

Robust Three-Dimensional Registration of Range Images Using a New Genetic Algorithm

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Abstract. 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. Registration is a fundamental stage in a 3D reconstruction process. Basically the task is to match two or more images taken in 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 images followed by an automatic registration process using a novel genetic optimization algorithm. Results for real range data are presented. This procedure focuses, on the problem of obtaining the best correspondence between points through a robust search method between partially overlapped images.

Keywords: Registration, range image, ICP algorithm, normal, genetic algorithm.

1 Introduction

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.

For a little more than one decade, with the introduction of the ICP Algorithm [1] there have been many variations to mitigate its deficiencies. This algorithm formulated a basic schema to obtain the alignment while minimizing the cost function and is based on the squares summation of the distance between points on the image.

Another approach to the registration of images consists of determining a set of matches through a search process instead of the classical approach based on distances. This approach consists in finding a solution close to the global minimum in a reasonable time. This can be done by means of a Genetic Algorithm (GA).

We propose 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 images pair using a Genetic Algorithm. Section 4 presents experiments realized, and in the Section 5, the conclusions of this work are presented.

2 Literature Review

Genetic algorithms have already been used for registration of 3D data. In their recent survey on genetic algorithms in computer-aided design [2], Renner and Ek'art mention a few related studies. In particular, Brunnstrom and Stoddart [3] 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. Robertson and Fisher [4] 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. Silva et al [5] 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 from the classical metric, based on the calculation of the mean square error between corresponding points on the two images after the registration. Yamany et al. [6] used a genetic algorithm for registration of partially overlapping 2D and 3D data by minimising the mean square error cost function. The method is made suitable for registration of partially overlapping data sets by only considering the points such that $p_i \in G_1 \cup G_2$, where G_1 and G_2 are space bounding sets for the two datasets. Unfortunately, the authors give very few details about their genetic algorithm, focusing on the Grid Closest Point transformation they use to find the nearest neighbour. Salomon et al. [7] apply a so-called differential evolution algorithm to medical 3D image registration. Differential evolution uses real-valued representation and operates directly on the parameter vector to be optimised. Otherwise, only the reproduction step is different from GA. On the other hand, this method requires much more computation than the simpler algorithm we use. In [7], differential evolution is used to register two roughly pre-aligned volumetric images of small size. The relative rotation is within $\pm 20^\circ$, which is comparable to the range our TrICP can already cope with. We need and propose a preregistration algorithm that can cope with arbitrary orientations.

A recent study on the use of genetic algorithms for range data registration appeared in [8]. Euclidean parameter space optimization is considered. To handle partially overlapping data, the median of the residuals is used as error metric. This improves the robustness but renders the method inapplicable to data overlaps below 50%. An advanced operator of dynamic mutation is introduced, which reportedly improves registration error and helps avoid premature convergence. An attempt is made to improve the precision by using dynamic boundaries. After the GA has converged, the

search space is reduced and the GA is applied again. However, using genetic algorithms for precise registration does not seem reasonable since faster and more precise iterative methods exist for registration of pre-aligned datasets.

3 Registration of a Pre-alignment Image Pairs to a 3D Surface Model Using Genetic Algorithms

The views to be registered are pre-aligned in order to obtain an initial overlapping area in both images. As it can be seen in Figure 1 the following steps for each point of sample size N taken in the overlapping area of one of the views, has a correspondent point that is searched for around the nearest points of the other view to be registered. This search is done because the best couple of points to obtain a transformation using Horn's method [9] are not always the points with less distance within an overlapping area. Two views could be badly aligned and present points with very short distances; however when joining the views using these points as a guide, their registration could be off. The initially pre-aligned images could be askew and the correspondent points with which the views would match best when applying a transformation, could be very close to the points with a minimum distance.

Given two images of ranges A and B where A is the image model and B is the image to be registered, searching the best points in A that match with a sample of points selected in B, is done by a genetic algorithm. The design is as follows.

3.1 Sampling

It is a random selection 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 better 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 overlapping area in A. Such a search is improved by implementing a K-d tree structure. Figure 1 graphically shows the establishment of a sub-domain.

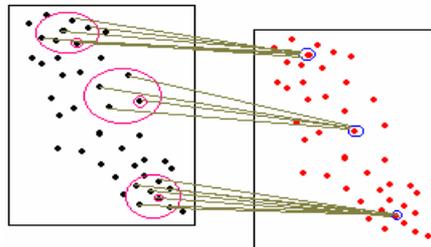


Fig. 1. Establishment of sub-domains, a) view A, b) view B

3.2 Diagram of Representation

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.

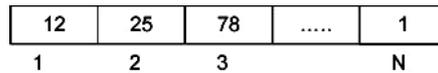


Fig. 2. Diagram of representation of a chromosome

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.

3.3 Aptitude Function

The aptitude function measures the standard deviation of the distribution of the distances between the points of the overlapping 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 standard deviation of this registration is assigned as the aptitude of an individual. The more accurate the individual, the smaller the error (1):

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

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

3.4 Genetic Operators

The proposal presented for a two-view registration applies a simple cross with only one crossing point, in which the parents' genetic content is exchanged on each side of the crossing point in order to generate two new individuals. 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.

4 Experiments and Results

All tests were performed using a computer with a 3.0G Intel processor and 1.0G RAM memory, running under the Microsoft XP operating system. The program was written in C++ and using Open GL to obtain the graphic representation of images. The data used were obtained using a Kreon sensor located at the Advanced Man-Machine Interface Laboratory at the University of Alberta, Canada.

The least average results were obtained with a 40% probability for the crossing operator and a 70% probability for the mutation operator. The size of the population was established to be 100 individuals, each one of which is formed by 10 pairs of points. Due to the fact that the GA model works on a specific problem, in order to find the best relationship between points that allows a transformation that correctly registers a pair of images with the objective of validating the correct performance of the methods ICP, ICP+Normals [10] and ICP+GA (See Figure 3), tests were performed to assure a point-to-point correspondence between the images, guaranteeing the existence of a unique solution to the problem. The convergence test was carried out fixing an error and running the method iteratively until it reached a convergence of 1×10^{-6} . The results of these experiments showed that the ICP+GA method converges more quickly as it is observed in the Figures 4 and 5.

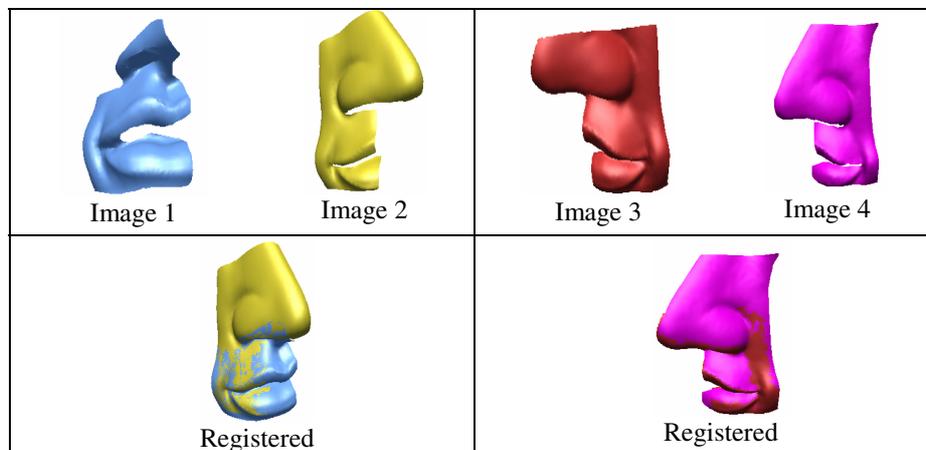


Fig. 3. Sample images 1 to 4 and their corresponding registration

Tests were made to compare the methods in the quality of the final registration using bad and good pre-alignments as benchmarks. The objective was to even measure the behavior of convergence of the methods when the images were rotated into their correct positions. Each test was carried out, keeping in mind that although

the were sufficiently rotated as to considered the pre-alignment like bad, there was no translation because of the neighborhoods of searches were constructed based on measures of Euclidean distance. In order to generalize the behavior in the final values of the registration were carried out 20 registrations with similar conditions of bad pre-alignment. Although, in some cases the methods not obtain values significantly different, one can observe that in general the method ICP +GA obtains the smallest error values that the other methods.

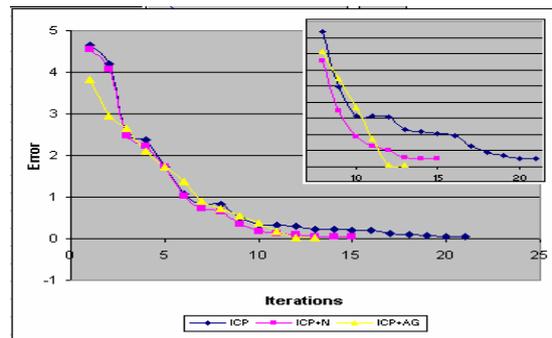


Fig. 4. Convergence Test 2 of the methods (Convergence= 1×10^{-6}) with images 1 and 2. (ICP = 21, ICP+N= 15, ICP+AG=13 iterations)

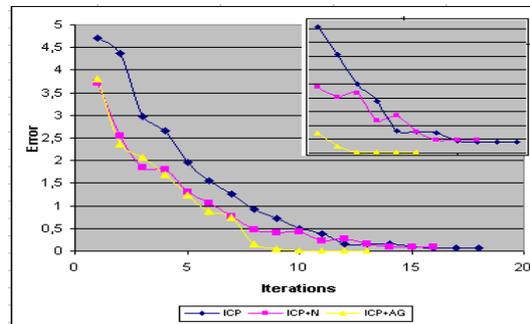


Fig. 5. Convergence Test 3 of the methods (Convergence= 1×10^{-6}) with images 3 and 4. (ICP = 18, ICP+N= 16, ICP+AG=13 iterations)

Additionally, the robustness of the method was proven, as it determined the maximum value of the angle for which the different methods converged in a good registration. Figure 6 shows the errors for different registrations with the variations in angles of each coordinate. The different methods obtain a correct registration for angles less than 40 degrees. For these cases the ICP+AG always produces the best registration. For angles greater than 40 degrees, the traditional methods present a significant increase in the error and we consider that it is not possible to reach a

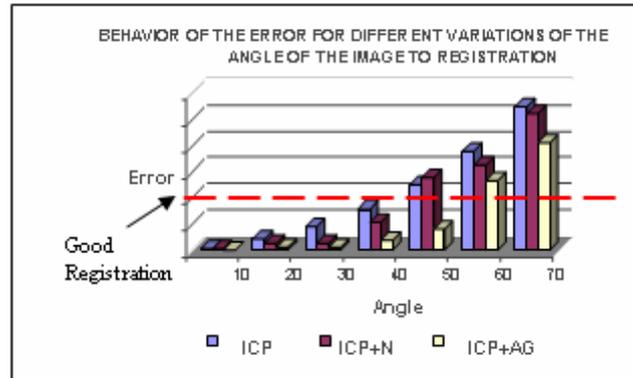


Fig. 6. Error of registration for different uniform variations in the angle. Dashed line shows the good pre-alignment limit.

correct registration for angles greater than 40 degrees. However the ICP+AG provide a good registration up to 50 degrees. Although the error continues to decrease after that point when using the other methods, there still is not correct registration.

5 Conclusions and Future Work

A semiautomatic 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 search 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 comparison of the results obtained through the different experiments shows a more precise convergence (using proposed method (ICP+GA) than the classical ICP method and one of its variants (ICP+Normals) can provide. However, the proposed method takes more computational time to find the solution.

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

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