debanga Raj Neog and Mithun Kumar Kar, "Hand Pose Recognition Using Geometric Features",

[4] tony Heap and Ferdinando Samaria, "Real Time Hand Trucking and Gesture Recognition Using Smart snacks", Proc. Interface to Real and Virtual Worlds, Montpellier, June 1995.

[5] Lars Bretzner, Ivan Laptev, Tony Lindeberg, "Hand Gesture Recognition using Multi-Scale Colour Features, Hierarchical Models and Particle Filtering", Proceedings of the Fifth IEEE International Conference on Automatic Face and Gesture Recognition (FGR.02), 2002.

[6] Mori, A.; Uchida, S.; Kurazume, R. Taniguchi, R. Hasegawa, T. and Sakoe, H. "Early recognition and prediction of gestures", Proceedings of International Conference on Pattern Recognition, pp. 560-563, Hong Kong, China, 2006.

[7] Naoyuki Kubota, "Human Detection and Gesture Recognition Based on Ambient Intelligence", Face Recognition, Book edited by: Kresimir Delac and Mislav Grgic,, pp. 262- 274. I-Tech, June 2007.

[8] D. E. Goldberg, Genetic Algorithms in Search, Optimization and Machine Learning. Reading, MA: Addison-Wesley, 1989.

[9] Holland, J. ,"Adaptation in Natural and Artificial Systems". University of Michigan Press, Ann Arbor, Michigan. 1975

[10] Sanghamitra Bandyopadhyay and Sankar K. Pal,"Pixel Classification Using Variable String Genetic Algorithms with Chromosome Differentiation", IEEE TRANSACTIONS ON GEOSCIENCE AND REMOTE SENSING, Vol. 39(2), pp. 303- 308, February 2001. Doi: 10.1109/36.905238

[11] Ting-Yu Lin, Kai-Chiuan Hsieh, and Hsin-Chun Huang, "Applying Genetic Algorithms for Multiradio Wireless Mesh Network Planning", IEEE TRANSACTIONS ON VEHICULAR TECHNOLOGY, Vol. 61(5), pp. 2256- 2270, JUNE 2012. Doi: 10.1109/TVT.2012.2191166

[12] I.Y. Kim, and O.L. de Weck, "Variable chromosome length genetic algorithm for progressive refinement in topology optimization", Springer Structural and Multidisciplinary Optimization Vol. 29 (6), pp. 445-456, 2005. Doi: 10.1007/s00158-004-0498-5.

[13] Jong-Bae Park, Young-Moon Park, Jong-Ryul Won, and Kwang Y. Lee, "An Improved Genetic Algorithm for Generation Expansion Planning", IEEE TRANSACTIONS ON POWER SYSTEMS, Vol. 15(3), pp. 916 - 922 , August 2000. Doi: 10.1109/59.871713

[14] Luis A. Gallego,Marcos J. Rider,Marina Lavorato, and Antonio Paldilha-Feltrin, "An Enhanced Genetic Algorithm to Solve the Static and Multistage Transmission Network Expansion Planning", Hindawi Publishing Corporation, Journal of Electrical and Computer Engineering, 2012, Article 12 pages. doi:10.1155/2012/781041

[15] James F. Frenzel, "Genetic Algorithms A new breed of optimization", IEEE potentials, pp. 21- 24, 1993

[16] [16] Brie, A. H., Morignot, P., Genetic Planning Using Variable Length Chromosomes. Proceedings of the 15th Internet Conference on Automated Planning and Scheduling, (ICAPS'05), USA, pp. 320- 329, 2005.

[17] J. Riquelme, M.A. Ridao, E.F. Camacho ,M. Toro, "Using Genetic Algorithm With Variable-length Individuals For Planning Two Manipulators Motion", 1997

[18] Ibraheem, N. A and Khan, R. Z., "Vision Based Gesture Recognition using Neural Networks Approaches: A Review", International Journal of Human Computer Interaction, vol. 3 (1), pp. 115-128, Malaysia, 2012.

[19] "Individual Aging Using Genetic Algorithms", proceeding of Australian new Zealand Conference on intelligent information systems, November, 1996.

[20] Burke, S Donald., De Jong, A. Keneth, Grefernstette, J. john, Ramsey, L. Connie, "Putting More Genetics into Genetic Algorithms", Evolutionary Computation, Vol. 6(4), pp. 387-410. 1998. Doi: 10.1162/evco.1998.6.4.387