A Robust Method for Registration of Partially-Overlapped Range Images Using Genetic Algorithms

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Abstract*— Registration is a fundamental stage in the 3–D reconstruction process. We consider the problem of Euclidean alignment of two arbitrarily-oriented, partially-overlapped surfaces represented by measured point sets contaminated by noise and outliers. Given two approximately aligned range images of a real object, it is possible to carry out the registration of those images using numerous algorithms such as ICP. Basically the task is to match two or more images taken at different times, from different sensors, or from different viewpoints. In this paper, we discuss a number of possible approaches to the registration problem and propose a new method based on the manual pre-alignment of the range images of arbitrarily-oriented surfaces followed by an automatic registration process using a novel genetic optimization algorithm in 3–D data registration. Results for real range data are presented with precision and robustness, combined with the generality of genetic algorithms. This procedure focuses on the problem of obtaining the best correspondence between points through a robust search method between partially overlapped images.

***Index Terms*— 3–D reconstruction process, range images, registration**

I. INTRODUCTION

Reconstruction is the process whereby real objects are reproduced within computer memory. Physical characteristics such as dimension, volume, and shape are represented in digital form. The task of surface reconstruction of 3–D objects from range images covers several stages: acquisition, registration, integration, segmentation, and adjustment, which when they are combined, transform a set of partial images of the object into a complete 3–D model [1].

The misalignment that is unavoidably produced when two or more images have been taken from different views, and without any control of the relative positions of the sensor and the object, becomes the central problem of registration. The purpose of the registration process is to align these views in such a way that the object's shape is recovered with the highest precision.

During this process two situations become evident. First, it is not possible to determine which of the coordinate system points of one image matches with the correspondence points of another image. This is known as the matching problem, and is the most time-consuming stage during the execution of the algorithm. Second, a transformation is required in the three-dimensional information of one of the images regarding its coordinate system and its relationship to the image that was chosen as its reference.

The objective here is to adjust both images using common information between them. Because of the inexact nature of the data and the uncertainness of the common surfaces, the procedure to calculate this transformation is iterative and is guided by the strategies and metrics that a particular algorithm uses. Due to this, the registration process is one of the slowest and most delicate stages in the process of 3–D reconstruction. The quality of the alignment process determines the quality of the model that will be obtained.

Since 1992, with the appearance of the ICP algorithm (Iterative Closest Point) [2], there are many variants which have appeared to mitigate the deficiencies of this method. This algorithm states a basic scheme for the obtention of the alignment, by minimizing a cost function based in the sum of the square of the distances between the points of the images; the basic procedures involves the features' identification, matching of corresponding features and the alignment of these correspondences by means of the evaluation of a metric for the error [2], [3]. This method is composed of two basic procedures: The first one is to find the correspondent points and the second one, to estimate iteratively the transformations for these points until satisfy a precision level.

Another approach for the registration of images consists in determining a set of correspondences through of a process of points correspondence searching, instead of the classical approach, based in distance. The approach based in searching presents several advantages against the distance based method, for instance: It does not require a fine pre-alignment, the data set of the image to be registered has not to be a subset of the reference image and besides, because it does not perform a combinatory exploration, guided through a domain created from the neighbors which are located around the point on the image to be registered, what permits to obtain a better correspondence between data.

In a general way, the approach based in searching consists in finding a solution near to the global minimum in a reasonable time and a way to perform this searching is by means of genetic algorithms (GA).

The Genetic Algorithms are computational method based in the natural evolution, in which, a population of individuals which represent a possible solution is evolved through a

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succession of cycles of selection, reproduction, mutation and replacement until finding the desired solution [4].

In this paper, we show a procedure based on a Genetic Algorithm for the registration of a pre-aligned image pair. This procedure focuses on the problem of obtaining the best match between points through a robust search method on images that are partially overlapped. This set of matches allows the calculation of transformation which precisely registers the images.

This paper is organized as follows: Section 2 presents a literature review. Section 3 describes the methodology used to do the registration of a pre-aligned image pair using a Genetic Algorithm. Section 4 presents realized experiments, and in Section 5, the conclusions of this work are presented.

II. ICP ALGORITHM (Iterative Closets Point).

A set of points is moved in a rigid way, in such a way they be aligned in the best possible way with the corresponding CAD model, through the following iterative procedure:

1. In the first iteration step, for every point of the image to be registered $X = (x_1; x_2; : : : ; x_n)$, it is calculated the nearest point to the reference image $Y = (y_1; y_2; : : : ; y_n)$, where every point x_i corresponds to the point y_i. This is the part of the algorithm which is more time consuming. As the first step result, it is obtained a sequence of the nearest points of the reference image corresponding with the sampled points on the image to be registered.
2. In the second step of every iteration, the rigid movement M is calculated in such a way that the transformed data points $M(x_i)$ be the nearest to its corresponding points y_i, where the target function to be minimized is:

   $$\sum_{i=1}^{n} \left\| y_i - M(x_i) \right\|^2$$

   This least squares problem can be solved explicitly. The translational part of M brings the mass center of X onto the mass center of Y. The rotational part of M can be obtained as the unitary eigenvector corresponding to the maximum eigenvalue of a symmetrical matrix $4x4$. The solution eigenvector is not more that the unitary quaternion of the rotational part of M.
3. In the third step, the positions of the data points are updated through $X_{new} = M(X_{old})$.

Now, the steps 1 and 2 are repeated, using the data of the updated points, while the change on the mean square error is kept under a pre-selected threshold. The ICP algorithm always converges monotonically at a local minimum, because of the value of the target function is always decremented in the steps 1 and 2. In a general way, the classical ICP can be seen in the algorithm 3.1.

```
Registration ICP()
begin
  while $Error < E_{MAX}$ do
      1.   Sampling Images
      2.   Matching Selection
      3.   Matching Rejection
      4.   Calculation of the Transformed
  end
end
```

Algorithm 3.1. Classical ICP.

III. MATCHING METHOD OF RANGE IMAGES USING A GENETIC ALGORITHM (ICP+GA)

The literature review about the problematic of registration reveals the numerous attempts to solve that problem. Among them, the ICP algorithm has an outstanding place, in spite of its serious limitations. Another approach to register to range images, is finding the geometrical transformation through a searching space, more than the searching based on correspondences of the methods based on ICP. In these case, the goal is finding a searching space of geometrical transformations, a solution which can be used to align precisely two views. A reasonable way to perform this searching is through the use of stochastic optimization techniques such as Genetic Algorithms. This approximation generally is considered to provide thick registration. However, several operators can be combined, such as heuristic local searching's, to obtain precise alignments during the convergence process.

The searching of precise alignments is a problem that can be approach from the view point of the optimization. The genetic algorithms are one of the recent tools that permit to find solutions by means of the searching in big spaces. The general principle of a genetic algorithm is to summit to a evolution process to a individuals population codified as chromosomes, which represent possible solutions of a searching problem. During the evolution, every individual is assigned with a fitness value obtained form a specifically defined function for the problem being solved. This function, called fitness function must be designed in such a way that favor to the most suitable as the solution of the problem. The assigned fitness to every individual is kept in mind to select the progenitors to participate in the reproduction process, which consists in interchange the genetic material contained in a couple of selected individuals to generate two new individuals or two new possible solutions of the problem, which, according to a mechanism of replacement, are incorporated into the population. The new descendent individuals are besides subjected to a mutation process, which consists in a random perturbation of its genetic material, with the objective of giving variability and to enrich the exploration of the possible solutions of the problem represented as chromosomes. Finally, after a determined number of fitness assignment, reproduction, mutation and replacement cycles, called generations, the best solution of the problem is chosen, that is to say, the individual with best fitness.

Brunnstrom and Stoddart [4] proposed a method that integrates the classical ICP method with a genetic algorithm to couple free form surfaces. Here an alignment is obtained with a genetic algorithm, which is later refined with the ICP. The main problem treated by Brunnstrom and Stoddart is to find a corresponding set of points between the two views. For it, dense samples are taken on both views and proceeding to perform the searching with a genetic algorithm that associates points between views, guided by the fitness function that goes counting the number of good correspondences using the invariants of translation and rotation, such as the relative orientation of the normal surfaces and the relative distance between points. In this thesis a chromosome represents a point assignation on both views.

Robertson and Fisher [5] proposed a parallel genetic algorithm which reduces the computational time, but its solution is not more accurate than the ones obtained with the first method. In this proposal, the individuals of a population are vectors formed by six parameters, which represent a transformation.

Silva *et al*. [6] proposed a method for the registration of range images, making two key contributions: The hybridization of a genetic algorithm with the heuristic optimization method of hill climbing, and a measurement of the performance of the interpretation of the surfaces different to the classical metric, based on the calculation of the mean square error between corresponding points on the two images after the registration. The performance measurement proposed in this work, consists in calculating the fraction of points that stay overlapped in the view A and in the view B after the registration. This method is specialized in searching the parameters of a transformation formed by six values, three parameters of rotation, and three parameters of translation.

Yamany *et al*. [7] used a genetic algorithm for registration of partially overlapped 2–D and 3–D data by minimizing the mean square error cost function. The method is made suitable for registration of partially Overlapped data sets by only considering the points such that $p_i \in S_1 \mathrm{~U~} S_2$, where S_1 and S_2 are space bounding sets for the two data-sets. Unfortunately, the authors give very few details about their genetic algorithm, focusing on the Grid Closest Point transformation they use to find the nearest neighbor.

Salomon *et al*. [8] apply a so-called differential evolution algorithm to medical 3–D image registration. Differential evolution uses real-valued representation and operates directly on the parameter vector to be optimized.

A recent survey about usage of genetic algorithms for range data registration was presented by Chow *et al.* [9]. For handling partially overlapped data, the media of the remainders is used as an error metric. This improves the robustness, but turns un-applicable the method when the overlapping is under 50%. An advanced dynamic operator of mutation is introduced, what improves the registration error, and helps to avoid early convergence. A trying to improve the precision is done, using dynamic borders. When the genetic algorithm has converged, the searching space is reduced, and the genetic algorithm is applied again.

It is difficult to compare the different algorithms. Every researcher uses a different image base, which makes it very difficult to compare results due to the different metrics each employs.

Sometimes, the strategy to pre-align the images can guide the process to a convergence which obtains an erroneous solution. As well, the strategies that exhaustively explore the space correspondences and transformations are computationally expensive. Although a reject may be made of the erroneous couples, this is not an adequate parameter to guarantee an adequate adjustment. Evaluation of the accuracy of the adjustment is another item that requires attention. It is the easiest way to compare the obtained model with another model, synthetic or real.

Another topic that aspects the performance of the method is the images' size. Modern scanners can offer elevated resolutions because the density of information of the images is high. Because of this, many sub-scanning strategies are proposed to reduce the number of corresponding points to guide the registration, the uniform random scanning, and the uniform scanning of the normals [10]. An-other consideration in the registration problem are the rejection rules.

These are many strategies to clean the matches, discarding the ones that are incorrect. One of the main rules is the exclusion of points at the boundaries. Its application is inexpensive and excluded regions are not overlapped. The parametric method offers advantages related to convergence speed and minimization to reach superior levels of accuracy. Therefore, it must be considered that the combination of parametric minimization methods form an acceptable registration.

Genetic algorithms have been previously applied to the registration problem; however, the complexity of the space search has become a major challenge. A proposal to use genetic algorithms in the registration problem of two views of approximately aligned range images is presented and described. This proposal is based on searching a set of points that when taken as entrance to Horn's method [11], a very good transformation is obtained that allows the integration of images with a very small margin of error. The algorithm 3.2 shows a general diagram of the proposed method.

In the following paragraphs it will be explained in detail each one of the stages that compose the proposed method.

```
ICP+GA Registration()
begin
    1. Pre-aligment and obtention of the overlapping area
    2. Points sampling
    3. Sub-domain determination
    4. Matching optimization by means of GA
end
```

Algorithm 3.2. Proposed Method for the registration of range images partially overlapped using genetic algorithms (GA).

A. *Pre-alignment and Obtaining of the Overlapped area*

Generally, as initial stage of the registration process, a previous process is required, which permits to find a global solution for range image registration. That is due to the fact that different types of acquisition devices generate partial images of the objects within different coordinates system. The coordinates system are altered due to occlusion problem in regions which are difficult to scan, or in objects of big size, when it is necessary to move to acquisition device. The reference coordinates systems in every image can be altered in terms of translation, rotation or a combination of both, however, the scaled parameter generally is not altered between partial samples, and is not considered a problem of the registration.

Because is possible to find images whose coordinates system different significantly, the proposed method requires an initial pre-alignment of the images. Usually, the performed works in registration of range images do not considers explicitly a pre-alignment stage, that to say, it is assumed that the images are close enough, or that the initial position of the views does not affect the registration process. The pre-alignment of the views improves the convergence time of the method, and warranties to find an adequate solution for the registration of images. Without a pre-alignment process, the registration method could take an excessive time to find the solution, or they could not find it. For example, the traditional registration method ICP, requires that the images be close enough to warranty the convergence. The problem of automatic pre-alignment is a research topic within registration, called thick registration, which tries to get the images close enough so that a fine registration method works rightly.

Once the image set has been pre-aligned, is possible to calculate a common area between two images (*A* y *B*). This area between the images is called overlapped area. The overlapped area consists in the set of pair points which have a distance lower that a threshold λ:

$$AB = \{(a_i b_l, a_k b_l, \ldots, a_p b_q) / i, k, \ldots, p \in I_A \wedge j, l, \ldots, q \in I_B\}$$

where I_A, I_B are the set of indexes of points in each one of the images *A* y *B* respectively, a_i is the closest point to b_j, this is, $Dist(a_i, b_j) = Min(Dist(a_r, b_j))/r \in I_A$.

The overlapped areas are necessary in the process of registration due to this ones are taken as reference to perform a right alignment. That is to say, every registration method searches, in general, to match rightly the overlapped area of the images. The overlapped area constitute the most important reference parameter in the registration process, and the adequate matches are searched on, therefore, on pairs of view which does not exist overlapped area is not possible to perform a right registration of the images.

B. Points Sampling

Given two images of ranges *A* and *B* where *A* is the image model and *B* is the image to be registered, it is a random selected set of *N* points that belongs to the overlapped area in *B* and establishes, for each one of them, a subset of points or sub-domain in *A*. The sub-domains contain m points near the closest point in *A* for each point in *B*. This approach of sub-domains reduces the space search and betters the global efficiency of the algorithm. The establishment of the domains has a critical computational step; that is, searching the closest point in *A* to each one of the points of the selected sample in *B*. Because this implies both calculating and comparing the distances to all the points which make up the overlapped area in *A*. Such a search is improved by implementing a K-d tree structure.

C. Sub-domain Determination

The division of the searching space into sub-domains, reduces the computational cost to find the right matching point of a selected point on the reference image. However, is not possible to warranty that inside the searching space of every sub-domains such point exists.

The probability of existence of a solution within every domain augments in relationship with the size of this. Thus, if every sub-domain has the size of the available points cloud, the probability to find the solution is 100% (See Figure 1).

The sub-domains are formed by the set of points P_i, in such a way that for every sample, $i \in B$, $P_i = (a_i, a_j, \ldots, a_k) / i, j, \ldots, k \in I_A$ and constitute a set of near points, circularly symmetric, this is, $Dist(\{a_i, a_j, \ldots, a_k\}, b_i) < \beta$, where β is the neighborhood radius, and I_A is the index of the points on the image.

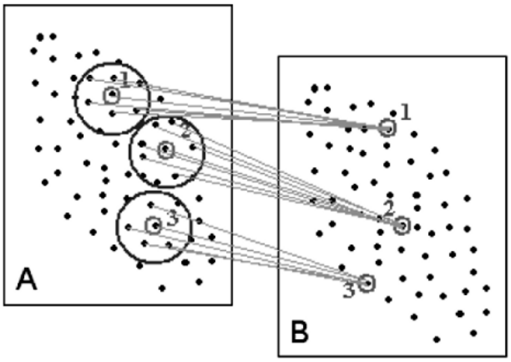

Fig. 1. Sub-domains determination.

D. Matching Optimization by Means of GA

The genetic algorithms constitute an adequate tool to solve the optimization problem due to its implicit parallelism in the searching, its ability to find and keep multiple optimal in every generation of the evolution and its ability to optimize non derivable criteria. In general, the GA codify every possible solution in individuals by means of representation schema; for every individual, it is estimated a fitness function which suggests the level of quality of the implicit solution within the individual. For every generation, every individual is evolved by means of the application of genetic operators as crossing and mutation. As it was stated previously, given two range images *A* and *B*, where *A* is the reference image and *B* is the image to be registered, the searching of the best points on *A* which couple with a points sample selected on *B*, is done by a genetic algorithm, which is composed by three elements: the representation scheme, the fitness function and the configuration of the genetic operators.

Representation scheme. It is represented as a chromosome of size N, that is, to each one of the points of the selected samples in view B there is a corresponding gene of the chromosome. Each gene contains an index that identifies a point within the neighborhood corresponding to a point as defined in view A. Figure 2 illustrates this representation.

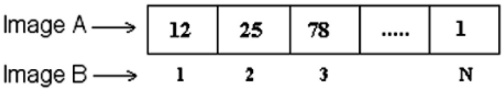

Fig. 2. Representation scheme of a chromosome.

Gene 1 corresponds to the first point of the sample, whereas gene 2 corresponds to the second point of the sample and subsequently to the *N−th* point of the sample taken in view *B*. For instance, in Figure 2 gene 1 contains value 12, which means that point 12 is found within the sub-domain corresponding to the first point of the sample in *B*. Twenty-five (25) is an index of a point-from-view *A* that belongs to a neighborhood of points close to point 2 of the sample taken in view *B*. Each point of the sample taken in view *B* has a defined neighborhood of points in view *A* from which the respective gene will take values.

Aptitude function. The aptitude function measures the average error between the points of the overlapped areas originating in the registration of the views. Each individual can be seen as a set of points with their respective couples translated into a transformation by Horn's method. The transformation is applied to the two views and the average error of this registration is assigned as the aptitude of an individual. The more accurate the individual, the smaller the error:

$$\varepsilon = \sqrt{\frac{\sum_{i=1}^{N}(P_i - R_i)^2}{N}}$$

Parameter P denotes each point in the overlapped area in view A obtained by applying each transformation. Parameter R is each point in the overlapped area in view B after applying the transformation.

Genetic operators. The proposal presented for a two-view registration applies a simple cross with only one cut point, in which the parents' genetic content is exchanged on each side of the cut point in order to generate two new (See Figure 3). In turn, the mutation operator varies the information of each gene according to the mutation probability, taking into account the defined neighborhoods for each point represented. That is, if gene i represents the i-th value of the sample taken in view B, and it has to be mutated, a respective point in the defined neighborhood is selected at random in view A, and it is changed by the former value.

The sampling of N points of view B, is only performed once during the whole of the genetic algorithm, what means that the genetic algorithm is specialized in the searching of points that get the best coupling with the selected sample. The pre alignment of the images permits to reduce the searching space for this procedure.

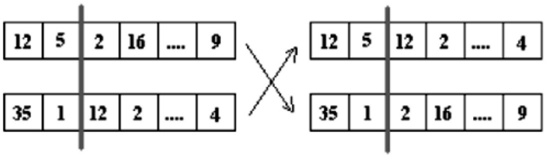

Fig. 3. Cross with a single cut point.

IV. EXPERIMENTS AND RESULTS

The procedure of optimization of the matching by means of GA, is validated with a set of tests, to demonstrate the effectiveness of the proposed method (ICP+GA), which correspond to: Analysis of the convergence of the error and the time, front to the methods ICP and ICP+N. Finally, it is demonstrated the robustness of the proposed method, with respect to the initial alignment of a pair of range images, front to ICP and ICP+N, by means of one intensive experimental test.

Comparison of the error and time convergence. This experiment consists in measuring the convergence of error and time for the registration of range image pairs of a scanned real object which serves as reference for the registration process. The error convergence test was executed fixing the error threshold at 1x10E-3 y 1x10E-6 and running the method iteratively until it converges. The results show that as for all the tests, the proposed method converges in less number of iterations (see Tables 1 y 2).

Table 2. *Convergence for 1x10E-3.*

Test	Iterations			Time (seconds)		
	ICP	ICP+N	ICP+GA	ICP	ICP+N	ICP+GA
Test 1	13	12	9	3.125	7.327	180.325
Test 2	17	15	11	6.325	15.327	235.235
Test 3	17	15	11	5.325	13.254	210.254

Table 3. *Convergence for 1x10E-6.*

Test	Iterations			Time (seconds)		
	ICP	ICP+N	ICP+GA	ICP	ICP+N	ICP+GA
Test 1	15	14	13	5.125	7.327	235.658
Test 2	21	15	13	8.251	19.325	220.325
Test 3	18	16	13	6.016	18.327	345.658

Analysis of the robustness of the method proposed with respect to the initial alignment. The test consists in the average of a set of 30 registrations of pairs of range images with different initial alignments. For each pair of images, the image to register is rotated each 5°, from 10° to 70° (see Figure 4). The images were registered with methods ICP, ICP+N and ICP+GA, and it were calculated the averages of these results for each angle.

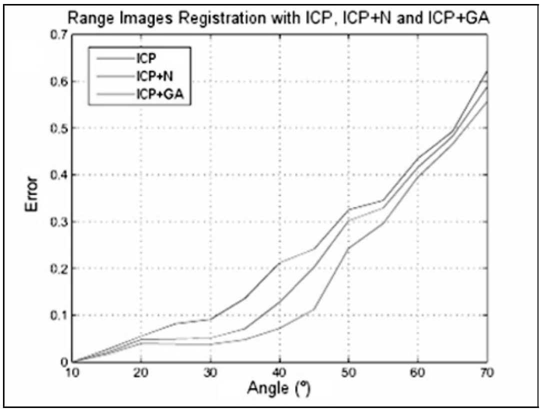

Fig. 4. Errors average of Registration with ICP, ICP+N and ICP+GA.

Figure 5 shows the difference of the errors average of the method ICP+GA with respect to methods ICP and ICP+N. the robustness of the method ICP+GA, it can be seen in the interval 20° to 55°, since this is able to generate registries with higher levels of precision. With reference to method ICP, the ICP+GA obtains the maximum difference in the improvement of the error in angles near 40°. On the other hand, with respect to method ICP+N, the maximum difference is in the angles near 45°. The difference from these angles, begins to decrease until 55°, from which, the errors obtained by the three methods are similar.

The analysis of the test of the differences of errors average made in this experiment, to demonstrate the robustness of the method proposed for registration of partially-overlapped range images using genetic algorithms, is validated statistically by means of the method of the confidence region.

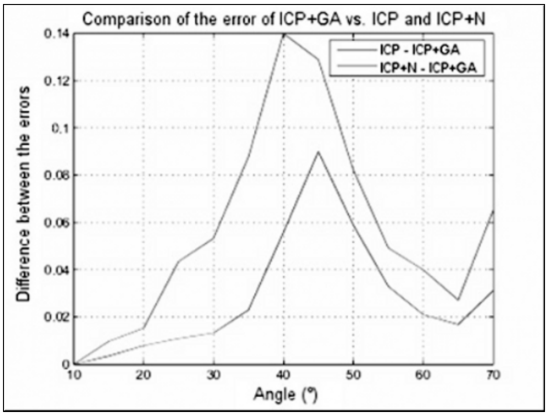

Fig. 5. Difference of the errors average of ICP+GA vs ICP and ICP+N.

Complete registration. The registration process is carried out registering each one of the images with the fusion of the previously registered images. The Figure 6 shows the sequence of the registration process that one obtains for each image of the object mask. Finally the registered object is shown in the Figure 6(f).

In all the cases a smaller registration error was obtained with the model GA (Error average = 0.1011), front to the ICP (Error average = 0.1196) and the ICP+N (Error average = 0.1104).

However, the differences of time between the ICP and ICP+N and the ICP+GA, it is significant for these tests in those that the images contain 35000 points on the average. The ICP and ICP+N methods, took on the average 1.5 minutes, to register each pair of views, while, the method ICP+GA, takes on the average 7 minutes for each pair of views.

V. CONCLUSIONS AND FUTURE WORK

A semi-automatic method has been proposed for the registration of multiple view range images with low overlap that is capable of finding an adequate registration without needing a fine preliminary pre-alignment of the images. This method is based on a genetic algorithm to perform a query of the best correspondence between a set of sample points, starting from an approach based on sub-domains that reduces the space search of the genetic algorithm which implies global algorithm efficiency.

The results obtained by means of the different made experiments, showed that the proposed method, converges to one better solution than methods ICP and ICP+N. The proposed method is more robust than ICP and ICP+N, with respect to the error, when the images to register have an initial alignment with rotation angles among 20° and 55°, which allows to register images without pre-alignment detailed. However, the proposed method uses more computational time in finding the solution.

For future work, the exploration of a parallel version to reduce the computational cost of the proposed method is suggested.

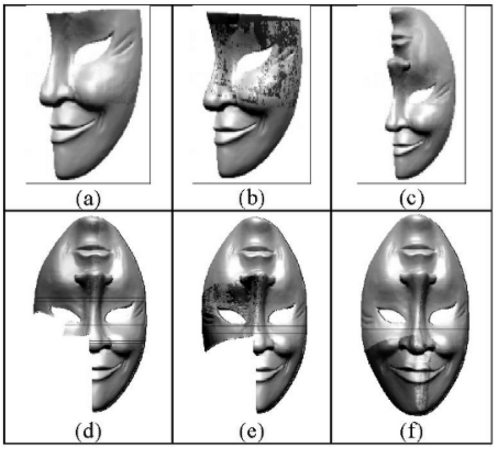

Fig. 6. Registration of the Mask with the ICP+GA method.

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