

Genetic Shape Fitting for Hand Gesture Modeling and Feature Extraction using Variable Length Chromosome

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Abstract

In this work; one of the artificial intelligent approaches has been used for hand modeling and for latter stages of feature vector extracting and gesture recognition. The proposed system composed of five stages; hand shape modeling, locating palm center, extracting geometric parameters such as wrist and finger's reference points, determining fingers' base and tip, features vector extraction, and finally classification. We have applied an innovated approach for hand modeling using variable length chromosomes genetic algorithm to extract appearance based features and locating the palm center coordinate using GA with a decreasing population size. Afterwards; wrist and fingers' reference points are determined which will be the brace for figuring out finger base and fingertip which will contribute in the extraction of the important features required for classification purposes. In this work we considered the former three stages of the aforementioned ones. The experimental results of the adopted system appeal effective and promising results for features extraction, finger identification and gesture classification.

Keywords: Gesture, Genetic Algorithms, Variable Length Chromosome, Feature Extraction.

Introduction

A The aim behind gesture analyzing and understanding is to enhance the performance of human-machine interaction by imitating human-human interaction [1][2]. However, researchers describe two different classification methods for gesture analysis, these methods are: vision based analysis, and glove based analysis methods [3] [4]. Vision based methods considered simple, and more available since the user is not obligated to be connected to the computer [4][5]. Glove based methods demanded the user to wear special hardware device that have some sensors attached to hardware gloves, such devices are cyber glove [5][3] and [6] which are cumbersome [4] and restrict the degree of naturalness [4] besides the idea that wearing same glove by multiple users produce good environments for diseases infection and distribution [4]. However, vision based can be sub classified into appearance based and 3D model based [4]. Appearance based can be summarized by comparing the predefined and stored features of the trained image with the features extracted from the input image and calculate the degree of matching between these features [4], while 3D hand model utilizes joint angles along with their segments to extract hand features [4]. Recently g marker is appeared in this field in which the user wears some colored glove to easy hand detection and tracking process [4].

Different algorithms have been utilized for hand gesture modeling, in this work, we adopted genetic algorithm (GA) for hand gesture modeling since the GA has proved its efficiency for solving various computational problems.

Genetic Algorithms: an overview

Genetic algorithms (GAs) are randomized search optimization techniques [7] directed by the natural evolution and genetics principles [8][7][9][10]. GAs have gained attention for its efficient, robust and adaptive search process in solving large, and higher complexity problems [9] such as operations research, optimization, and combinatorial search problems [7][11] by producing results near to optimal solution

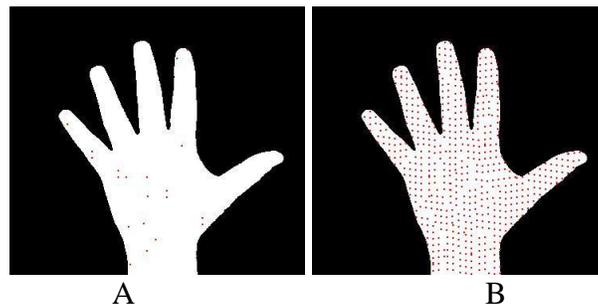
[7][11][9] using an implicit parallelism strategy [9]. GA nature is probabilistic [12] rather than other methods that are deterministic [12] which can produce different solutions for the same problem [7][12]. Goldberg [7] shows full description and complete explanation of GAs approaches.

Related Work

Stergiopoulou, E. and Papamarkos, N. [13] applied artificial intelligent approach for capturing hand shape using self-growing and self-organized neural gas, while Hasan M. and Mishra P.[4] applied statistical approaches for fitting hand shape using dynamic circular matching. Limited research work in the literatures that utilize GA with variable length chromosomes since it depends on the characteristics of the optimization problem. However, Kim and Kwak [11] proposed variable chromosome length genetic algorithm for two structural topology optimization problems: a short cantilever problem and a bridge problem. Horia and Morignot [14] describe a genetic planning system using variable length chromosomes model, the planning model is a type of STRIPS domains. Riquelme J. et al. [15] suggested genetic algorithms with variable length chromosomes to find the coordinated motion plans of two manipulator robots. Individuals are represented by an increasing synchronization path of coordinate's sequence.

Hand Shape Morphology Algorithm

The adopted Genetic Shape Fitting using Variable Length Chromosome (GSF_VLC) algorithm is used to capture full hand morphological representation by increasing the chromosome length gradually, and to decide the fitted length of chromosome. Fig. 1 shows a portray description of the adopted algorithm.



A) Best individual generated in the initial population. B) Best individual generated in the final generation.

Fig. 1. *Initial individual and final individual result for pixels distribution model.*

Chromosome and Gene Structure

Formally the chromosome is represented by a list of action genes [14] or Basic Element Circle (BEC) and each BEC is represented by two parameters; the position of x- and y-coordinate of a particular point, and the value of image intensity stored in the x, y coordinate. The generated BEC are checked at the instantiation time for achieving compatible stipulations of chromosome construction. The imposed conditions for newly generated BEC are:

- 1) Overlapping BEC: Checking for BEC points overlapping status, the randomly generated point overlaps with the already existed points. To avoid the overlapping case, each BEC should not infiltrate the area of another BEC.
- 2) Repetition BEC: Checking for BEC point's repetition status, in case of the randomly generated point is previously generated.
- 3) x- and y-coordinates intensity value: The value of the randomly generated BEC should be equal to one, to guarantee that the randomly generated point is in the hand area.

Fitness Function

To evaluate the suitability of an individual, two factors are considered; 1) the BEC overlapping factor, 2) the length of an individual. Let L_i be the individual length and o_i be its overlapping percentage for an individual i , the evaluated function can be expressed by the following function:

$$\text{Fitness}_i = F(g(L_i), h(o_i)) \quad (1)$$

Where $F, g,$ and h are appropriate functions normalized to lie in the range $[0, 1]$. The function g is selected to be monotonically increasing function [16] defined as:

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

Where \max and \min represent the maximum and minimum chromosome length. The function h is selected to be a decreasing function [16][17].

$$h(x) = \begin{cases} 1.0 & \text{if } x < c1 \\ 1 - \frac{x}{\text{Ovp}} & \text{if } c1 \leq x < c2 \\ 0.0 & \text{otherwise} \end{cases} \quad (3)$$

Where c represents the percentage of overlapped BEC genes in a particular individual, the range $[c1, c2]$ restricted the overlapped genes. Individual less than $c1$ considered as a perfect and fitted in that iteration [16]. Finally the function F can be modeled by combine $g(x)$ and $h(x)$ in a specific form:

$$F(a_i, b_i) = ((a_i \times \beta) + (b_i \times \alpha)) \quad (4)$$

Where β and α are constant values in the range $[0, 1]$, and the a_i equal $g(x)$ and b_i equal $h(x)$.

Initial Population with Variable chromosome length

The initial population scheme randomly generates chromosomes length confined in a specific range $[n, m]$ which represents the lower bound and upper bound of a uniformly distributed random number [18][15] respectively, with checking the constraints of newly generated BEC.

Selection and Crossover Operation

Tournament selection strategy and one-point uniform crossover has been used. In crossover process, two different cutting points are selected randomly from both parent chromosomes with range from $[1, \text{Length}-1]$ according to crossover probability P_c , as result of performing recombination process some genes will be a replicated copy from the parents, this problem is solved by removing them from the new offspring list.

Proposed Artificial Mutation

Our proposed mutation adds a fixed number into the four directions of each gene coordinates. According to the mutation probability P_m , generate four genes in four directions restricted with the radius R previously defined where R is an integer number equal to 5, and check the newly generated four genes if they satisfy the

predefined gene's. However, a predefined joining percent was used to determine the number of genes every time attached to current chromosome length. Figure 2 shows mutation steps.

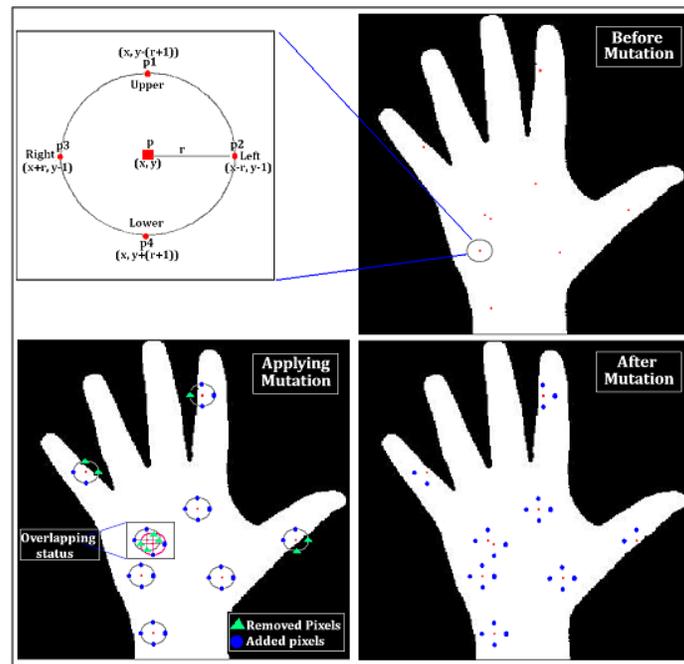


Fig. 2. Mutation operation steps.

Termination Criteria

An estimation number of pixels that should distribute over the segmented area is calculated by dividing the number of pixels in the white intensity of the segmented area by the circle circumference $C_{cir} = 2 \times r \times \pi$, the estimated number of pixels $Epixel_x$ can be computed by:

$$Epixel_x = \frac{P_{i_w}}{C_{cir}} \quad (5)$$

Where P_{i_w} is the number of white's intensity pixels. After each iteration checking for a significant convergence between the best solution length achieved and $Epixel_x$

Experimental Results

This section presents experimental results of applying the proposed GSH_VLC algorithm on a set of different segmented hand gesture images as shown in detail in figure 3 and figure 4. The database used contains 100 different hand images from two volunteers. Setting parameters of the tested image in Fig. 3 is demonstrated in Table I.

Locating Initial Palm Center

For locating the initial location palm center, Decreasing Population Size Genetic Algorithm (DPS_GA) algorithm have been suggested. Since the consequence of applying GSF_VLC algorithm is well arranged distributed points, DPS_GA algorithm bases on that points to extract the initial palm center. Figure 5 explains an example of palm center locating using DPS_GA algorithm.

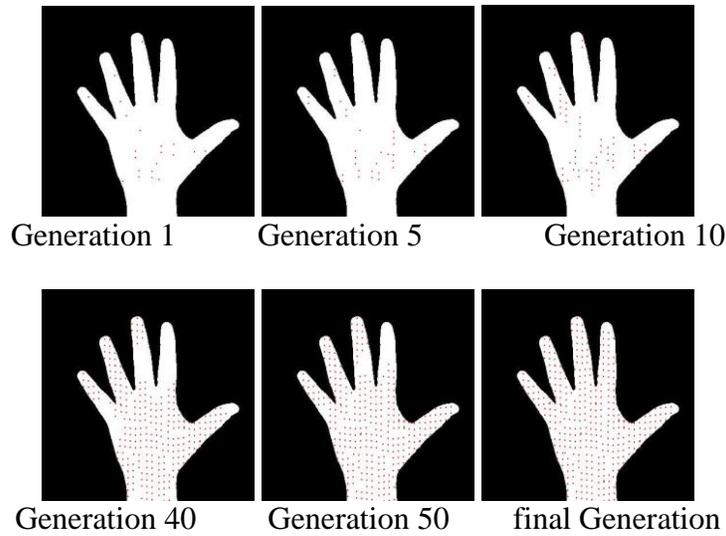


Fig. 3. Evolution stages of genetic pixels distribution through hand image.

TABLE I: PARAMETERS SETTING OF TESTED IMAGE IN FIG. 5.

Parameter	Setting
Population Size	10
Initial gene lengths	[5,20]
Generation	70
pc	0.6
pm	0.01
Diameter	18
Predicted Number of Pixels	601
Max length (number of pixels) reached	351
elitism factor, increment chromosome length	30%

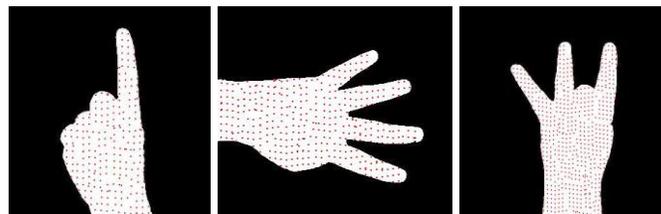
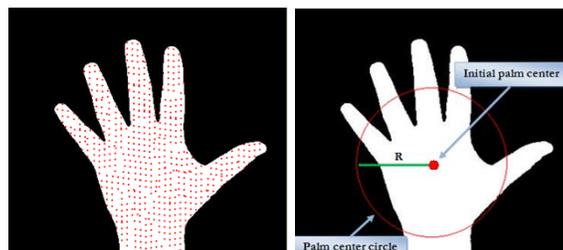


Fig. 4. Demonstration of GSH_VLC algorithm implementation.



A) The best individual length achieved in hand modeling algorithm. B) Locating the initial palm point with a circle that represents the maximum palm radius.

Fig. 5. *Locating initial palm center point*

Chromosome and Gene Structure

In GSF_VLC algorithm a candidate solution or a chromosome represents a hand gesture while in DPS_GA algorithm a candidate solution represent a single point (pixel) in the hand modeled by GSF_VLC algorithm. The optimal solution is represented by a single point which is consisting of a gene that describes x- and y-coordinates.

Algorithm Description

The algorithm starts by calculating the interior distances among the population points and assign a value to each point in the population, these distances are utilized in the evaluation of fitness function, depending on the fitness measurement of each point, the population size decreases with a predefined percentage. The new population size looped through various generations until only one point from the whole population is remained. Since we are concerned in minimizing the population size and stemmed on center point, GA operators' steps are skipped in this algorithm. Empirically determined, the diameter initial setup is $dim = 30$, and $initial\ population\ size = Best\ individual\ length$ achieved using GSF_VLC algorithm .

Calculation of Interior Population Distance

The average distance between each point in the population and the whole interior population points are calculated, in which each point has a different average length distance using Euclidean distance measure. This step is preliminary for computing each point's fitness function.

Fitness Function Evaluation

For fitness evaluation purposes, two aspects should be considered: 1) point's density this term refers to the number of pixels available inside the circle of each point per circle area, and 2) points' distance which relies of using the utility of calculating the average points' distance over the population size.

Let Np_c represent the number of points per individual point's circle and let C_{area} be circle area defined with R for an individual point p_i , then density function f_{dens} can be defined by:

$$f(p_i)_{dens} = \frac{Np_c}{C_{area}} \quad (6)$$

For the distance length function f_{dist} an increasing monotonically function [16] is selected to be expressed by the following formula:

$$f(p_i)_{dist} = \left\{ 1 - \frac{p_{i,dist} - min_{dist}}{max_{dist} - min_{dist}} \right. \quad (7)$$

Where $p_{i,dist}$ represents the distance length of a particular point p_i , min_{dist} and max_{dist} is the minimum and maximum distance length attained in a specific population.

The function F can be modeled by integrating $f(p_i)_{dens}$ and $f(p_i)_{dist}$ functions in a specific formula, and the fitness function can be defined by:

$$Fitness(p_i) = F(f(p_i)_{dens} + f(p_i)_{dist}) \quad (8)$$

Where $(p_i)_{dens}$, and $f(p_i)_{dist}$ functions are normalized to lie in the range [0, 1].

Termination Criteria

Two possible solutions are available in this case. Either by take the average of the remaining nominated points=N points so the palm initial center will be an estimated value from attending points in palm area, or let nominated points=1 and in this case only the survival point will represent the center of hand palm. However, after finalizing the center coordinates, the palm radius value is used to depict a circle using Bresenham circle drawing algorithm with the maximum diameter value achieved.

Implementation Results

The implementation results of applying DPS_GA algorithm is shown in Figure 6 with different samples of hand gestures along with the maximum radius that form palm center circle, the calculated palm center has been amendment in order to obtain (x, y) that fits in the middle of the hand palm.

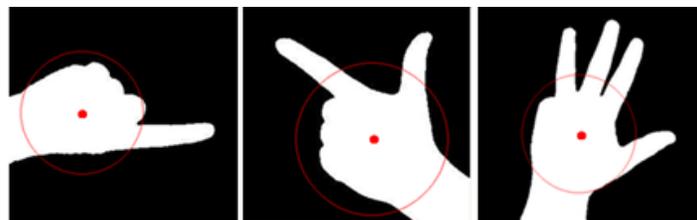


Fig. 6. Samples of initial palm center locating.

Extract Fingers and Wrist Reference Points

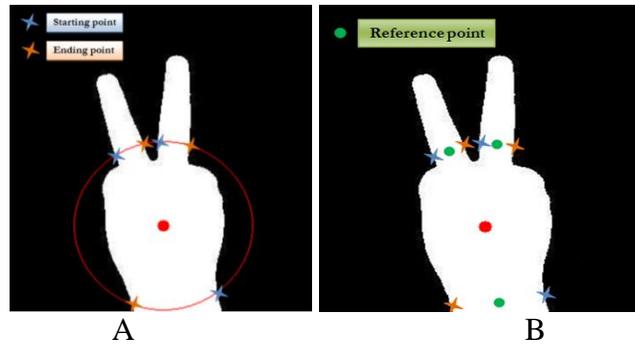
Fingers and Wrist Reference points Extraction (F_WRPE) algorithm proposed for locating fingers' reference points depends on the maximum R value attained during extraction final palm center.

The algorithm starts by tracing each pixel on palm center circle in a clockwise direction from 0o to 360o degree. F_WRPE algorithm steps are explained as follows:

- Step 1) Calculate each pixel value on the circumference that constitutes palm center circle.
- Step 2) Searching circle perimeter pixels for a black pixel which indicates a non wrist or fingers region is discovered yet and continue until the first white pixel are counted which represents a wrist or fingers region is discovered.
- Step 3) Mark this white pixel as the **StartPoint** of this area, and keep counting the white pixels over the circle circumference until a black pixel is counted which represents the finishing of a segmented region either wrist or fingers.
- Step 4) Mark this black pixel as the **EndPoint** of this area.
- Step 5) The process continues applying steps (3) - (5) until all pixels on circle perimeter are traced and stopping when the degree 360° is satisfied.
- Step 6) The resultant of this algorithm is the extraction of wrist area and fingers area by assigning border points represented by **StartPoint** and **EndPoint** for the wrist and fingers area.

To locate the wrist area, Euclidean distance used to measure the distance difference between the start point and end point of the segmented regions and the larger difference represents the wrist area.

Wrist and fingers reference points are locating by calculating the average point of the StartPoint and EndPoint of the extracted area. Practical example of applying F_WRPE algorithm steps is shown in Fig. 13.

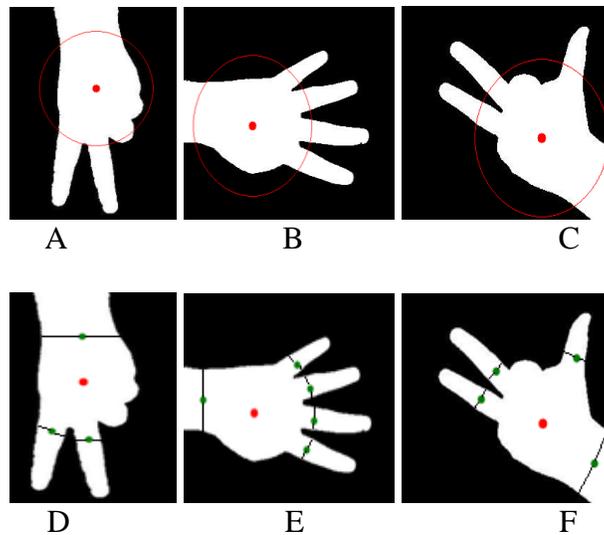


A) Assigning border point for the detected wrist and finger areas. B) Calculating the reference point corresponding to the border point.

Fig. 7. Applying F_WRPE algorithm.

Experimental Results

In this section an implementation results of applying F_WRPE algorithm for locating the wrist and fingers reference points is depicts in Figure 14.



A, B, C: represent the palm circle. D, E, F: the corresponding extracted reference points for each of A, B, and C respectively.

Fig. 8. Different samples explain the extracting of wrist and fingers reference points.

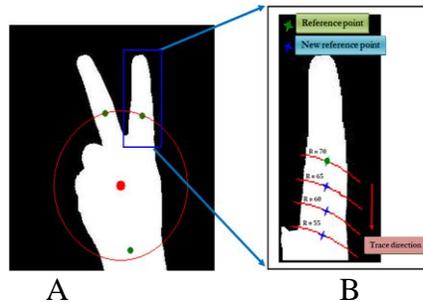
Extracting Fingers Parameters

To extract fingers parameters, two algorithms are suggested: Finger Base Detection (FBD) algorithm and FingerTip Detection (FTD) algorithm to specify finger base and tip respectively.

Finger Base Detection (FBD) Algorithm Description

The FBD algorithm utilizing the extracted finger border points along with the reference point. FBD algorithm can be summarized as follows : for each finger with the current R value, compute the slope of the line between the palm center and the StartPoint, and palm center with the EndPoint to calculate the distance of slope difference between the border points and generate the BaseDistance. The loop continues by

decreasing R and calculates the new border finger points for each R by tracing the left side and right side of the reference point. The loop stops when reached into an approximated distance of finger base. the approximated distance is estimated by applying some distance factor λ to the actual BaseDistance. empirically $\lambda=0.8$ of the actual distance, and R decrment by 50 degrees. Figure 15 depicts these steps.

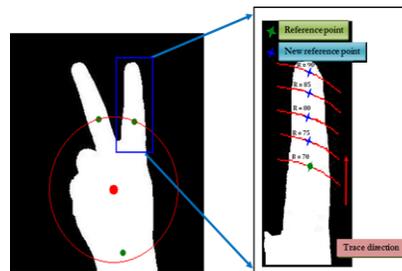


A) Hand with fingers after locating wrist and fingers reference points. B) Section part of the right finger to show the process of FBD algorithm. (Radius value here is estimated value close to real applied values.)

Fig. 9. *Overview of Fingers Bases Detection algorithm.*

Finger Tip Detection (FTD) Algorithm Description

This mechanism process of FTD algorithm is similar to FBD algorithm with slightly different in paramters settings which is the R value. Since the current algorithm trying to find out the fingertip, the R is increasing at each iteration explained in Figure 16.



A) Hand with fingers after locating wrist and fingers reference points. B) Section part of the right finger to show the process of FTD algorithm. (Radius value here is estimated value close to real applied values.)

Fig. 10. *Overview of Fingers Tips Detection algorithm.*

Experimental Results

Samples of applying FBD and FTD algorithms to extract fingers bases and fingertips are shown in Figure 17. The fingers are numbered from left to right.

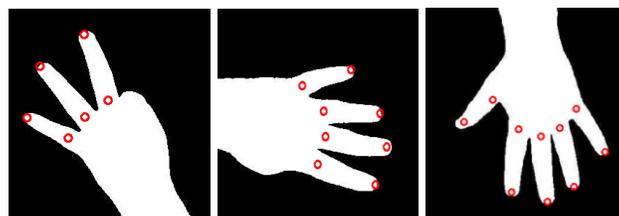


Fig. 11. *Extracting finger bases and fingertips.*

Conclusion and Future Work

In this work a novel algorithms have been adopted for modeling hand shape, calculating initial and final palm center, locating wrist and fingers reference points, and finally determining finger base and tip. The latter parameters are the promising finger characteristics towards extracting features vector. GA with variable length chromosome have utilized for shape fitting, the results are effective and dominant the segmented hand. in the future work, The extracted finger base and tip along with the palm center are used to extract two features. In which our aim is to represent a lot of characteristic with minimum size of the feature vector. Finally Gaussian classifier model is used for fingers classification and gesture recognition.

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