

# Matching Contours in Images through the use of Curvature, Distance to Centroid and Global Optimization with Order-Preserving Constraint

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**Abstract:** This paper presents a new methodology to establish the best global match of objects' contours in images. The first step is the extraction of the sets of ordered points that define the objects' contours. Then, by using the curvature value and its distance to the corresponded centroid for each point, an affinity matrix is built. This matrix contains information of the cost for all possible matches between the two sets of ordered points. Then, to determine the desired one-to-one global matching, an assignment algorithm based on dynamic programming is used. This algorithm establishes the global matching of the minimum global cost that preserves the circular order of the contours' points. Additionally, a methodology to estimate the similarity transformation that best aligns the matched contours is also presented. This methodology uses the matching information which was previously obtained, in addition to a statistical process to estimate the parameters of the similarity transformation in question. In order to validate the proposed matching methodology, its results are compared to those obtained by the geometric modeling approach proposed by Shapiro and Brady who are well known in this domain.

**Keywords:** Image analysis, alignment, registration, geometric modeling, dynamic programming.

## 1 Introduction

As far as Computational Vision is concerned, one of the main and more complex problems encountered is the alignment and recognition of objects represented in images. These tasks are very important in several applications of Computational Vision as is the motion analysis of objects along image sequences, the quality inspection of objects from images, the objects' recognition from images, the evolution analysis of patients' diseases from medical images, etc. The complexity

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involved is essentially due to the different projections that objects can assume in images; for instance, due to the existence of varied cameras viewpoints, or even as a result of deformations that the objects may undergo.

To measure the similarity between two objects represented in images, or between two configurations of an object, it is possible to resort to techniques based on the signals used to represent those objects. In these techniques, images are regarded as being 2D signals that characterize the gray level (or color) of the images' pixels. Examples of such techniques are those based on Fourier or wavelet transforms. For instance, in [Daugman (2003)] a method based on Gabor wavelets is used to identify persons through the recognition of their iris, and in [Orchard (2007)] medical images from multimodal sources are aligned using an exhaustive search procedure based on the Fourier transform.

Another class of techniques used to measure the similarity between two objects in images is based on the analysis of their shapes. To apply these techniques, one must begin by extracting features from the objects' shapes, such as a group of points, segments, boundaries, surfaces or skeletons. In Computational Vision, this task is usually known as object segmentation.

There are several techniques to obtain the segmentation of objects represented in images; for example, those based on: image gradient, [Canny (1986)], deformable models, [Kass, Witkin and Terzopoulos (1988), Cootes and Taylor (1992), Xu and Prince (1998), Tavares, Carvalho, Oliveira, Vasconcelos, Gonçalves and Pinho (2007), Vasconcelos and Tavares (2008)]; level set methods, [Wang and Wang (2006), Wang, Lim, Khoo and Wang (2007a), Wang, Lim, Khoo and Wang (2007b)]; as well as physical modeling, [Gonçalves, Tavares and Jorge (2008)]. For a review on object segmentation see, for example, [Zhang (2001), Zhang and Lu (2004), Gonzalez and Wood (2008), Ma, Tavares, Jorge and Mascarenhas (2009)].

Frequently, following the segmentation of the objects from the input images, the matching between the extracted objects' features are then accomplished. Then, some techniques use the matching found in order to determine the objects' similarity by attributing a cost to each correspondence found. However, other techniques begin by trying to align the objects, based on the above mentioned matching process and, subsequently proceed to determine their similarity by comparing the aligned objects. Usually, this image alignment is referred to as image registration.

The problem in determining the matching between objects' feature points, has resulted in the appearance of several approaches that try to achieve the best possible global matching. To achieve this goal, one can use, for example: spatial information of the intensity gradient, [Lucas and Kanade (1981)]; modal matching, [Scot and Longuet-Higgins (1991), Shapiro and Brady (1992), Sclaroff and Pent-

land (1995), Tavares (2000), Carcassoni and Hancock (2003), Bastos and Tavares (2006); shape context, [Belongie, Malik and Puzicha (2002)]; shape signature, [Otterloo (1991), Cohen and Guibas (1997): Oliveira and Tavares (2007), Gonzalez and Wood (2008), Oliveira (2008)]; or probabilistic criteria, [Moisan and Béranger (2004), Keren (2009)].

When the similarity of the objects' feature points is quantified in the form of a cost matrix, the matching problem can be considered as being an optimization problem, and assignment algorithms are thus used. Examples of optimal approaches for this purpose are: linear programming, [Bastos and Tavares (2006)]; graph search, [Roy and Cox (1998)]; bipartite graph matching, [Fielding and Kam (2000)]; concave optimization, [Maciel and Costeira (2003)] and dynamic programming, [Scott and Nowak (2006), Oliveira and Tavares (2008)]. Non-optimal approaches include greedy algorithms, [Wu and Leou (1995)] and simulated annealing, [Starink and Backer (1995)].

This paper begins by referring to previous work which has been developed in order to determine the best global matching between objects' feature points. Then, a novel methodology is proposed to build a robust affinity matrix by using the curvature value and its distance to the correspond centroid from each point that is to be matched. Following this, comparative results between the proposed methodology and the geometrical approach suggested by Shapiro and Brady, [Shapiro and Brady (1992)], are presented. Our preference in relation to the methodology used by Shapiro and Brady as a reference approach is mainly due to the following facts: it is widely known in the image analysis domain, it presents a reasonable computational cost and it usually produces good matching results. Next, a methodology is presented to estimate the similarity transformation that best aligns objects which have been previously matched. In order to achieve this, this methodology defines the contours in the complex plane and then, by using the matching information and statistical processing, it estimates the similarity transformation parameters. Finally, in the final section, some results and conclusions are presented.

## **2 Previous work**

This work appears as a sequence to the projects described in [Tavares (2000), Tavares, Barbosa and Padilha (2000)] which considered matching methodologies for characteristic points in images based on physical modeling or geometric modeling complemented with modal matching, [Shapiro and Brady (1992), Sclaroff and Pentland (1995)]. Briefly, the methodologies were used to determine the matching between objects' characteristic points, through the construction of an affinity or cost matrix. Next, the cost matrix obtained was used in the process of obtaining the desired correspondences by using a pure local searching approach: one point is

just matched with its best candidate if in the case of this second point the first one is also the best matching candidate.

In [Bastos and Tavares (2006)], the work previously described in [Tavares (2000), Tavares, Barbosa and Padilha (2000)] was improved by taking into consideration optimizations methods in the establishment of the desired matching. Thus, the matching was formulated as a classic assignment problem and solved by considering three traditional algorithms, [Dell' Amico and Toth (2000)]: the usual Hungarian method; the Simplex method for Flow Problems, [Löbel (2000)], and the LAPm, [Volgenant (1996)]. The results obtained were considerably better than those obtained using the original local approach; however, crossed correspondences still appeared very frequently, [Bastos and Tavares (2006)].

In [Oliveira and Tavares (2008)] an assignment algorithm with order restriction based on dynamic programming was applied to the previously built affinity matrices by using the geometrical modeling suggested by Shapiro and Brady, [Shapiro and Brady (1992)]. This new optimization algorithm successfully solves the crossed matches problem and considerably improves the execution time of the complete matching process. However, the execution time is still high for some possible applications; essentially due to the fact that the methodology used by Shapiro and Brady needs to solve an eigenvalue/eigenvector problem from two modeling matrices that can assume large dimensions ( $n \times n$  and  $m \times m$ , with  $n$  and  $m$  being the numbers of the objects' points to be matched). Additionally, the above mentioned methodology is very sensible to the objects' shapes and also to some of the considered parameters, such as the eigenvectors' signals and the number of eigenvectors to be used in the construction of the cost matrix.

Thus, the principal goal of this work was to develop a faster, more efficient and robust methodology to obtain a novel affinity matrix that, when complemented to an optimization algorithm which preserves the circular order of the objects' contour points, allows for the establishment of the best global matching between objects' contour points without having crossed correspondences.

### 3 Matching methodology

Transformations of similarity, that is, geometric transformations involving translations, rotations and scaling, can originate changes in an object's position, dimension and orientation, whilst always maintaining its shape. Moreover, if the shapes involved are polygons, then the known property: *two polygons are similar (have the same shape) if the corresponding angles have the same amplitude and the lengths of the corresponding sides are directly proportional*, can be used to decide if they are similar and also to establish their matching. The adopted matching methodology

considers this property to build a cost matrix that quantifies the similarity between the contour points of two objects. One should notice that if a discrete contour is closed, then it can be considered as being a polygon.

### 3.1 Cost matrix construction

Let *contour 1* and *contour 2* represent two contours to be matched, defined by a sequence of  $n$  and  $m$  ordered points, respectively. For each contour, a sequence of the angles' amplitude associated to its points can be established. Thus, point  $P_i$  of *contour 1* corresponds the angle's amplitude  $\alpha_i$  and point  $P'_j$  of *contour 2* corresponds the angles' amplitude  $\theta_j$ .

Now, consider a contour and three of its consecutive points  $P_{i-k}$ ,  $P_i$  and  $P_{i+k}$ , where  $k$  is an integer positive number. Here, it is defined as the curvature angle associated with point  $P_i$  the angle whose vertex is  $P_i$ , one side contains point  $P_{i-k}$  and the other side contains point  $P_{i+k}$ . Three points define two angles, the first whose amplitude is lower or equal to  $180^\circ$  and another whose amplitude is greater or equal to  $180^\circ$ . To build the sequences of angles, the angle' amplitude defined in counter clockwise direction and from the line segment  $[P_i P_{i-k}]$  to the line segment  $[P_i P_{i+k}]$  is taken into consideration.

To improve the results, the value of parameter  $k$  could be adjusted, depending on the point sets of the contours. For instance, if the contours are defined by few points, then small values of  $k$  (near 1) provide better results. On the other hand, if the contours are defined by a larger number of points, then the value of  $k$  should be increased. The experimental results which will be presented were obtained by considering  $k = 10$ , due to the fact that this value revealed to be adequate in our preliminaries experiments. Additionally, one verified that values lower than 10 and not significantly higher than this value do not originate considerable differences in the matches found.

Therefore, an angular cost matrix,  $A$ , can be defined in such a way that each element  $a_{ij}$  represents the difference between the angles' amplitude  $\alpha_i$  of *contour 1* and the angles' amplitude  $\theta_j$  of *contour 2*:

$$a_{ij} = |\alpha_i - \theta_j|.$$

Matrix  $A$ , when used as cost matrix together with an optimization algorithm that preserves the contours' point order in the matching, can originate suitable matches if the two contours are defined by few points and the numbers of points that define them are approximately equal. However, in other cases, the matching results can be unstable, [Oliveira (2008)]. Thus, along with the curvature information, it is necessary to consider more relevant information about the objects to be matched in order to suppress the instability verified.

As has been previously referred, if two objects are similar, then the lengths of homologous elements are directly proportional. Thus, if the scaling effect is suppressed, the distance between two elements in an object is equal to the distance of the homologous elements in the other associated object. Here, this property is used to define a new cost matrix,  $D$ , based on the distance of the contours objects' points to the correspondent centroid.

Let's take the following two contours, *contour 1* defined by  $n$  points and *contour 2* defined by  $m$  points into consideration. For *contour 1*, let  $\bar{X}_{d1}$  represent the weighted average of the distances of its points to its centroid with coordinates  $(x_c, y_c)$ , as defined in [Oliveira (2008)]. Now, consider the sequence of distances to the centroid of the *contour 1*'s points:  $d1_1, d1_2, d1_3, \dots, d1_n$ , where for each *point*  $P_i$  with coordinates  $(x_i, y_i)$ :

$$d1_i = \sqrt{(x_i - x_c)^2 + (y_i - y_c)^2} / \bar{X}_{d1}.$$

Based on the same principle, the sequence of distances to the centroid of *contour 2* can be established:  $d2_1, d2_2, d2_3, \dots, d2_m$ .

Next, a new matrix  $D$  can be defined by calculating the differences between the previously defined two sequences. Therefore, each element  $d_{ij}$  of matrix  $D$  is:

$$d_{ij} = |d1_i - d2_j|.$$

Finally, by adding the information of angular costs, represented in matrix  $A$  and the information of the distance to the centroid represented in matrix  $D$ , the final cost matrix  $C$  can be defined:

$$C = w \times D + (w - 1) \times \bar{X}^{-1} \times A,$$

where  $w \in [0, 1]$  represents the weight attributed to the distance to the centroid and  $\bar{X}$  is the average of the curvature angles of the contour defined by fewer points. Seeing that all elements of matrix  $D$  vary around 1 (one) whereas the elements of matrix  $A$  do not, matrix  $A$  is multiplied by the factor  $\bar{X}^{-1}$ . Consequently, the elements of matrix  $(\bar{X}^{-1} \times A)$  also vary around 1 (one) and, in this way, the effect of the parameter  $w$  is more stable.

In summary, the distance to the centroid information included in matrix  $C$  gives stability to the global matching and the curvature information improves the local matches, [Oliveira (2008)]. Moreover, each element  $c_{ij}$  of matrix  $C$  represents the match cost between point  $i$  of *contour 1* and point  $j$  of *contour 2*. Furthermore, the bigger its value is, the smaller is the affinity between the respective points.

After having done several preliminary experiments which consider contours of different dimensions and shapes, the following can be concluded: (a) When the contours are defined by a reduced number of points and the difference between the number of points that defines them is insignificant, the low value of parameter  $w$ , which reflects a reduced influence of the distance to centroid information and a high influence of the curvature information, provides better results. (b) When the contours are defined by a large number of points or there is a considerable difference between the numbers of points that define them, a value of parameter  $w$  near 1 (one), which represents the high influence of the distance to centroid information and the low influence of curvature information, provides better results.

The results presented in this paper were obtained by using  $w = 0.8$ ; because of the fact that, in the experiments done, this value was proven to be a good compromise between the effect of the curvature information and the distance to centroid information. However, in a number of other particular applications, different values of  $w$  combined with various values of  $k$ , could originate better results.

The computational complexity of all the processes involved in the building of the cost matrix  $C$  is  $O(r \times n \times m)$ , where  $r$  is a constant value. For the sake of simplicity, one can only consider  $O(n \times m)$ . In all the references to computational complexity throughout this paper this simplification has been applied.

### 3.2 Optimal global matching

To determine the global matching based on the previously defined cost matrix, a cost optimization algorithm has been used. Due to the fact that the order of the contours' points must be preserved, in order to avoid crossed matches, an optimization algorithm that respects this restriction should be employed. Let us consider a cost matrix  $C$ , of dimension  $n \times m$ , representing the matching cost of the  $n$  points of *contour 1* with the  $m$  points of *contour 2*. The matching problem could be formulated as:

- Decision variables:

$X = [x_{ij}]$ , where:

$$x_{ij} = \begin{cases} 1, & \text{if point } i \text{ (contour 1) matches point } j \text{ (contour 2)} \\ 0, & \text{otherwise} \end{cases};$$

- Objective function:

$$\min f = \sum_{i=1}^n \sum_{j=1}^m x_{ij} c_{ij};$$

- Constrains:

$$\left\{ \begin{array}{l} \sum_{j=1}^m x_{ij} = 1, \quad i = 1, 2, \dots, n; \\ \sum_{i=1}^n x_{ij} \leq 1, \quad j = 1, 2, \dots, m; \\ \text{The matching must preserve the circular order.} \end{array} \right.$$

In order to solve this problem, we have chosen the algorithm based on dynamic programming proposed in [Oliveira and Tavares (2008)], because it satisfies all the above mentioned conditions in addition to the fact that it is very fast. In summary, the algorithm selected determines the global matching of type one-to-one that minimizes the sum of all individual matches. If a contour is defined by  $n$  points and the other by  $m$  points, with  $n \leq m$ , only  $n$  matches are established, thus excluding the  $(m - n)$  points of the contour defined by a greater number of points from the matching. Its computational complexity is  $O(n \times m \times (m - n + 1))$ , [Oliveira and Tavares (2008)].

#### 4 Similarity transformation estimation

The process of image alignment, usually referred to as image registration, is fundamental in many applications such as in medical imaging and image recognition.

A commonly used methodology to align two objects in images consists of applying a series of transformations to one of the original images in order to increase the similarity between them. Whenever it is impossible to further enhance the similarity found between the images, or in the case of the convergence criteria being satisfied, the objects are considered to be aligned.

Frequently, the alignment problem is associated with the matching problem. Thus, in order to align the objects the matching between their homologous elements must first be established. Then, based on the matches found, the parameters of an alignment function can be estimated. The methodology which has been proposed is of this class: it only considers similarity transformations, which are solely based on rotations, scaling and translations.

##### 4.1 Local rotation, scaling and translation

Let  $[AB]$  and  $[A'B']$  represent two straight line segments in the plane. When aiming to determine the similarity transformation  $T$  that aligns these two segments, the following condition must be verified:

$$T([AB]) = [A'B'] .$$



Without loss of generality, we can assume that  $T(A) = A'$  and  $T(B) = B'$ .

A point on a plane can be represented in a unique way by a complex number. Thus, considering the segments defined in the complex plane  $C$ , the similarity transformation  $T$  can be defined as a function that applies a scaling and a rotation around the origin point,  $O = 0 + 0i$ , followed by a translation. Thus, mathematically,  $T$  can be defined as:

$$T : C \rightarrow C$$

$$z \mapsto z' = wz + u$$

where  $w$  and  $u$  are complex numbers. In this way, through the definition of  $T$ , two independent simultaneous equations can be defined:

$$\begin{cases} T(A) = A' \\ T(B) = B' \end{cases} \Leftrightarrow \begin{cases} wA + u = A' \\ wB + u = B' \end{cases}$$

By solving these simultaneous equations in order to find  $u$  and  $w$ , the parameters of function  $T$  can be determined. The absolute value of  $w$  represents the scaling and its argument represents the rotation angle amplitude.  $Re(u)$  and  $Im(u)$  represent the translation in the  $x$ -axis and  $y$ -axis directions, respectively.

#### 4.2 Global rotation, scaling and translation

Supposing that a global matching of type one-to-one had already been established, and it was defined by a function  $g$  like the following one (given by column):

$$g = \begin{pmatrix} P_1 & P_2 & \dots & P_n \\ P'_1 & P'_2 & \dots & P'_n \end{pmatrix},$$

where the first row represents the points of *contour 1*, the second row represents the corresponding points of *contour 2* and  $n$  is the number of singular matches established; that is, the number of the points of the contour which has been defined by fewer points.

If a contour is defined by  $n$  points, then it is possible to define, at the upmost,  $(n^2 - n) / 2$  distinct line segments connecting its points. Thus, for each segment defined by two points of *contour 1*, the transformation of similarity  $T$  that transforms it into the corresponding segment of *contour 2* is determined, and, at the upmost,  $(n^2 - n) / 2$  distinct values for local scaling, rotation angle and translation vector can be obtained.

In this paper, in order to estimate the global parameters of the similarity transformation involved between two previously matched contours, a statistical processing

of the local parameters determined has been made. First, the outsider values are excluded; then, the averages values of the rotation angles, scales and translations are calculated by using the remaining values. We consider that a value  $x_i$  is an outsider, if  $|\bar{X} - x_i| > \sigma$ , where  $\bar{X}$  is the average of all values and  $\sigma$  is the standard deviation. The option for average solutions was a consequence of its simplicity and also because good results in the preliminaries experiments that were done were always achieved. However, other statistical approaches could be considered, possibly originating different results. Notice that the elimination of the outsiders is important, because the average is a statistic parameter that is very sensitive to extreme values. Moreover, the contour pairs which have been used have a significant non-similarity component between them; thus one may expect some local transformations values to be very different to the global transformation parameters.

The computational complexity of the methodology developed to estimate the similarity transformation between two previously matched contours is equal to  $O(n^2)$ , being  $n$  the number of points matched.

## 5 Results and conclusions

So as to validate the proposed matching algorithm, based on CDCI (curvature and distance to centroid information), its results were compared with those obtained by using the geometrical modeling and modal matching proposed by Shapiro and Brady, [Shapiro and Brady (1992)]. As has been previously referred, the reference methodology that was chosen was mainly due to the fact that it is widely known in the image analysis domain, it is not very demanding in computational terms, in particular in terms of execution speed, and the fact that it usually produces good matching results. Before presenting the results obtained, we provide a brief summary of Shapiro and Brady's methodology in the next subsection.

### 5.1 Shapiro and Brady's methodology

Briefly, the first step is to build two squared *proximity matrices*,  $H_1$  and  $H_2$ , also called *shape matrices*, one for each contour which is to be matched, defined by the  $n$  and  $m$  points, respectively. To build the matrix  $H_1$  of *contour 1*, the *Gaussian-weighted* distances between all of its points should be calculated. Thus, each element  $h_{ij}$  of  $H_1$  is given by:

$$h_{ij} = e^{-r_{ij}^2/2\sigma_1^2},$$

where  $r_{ij}^2 = \|x_i - x_j\|^2$ ,  $x_i$  and  $x_j$  are points of *contour 1* and  $\sigma_1$  is a parameter that depends on the *contour 1* shape and controls the interaction between its points. In an analogous way, the matrix  $H_2$  is built for *contour 2*.

To determine the best value of  $\sigma_i$  ( $i = 1, 2$ ), several preliminary experiments were carried out. Usually, the value  $\sigma_i = d_i/\sqrt{2}$ , where  $d_i$  is the average distance between all points of the *contour*  $i$ , was the one which originated the best matching results. Thus, the results presented by this paper were obtained by using this value.

The two proximity matrices,  $H_1$  and  $H_2$ , are real, squared and symmetric. Thus, all eigenvalues are real and all eigenvectors, commonly called *modes*, are orthogonal. To make their singular value decomposition (SVD), an algorithm presented in [Press, Teukolsky, Vetterling and Flannery (2002)] based on the *Jacobi Transformations of a Symmetric Matrix* was used.

The Jacobi method is absolutely foolproof for all real symmetric matrices, but for large matrices it is slower than the *QR* method, for instance, [Press, Teukolsky, Vetterling and Flannery (2002)]. However, the Jacobi algorithm is much simpler than the more efficient methods.

The number of operations involved in the implemented Jacobi routine varies from  $18n^3$  to  $30n^3$ , [Press, Teukolsky, Vetterling and Flannery (2002)]. In a simplified manner, to make the SVD of the two matrices  $H_1$  and  $H_2$ , the total complexity of the algorithm is  $O(n^3 + m^3)$ .

The sign of each eigenvector is not unique, since that by switching its signal the orthogonality of the basis is not violated. However, it is vital that both sets of eigenvectors have *consistent* directions, since they are used to build the affinity matrix  $Z$ . Thus, a signal correction algorithm is needed.

In order to choose the signal of each eigenvectors, the approach presented in [Shapiro (1991)] was implemented. Briefly, it can be described as follows: Let  $V_1$  and  $V_2$  represent the sets of unitary length eigenvectors of matrices  $H_1$  and  $H_2$ , respectively, considering that the eigenvectors are ordered according to the descendent order of the correspondent eigenvalues. Next,  $V_1$  is considered to be the reference basis and the axes in  $V_2$  are oriented one at a time, by choosing the direction (that is, the vector's signal) for each one that maximizes the alignment of the two vectors' features set. Details of this approach can be seen in [Shapiro (1991)].

Finally, the affinity matrix  $Z$  is built by measuring the squared Euclidean distance between the features' vectors. In the implementation carried out by this study, only 25% of the eigenvectors were used, because this value was proved to be efficient in many cases, [Tavares (2000)]. Considering  $k$  to be the number of eigenvectors used,  $v_{1,p}(i)$  the  $i$ -element of  $p$ -vector from the ordered set  $V_1$  and  $v_{2,q}(j)$  the  $j$ -element of  $q$ -vector from the ordered set  $V_2$ , each  $z_{ij}$  of matrix  $Z$  is given by:

$$z_{ij} = \sum_{r=1}^k (v_{1,r}(i) - v_{2,r}(j))^2.$$

The values of each  $z_{ij}$  vary between 0 (zero) and 4 (four). A perfect match is indicated by the value 0 (zero), while a value of 4 (four) indicates an inappropriate match. The computational complexity involved in the building of the matrix  $Z$  is  $O(n \times m \times k)$ .

As has been previously referred, to obtain the global matching that minimizes the sum of all matches, considering  $Z$  as the cost matrix, the algorithm based on dynamic programming proposed in [Oliveira and Tavares (2008)] was used.

## 5.2 Experimental results

The main goal of this work was the evaluation of the quality of the matches found based on CDCI by comparing the results obtained with those resulting from the use of the cost matrix established by geometric modeling as proposed by Shapiro and Brady. To make the comparison between the two matching methodologies possible, the same algorithms for both methodologies were used, except for those used to build the cost matrices. The algorithms were implemented in C++ language, using Microsoft Visual Studio 6. All the experiments were carried out in a PC with an AMD Turion64 microprocessor at 2.0GHz, with 1.0GB of RAM and running Microsoft Windows XP.

In the following experiments which will be presented, the contours used were extracted from the images available in the database “*silhouette database(1032 shapes)*”, organized by the Laboratory for Engineering Man/Machine System (LEMS). Two image classes were considered: class “hammer”, with a total of 32 images, and class “tool”, with a total of 41 images.



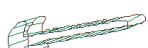
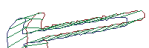


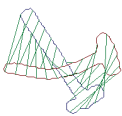
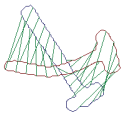








For the images used, the contours extraction was easy and no special segmentation technique was used. The flowed segmentation approach can be divided in three steps: first, the images were binarized; then, the objects’ inner points were eliminated; and finally, the contours’ points were ordered through the use of a contour tracking algorithm.

Shapiro and Brady’s methodology is based on the singular value decomposition of the proximity matrices of the two contours to be matched. Thus, for large proximity matrices, this methodology requires a high computational effort, even if a faster algorithm is used to solve the associated eigenvalues/eigenvector problem. Thus, in the comparisons that have been carried out, only contours defined by less than 200 points were used.

In Table 1, some examples of the matches found by using the cost matrix based on CDCI as well as by using the cost matrix based on the Shapiro and Brady’s methodology can be observed. In the same table, the numbers of points that define each contour and the total of computational time required (that is, to extract

the contours, build the cost matrix, establish the matches, determine the similarity transformation and align the contours) are also presented. The examples shown were chosen to permit the simple visualization of the original contours and the matches established. In addition, and bearing the same goal in mind, only pairs of contours where the rotation angle involved was reduced are shown. Furthermore, in each case presented, only 25% of the matches found are represented.

Table 1: Examples of matches obtained and the associated computation times required by the proposed methodology (CDCI) and Shapiro and Brady’s methodology (in which just 25% of the matches found are represented by green lines).

Objects and nº of contours points		Methodology used	
		CDCI	Shapiro and Brady’s
 "hammer01" 141 points	 "hammer02" 139 points	 Time: 0.016 s	 Time: 2.813 s
 "hammer25" 193 points	 "hammer26" 126 points	 Time: 0.047 s	 Time: 4.766 s
 "tool27" 105 points	 "tool23" 189 points	 Time: 0.062 s	 Time: 5.094 s
 "tool09" 200 points	 "tool03" 185 points	 Time: 0.047 s	 Time: 7.844 s

In Table 2, some examples of contours alignment, obtained by the proposed alignment methodology, are illustrated. In these cases, the matches were previously obtained by resorting to CDCI.

The matching results and respective alignments are presented in Table 3 for the two matching methodologies under comparison. The classification of the quality of the matches and alignments found was made through visual observation.

In Table 4, a comparison of the total computational time needed by both methodologies is made. The results presented were obtained by taking more than 150

Table 2: Examples of alignments obtained using the proposed algorithm to estimate the similarity transformation involved between two matched contours (the matches were found by using CDCI).


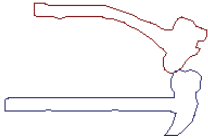
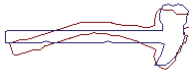


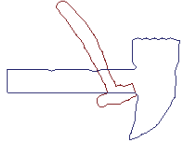
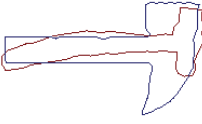


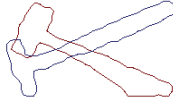
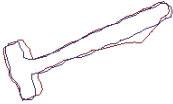


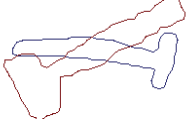
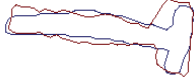


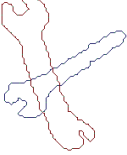
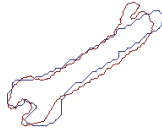


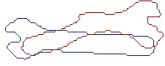
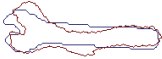

Original images	Contours in their original positions	Aligned contours
 "hammer03"		
 "hammer30"		
 "hammer13"		
 "hammer28"		
 "hammer21"		
 "hammer35"		
 "hammer27"		
 "hammer38"		
 "tool12"		
 "tool05"		
 "tool16"		
 "tool19"		

Table 3: Summary of the matches and alignments obtained by using the methodology based on CDCI and Shapiro and Brady’s methodology, when considering contours defined by 100 to 200 points.

Methodology based on CDCI						
Image classes	Matching			Similarity transformation		
	Good	Satisfactory	Bad	Good	Satisfactory	Bad
“hammer”	100%	0%	0%	100%	0%	0%
“tool”	100%	0%	0%	100%	0%	0%
Shapiro and Brady’s methodology						
“hammer”	51%	24%	25%	58%	17%	25%
“tool”	54%	31%	15%	59%	26%	15%

experimental cases for each methodology into consideration.

Finally, to show how instable the Shapiro and Brady’s methodology can be, Table 5 presents four experiments made with two different values of  $\sigma_i$ , and one can clearly see how a reduce change on this parameter can affect the results obtained.

Table 4: Total computation times required by each of the two methodologies compared when considering contours defined by 100 to 200 points.

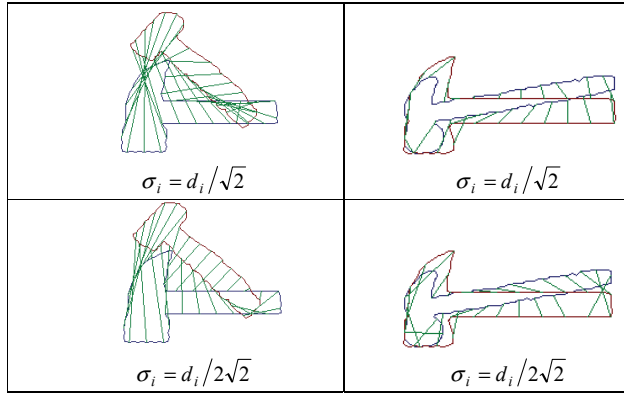
Images classes	Total time [s]					
	Methodology based on CDCI			Shapiro & Brady’s methodology		
	Min	Average	Max	Min	Average	Max
“hammer”	< 0.01	0.03	0.08	1.11	2.46	10.10
“tool”	0.01	0.04	0.08	1.13	4.86	8.63

### 5.3 Results discussion

In all the experimental tests which considered the contours of classes “hammer” and “tool”, the methodology based on CDCI always presented good matches, and consequently, good estimations for the similarity transformation in question. However, when Shapiro and Brady’s methodology was used, only 51% and 54% of good matches were obtained for the classes “hammer” and “tool”, respectively.

In some experiments, the matching obtained as a result of Shapiro and Brady’s methodology were of bad quality or did not make any sense (for example, the matching between the contours “hammer08” & “hammer39” represented in Table 5). This happened in 25% and 15% of the matches for the classes “hammer” and “tool”, respectively.

Table 5: Matching of the contours “hammer08” & “hammer39” on the left and “hammer01” & “hammer04” on the right, using Shapiro and Brady’s methodology with the indicated values for the parameter  $\sigma_i$ .



Shapiro and Brady’s methodology was very unstable in several experiments that were carried out. In fact, in some cases where bad matches were established, good matches could have been obtained if the methodology parameters had been adjusted for these particular cases. However, as a consequence of this, some previous well established matches would have been worse if these new parameters had been adopted instead. For instance, as Table 5 illustrates, by considering  $\sigma_i = d_i / 2\sqrt{2}$ , the matching between the contours “hammer08” & “hammer39” improved, but the matching between the contours “hammer01” & “hammer04” became worse.

Obviously, the similarity transformation parameters depend on their previous matching. When the matching was good, the estimated values for the similarity transformation were also good. When the matching was of satisfactory quality, the estimated values for the similarity transformation were good in a considerable quantity of the cases analyzed, and satisfactory in the others. When the matching was bad, the alignments were also usually bad. These final last observations confirm that the statistical processing done on the parameters seems to be appropriate.

In addition, some experiments were carried out by using contours defined by fewer points, but, in general, the quality of the matches obtained by both methodologies under comparison was like the one previously described.

In relation to to the execution times, the methodology based on CDCI required less execution time as was to be expected.



## **6 Final conclusions and future work perspectives**

An important fact that should be emphasized is that the methodology based on CDCI was proven to be robust for the classes of objects used. In fact, the results were always good, independently of the contours' shapes and the numbers of points which define them. In addition, this methodology was proven to be more adequate to match contours defined by ordered points than the methodology used by Shapiro and Brady.

The methodology presented to estimate the similarity transformation produced good results as well, mainly when used in combination with the matching methodology based on CDCI.

As a future work perspective, one possibility could be the matching of all contours presented in images. That is, each image can have more than one contour and the goal would be the establishment of the best matching of each contour of one image with the corresponding contour of the other image. In order to achieve this, a similarity measure would be needed to decide which pairs of contours should be matched.

Another possibility could be the development of a new methodology to match objects defined by sets of points without the order requirement, which would permit the consideration of the objects' inner points. Several methodologies of this kind already exist, but in general they are quite sensitive to the objects' shapes, to the image acquisition systems or even to the geometric transformation involved.

The usage of the methodologies proposed in this paper to match and align organs presented in medical images is another task which should be addressed in the near future.

**Acknowledgement:** The first author would like to thank the Portuguese Fundação Calouste Gulbenkian for his PhD grant. Authors would like to express their deep gratitude to Dr. Vanessa Esteves from University of Porto – Portugal for her valuable help in the writing process of this paper.

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