Robust point correspondence matching and similarity measuring for 3D models by relative angle-context distributions

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Received 4 February 2005; received in revised form 5 July 2007; accepted 15 August 2007

Abstract

Robust solutions for correspondence matching of deformable objects are prerequisite for many applications, particularly for analyzing and comparing soft tissue organs in the medical domain. However, this has proved very difficult for 3D model surfaces, especially for approximate symmetric organs such as the liver, the stomach and the head. In this paper, we propose a novel approach to establish the 3D point-correspondence for polygonal free-form models based on an analysis of the relative angle distribution around each vertex with respect to relative reference frame calculated from principal component analysis (PCA). Two kinds of distributions, the Relative Angle-Context Distribution (RACD) and the Neighborhood Relative Angle-Context Distribution (NRACD) have been defined respectively from the probability mass function of relative angles context. RACD describes the global geometric features while NRACD provides a hierarchical local to global shape description. The experiments and evaluation of adopting these features for the human head and liver models show that both distributions are capable of building robust point correspondence while the NRACD gives better performance because it contains additional information on the spatial relationship among vertices and has the ability to provide an effective neighborhood shape description. Furthermore, we propose a similarity measure between correspondence ready models based on relative angle-context distribution factors. The experimental results demonstrate that this approach is very promising for model analysis, 3D model retrieval and classification.

Keywords: 3D model matching; Point correspondence; Relative angle distribution; Similarity analysis

1. Introduction

The ability to establish robust correspondence between 2D images and more recently, 3D objects is frequently a central issue in many image analysis paradigms, such as structure-from-motion [1], stereopsis [2], optical flow analysis [3], and deformable or morphable models [4,5], etc. This is particularly true in the medical and biological domains where robust solutions to the correspondence problem is vital to many applications such as organ growth measurement [4], histological section alignment [6], aesthetic surgical planning [7]. Recently, correspondence algorithms are becoming the fundamental building block for object segmentation techniques that make use of the classical as well as statistical deformable models [8–12] and for the construction of point distribution models [13]. A recent survey shows that solving the correspondence problem continues to be the central issue in many medical image registration algorithms [14].

With the increasing availability of large collections of 3D graphical models for a variety of applications, tech-
niques that have been developed for image analysis, classification and content-based retrieval of 2D images are being extended for 3D models. This makes 3-dimensional morphological analysis [15], model classification [16], 3D graphical model indexing and retrieval [17] fast growing areas of active research. Among the many research issues that have been brought forth by these new topics, 3D correspondence problems have been identified as a major challenge and a prerequisite for many applications. For the last decade, researchers in the medical domain have been investigating robust techniques for 3D point correspondence matching of organs or anatomical structures. One of the most common approaches to determine the correspondence between sets of 3D model data is to match distinctive local features such as local geometric invariants. As a general method, one of the advantages of local invariants such as corners or curvature is that they are insensitive to occlusion [9,18]. Such features, however, are very sensitive to noise, although a multi-scale framework could alleviate this problem [19]. Usually for most applications the amount of local information is insufficient for robust matching, especially in 3D space. Modal matching was introduced in 1995 to find feature correspondence and perform object recognition [20,21]. They described objects in terms of generalized symmetries, which were defined by the object’s eigenmodes. Since eigenmodes could provide a global to local ordering of shape deformation, point correspondence between two surfaces can be reliably determined by comparing their trajectories in this modal space. However, the technique that requires the calculation of eigenmodes and their interpolation for 3D points-set mass is computationally very expensive. Recently, Walkers et al. [22] tried to determine a globally consistent set of correspondences across all of the face images in a set using the transformation of a grid. However, the algorithm could not handle significant changes in scale and orientation, which are inevitably present for many medical applications.

In this paper, we focus on the problem of searching for the correspondence between the same classes of 3D graphical models that differ from each other through some form of non-linear deformation. Such models frequently occur in medical applications as the results of soft-tissue organ segmentation. The challenge posed by such soft-tissue organ models is that it is frequently difficult to define landmarks or to obtain salient geometric features from the model surfaces. To overcome this problem, we propose an intuitively simple but very effective and robust feature for 3D point correspondence matching. The feature is based on the distribution of Relative Angles (RAnGs) in the vertex set. We introduce a vertex context descriptor, which is called Relative Angle-Context (RAC), to describe the shape of the surface around a vertex. We show that RAC is able to capture the global geometric information of the model from the point of view of any vertex as well as its local structures by associating each vertex of the model with a probability distribution of angles between vectors linking pairs of vertices. The correspondence between points or vertices in a pair of models can then be cast as a problem of searching for a pair of points or vertices in the two matching models which have the most similar distribution. The experimental results indicate that our technique could establish robust point correspondence for 3D medical objects even for near spherical, as well as approximately symmetric organs such as livers and human heads, which have been shown to be very difficult for many local-invariant based algorithms. More importantly, since the algorithm is based on the distributions of the global and local relative angles context, it possesses the general qualities of statistical methods such as computational efficiency and robustness (insensitivity to noise). The other advantage of our method is that, for the surface points which have no truly ‘accurate’ correspondences, it could locate to correspondence region within a small neighborhood of the points. We show that the resulting point correspondence could be used to (i) construct active shape models (ASM) which requires knowledge of one to one point correspondence between all the sample models, and (ii) to compute the similarity between models of organs.

2. Literature review of statistical based geometric point correspondence matching

In the following, we will focus our review on previous approaches to point correspondence matching and model classification based on statistical analysis of geometric features. As a traditional but still very popular statistical approach, histograms have been widely investigated for representing, analyzing and characterizing 2D and 3D shapes. Unlike other feature representation, a histogram representation possesses an inherent structure which is governed by the probability density distribution of the underlying random variable. The most important advantages of histograms include computational efficiency, robustness to noise, invariance to image transformation and significant data reduction. There exist some techniques that construct histograms from shape attributes. For example, Evans et al. [23] proposed a two dimensional histogram of pair wise attributes for each line segment in the images to recognize objects. This approach was extended by DiMauro [24] by restricting the histogram binning only to segment pairs located in a region of interest. Huet et al. [25] proposed the construction of two-dimensional histograms based on relative angles and positions of directed segments in an image and found they were very effective and robust in 2D shape indexing and retrieval. A similar idea has been used by Belongie et al. [26] who used the distribution of relative coordinates of the vectors originating from a point as the shape context to solve for correspondence between similar 2D shapes.

Histogram-based retrieval has also been shown to operate effectively for indexing 3D volumetric or polygonal data, when the histogram is computed from surface normal information [27]. Recently, our group proposed an optimal classification representation of 3D head models based on surface normal orientation statistics [16]. In this work, the distribution of the surface normals are mapped to the
Extended Gaussian Image (EGI), and the optimal transformation of the distributions are found through an application of Genetic algorithm (GA). In [28], surface normal orientation histogram is used as a morphological signature for each vertex in the surface. The authors used local orientation histogram as a shape representation for finding correspondence in deformable cortical surface matching. Osada et al. matched 3D Models with shape distributions [29], in which the signature of an object was represented as shape functions that measure the global geometric properties. In their paper, simple measurements such as angles, distances, areas and volumes of objects were employed as shape functions and good object classification results were achieved.

Rueckert et al. used a non-rigid registration method which is performed by manipulating a grid of B-spline control points. However, their approach does not define one-to-one point correspondence [30]. Davies et al also proposed an approach to statistical shape modeling based on a minimum description length [31]. They derived an objective function that provides a principled measure of the quality of a statistical shape model. However, as a stochastic optimization technique, the approach is very time consuming. To overcome this problem, Chui et al. proposed a unified non-rigid feature registration method for brain mapping [32]. They used an iterative joint clustering and matching strategy which effectively reduces the computational complexity. Furthermore, the method has the ability to fuse different types of feature. However, since the algorithm uses some specific features of brain structure, it is difficult to be generalized.

In 1998, to achieve robust correspondence matching between 2D shapes that is invariant to the affine transform, our group proposed an affine-invariant active contour model that makes use of an affine invariant feature computed from the area of a triangle defined by sets of three vertices along a digital curve [8]. The resulting paradigm which we called the AI-Snake has been successfully applied to model-based object segmentation [8], shape retrieval [9], and detection of parallelism [10]. Recently, the approach has been extended to the 3D case [11,12] for the segmentation and shape modeling of 3D brain structures. In three dimensions, the tetrahedron volumes formed by different layer neighbors are used as affine-invariant feature vectors associated with each of the vertices for a 3D deformation model. Furthermore, based on these feature vectors, the point correspondence could be efficiently established in a hierarchical paradigm. The volume of the tetrahedron formed by the nearest neighbors of a vertex reflects the local surface structures around it while the volumes of the larger tetrahedrons capture the global properties of the 3D model. In this way, high-curvature regions could be easily distinguished from flat segments of surface. However, in recent research, we found that such an affine invariant feature vector is not sufficient to define or detect the point correspondence for approximately spherical and/or symmetric 3D objects such as the liver, the stomach and the head. Such organs do not exhibit significant differences in surface curvature as we move from one part of the object to another. For example, vertex A and vertex B on the liver model shown in Fig. 1 basically have the same local and global structures on the approximate half-sphere surface, which makes the correspondence matching process become ineffective or even fail. Obviously, for spherical models where many local regions have similar curvatures, we should focus not only on curvature information but also the direction and location of the vertices when we try to identify potential correspondence. In forming a robust attribute vector, these properties must be taken into account along with the shape information. In [33], we proposed a shape signature based on the computation of a spoke vector histogram for hand-drawn sketches. We further show theoretically that this signature is affine-invariant [8] and is very computationally efficient and robust for shape retrieval. In this paper we extend this shape feature to three-dimensional space and propose a vertex signature on a 3D surface that can be used to construct robust point correspondence for 3D graphical models, particularly for approximately spherical and symmetric objects. Previous work on relative angle histograms as reviewed above focused mainly either on the 2D domain or on distinguishing and classifying the shape of 3D objects. Our contribution is the proposal of a new way of defining and constructing a relative angle histogram from a 3D model and to show how it is used to solve the correspondence problem for 3D objects, particularly for objects that do not possess significant differences in surface curvature and are approximately symmetrical. Usually histogram based approaches could not achieve adequate descriptions since they do not capture spatial information. Our approach is to represent the shape context for each vertex of a 3D model as a probability distribution sampled from a Relative Angle-Context (RAC) which measures the geometric properties of the 3D model. We call this signature a Relative Angle-Context Distribution (RACD). Samples from the distribution can be computed quickly and easily from any 3D surface model. Our hypothesis is that corresponding points on similar 3D shapes should have consistent RAC distributions. Our approach works directly on the original vertices-set of a 3D model, making few assumptions about their format, organization and structures, therefore the approach can be used for corresponding matches and similarity queries in a wide variety of 3D database. Secondly, Relative Angle-Context distributions are invariant to all transformations used in similarity estimations, i.e. transla-
tion, rotation, and uniform scaling. Furthermore, its inherent statistical characteristics ensure that RAC distributions are insensitive to small perturbations due to noise, cracks and insertion/removal of polygons.

Unlike 2D domains, the construction of a reference frame is a challenge for 3D applications with angles or directions based signatures. Osada et al. [29] measure the angles between three random points on the surfaces, and in Wong et al. [16], the authors adopted an absolute reference frame. The latter requires that the orientation of models needs to be carefully initialized. Belongie et al. [26] proposed a relative frame based on treating the tangent vector at each point as the positive x-axis which is not particularly robust for most models. In our RAC distribution based approach, specifically, the three principal axes of our relative reference frame are obtained from principal component analysis (PCA) of the vertex distribution of 3D models. It was expected that using models belonging to the same category would give rise to similar principal axis orientations, and our experiments verified this expectation. Although the proposed approach is applicable to object classification for 3D models in general, we focus our study here on detecting and quantifying the dissimilarities between the same classes of medical organs. This is particularly important for the use of morphological analysis of 3D organs for the location of pathological changes, quantifying organic deformation and to characterizing abnormal organ shapes [34,35].

The rest of the paper is organized as follows. Section 3 presents the definition of Relative Angle-Context distributions and gives the formulation of two types of probability mass functions RACD and NRACD for a vertex on the model surface. Section 4 proposes a Discrepancy Factor df that is appropriate for correspondence matching and a Similarity Factor sf for the subsequent quantification of similarity between models. The experimental results and evaluation design are presented in Section 5 and we present conclusions in Section 6.

3. Relative angles in principal reference frame and Relative Angles-Context Distributions

3.1. Principal component frame in 3D models

Let us describe a generalized surface model \( R \), either open or closed, as being represented by a vertex-set \( V \) and a patch-set \( P \). Let \( v_i \) be defined as the \( i \)th vertex of the model, where \( v_i \in V \) and \( 1 \leq i \leq N \); \( p_l(v_{i1}, v_{i2}, ..., v_{in}) \) is the \( l \)th patch of the model surface \( p_l \in P \) and \( 1 \leq l \leq M \). Actually, \( p_l \) is a free-form polygon defined by vertex \( v_{i1} \) to \( v_{in} \). In 3D Euclidean space, the coordinates of vertices \( v_i \) can be denoted as \( v_i = (x_i, y_i, z_i)^T \). The centroid \( O \) (center of mass) of this object model can be easily computed from:

\[
O = \frac{1}{N} \sum_{i=1}^{N} v_i.
\]  

Without lost of generality, \( V \) can be transformed to the center of the mass \( O \) and if we treat the set of \( v_i \) as 3D random variables, we could find the positive definite covari-

![Figure 1. (a) Very different RACD curves for two vertices which have similar local features in the different locus of the surface. (b) RACD curve of vertex A. (c) RACD curve of vertex B.](image-url)
 variance matrix $C$ from the transformed version of $V$, noting that the standard deviations and correlations are not affected by the center of mass transformation. From $C$, the three largest eigenvalues of $C$ ($\lambda_1 \geq \lambda_2 \geq \lambda_3 \geq 0$) can be calculated. The matrix $E_1 = \{e_i\} (1 \leq i \leq 3)$ formed by the eigenvectors $e_i$ is an orthogonal matrix and there exists $E^T E = I$, where $I$ is the identity matrix.

From $CE_1 = \lambda_1 e_1$, the covariance matrix $C$ can be diagonalized by

$$E^T CE = \Lambda = \begin{bmatrix} \lambda_1 & 0 & 0 \\ 0 & \lambda_2 & 0 \\ 0 & 0 & \lambda_3 \end{bmatrix},$$

or we can express it in another way: $C = EE^T$. Now we choose $U$ as linear combinations of $V$ such that $U = E^T(V - O)$, and the covariance matrix of $U$ can be diagonalized to: $Cov(U) = E^T CE = \Lambda$. That is, the variance between the set of $U_i$ can be calculated as:

$$Cov(U_i, U_j) = Cov(e_i^T x, e_j^T x) = e_i^T Ce_j = \begin{cases} \lambda_i & \text{for } i = j \\ 0 & \text{for } i \neq j \end{cases}$$

$U_i (1 \leq i \leq 3)$ is known as the $ith$ principal component (PC) of the original variables $V$ and here, we use these three PCs of the 3D model to establish a relative reference frame for the object. In other words, the relative coordinate system of a 3D graphical model can be constructed by employing $U_1$, $U_2$ and $U_3$ as the orthogonal axes of a new coordinate system, and having its origin located at the center of mass $O$ of the 3D model (as shown in Fig. 2).

### 3.2. Relative angles in the vertex context

For each vertex $v_i$ on the surface model, $N - 1$ spoke vectors $v_i\tilde{v}_j$ $(1 \leq j \leq N, j \neq i)$ can be derived from $v_i$ and the angle between the $jth$ spoke vector of $v_i$ and the first principal axis $U_1$ can be computed from:

$$\theta_j(v_i) = \arccos \left( \frac{(v_i\tilde{v}_j \cdot \tilde{U}_1)}{|v_i\tilde{v}_j||\tilde{U}_1|} \right),$$

where $\cdot$ is the dot-product. Furthermore, two base-planes $\Pi_{12}$ and $\Pi_{13}$ are defined by $U_1, U_2$ and $U_1, U_3$, respectively. We use these planes to determine the signs of the relative angles. For example, if a spoke vector roughly points to the positive direction of the normal of plane $\Pi_{12}$, the corresponding angle will be given a positive sign. Formally, since the plane equations of $\Pi_{12}$ and $\Pi_{13}$ are $e_i^T v_i = 0$ and $e_i^T v_i = 0$ respectively, the signed angles between spoke vectors and the first principal axis $U_1$ can then be represented as:

$$_{ij}(v_i) = \begin{cases} \theta_j(v_i) & \text{if } e_i^T v_i > 0 \\ -\theta_j(v_i) & \text{if } e_i^T v_i < 0 \\ \theta_j(v_i) & \text{if } e_i^T v_i = 0 \& e_i^T v_i > 0 \\ -\theta_j(v_i) & \text{if } e_i^T v_i = 0 \& e_i^T v_i \leq 0 \end{cases}$$

This way, we have extended the range of angles for the spoke vectors from $[0, \pi]$ to $[-\pi, \pi]$. Furthermore, we can normalize these angles to $0 \sim \pi$ and define the $jth$ Relative Angles (RAngs) of vertex $i$ as:

$$\text{RAng}_{ij} = \begin{cases} \theta_j(v_i) & \text{if } \theta \geq 0 \\ 2\pi + \theta_j(v_i) & \text{if } \theta < 0 \end{cases}$$

It is trivial to note that with respect to the relative reference frame of the model, these Relative Angles are translation, rotation and scale invariant. This is a major advantage of this representation over other local geometric attributes.

It is not difficult to see that the RAngs describe the geometric structure of the vertices as seen from a given point of the 3D model. In addition, the distribution of RAngs characterizes the spatial relationship between a vertex and both its near as well as distant neighborhoods. In this way, shape properties as well as relative location information can be captured in the same distribution curve associated with the vertex. Consequently, based upon this representation, point correspondence can be estimated between vertices that have a similar distribution but belonging to different models. Furthermore, as a statistical feature like that of the histogram, distribution of Relative Angles has many other advantages including computational efficiency, insensitivity to noise, and ease with which it may be normalized. There are also established metrics for comparing such probability distributions. In the following sub-sections, we define two forms of Relative Angle-Context (RAC) distributions and use them as geometric signatures for the model vertices.

### 3.3. Relative Angle-Context distributions for the model vertices

Let us consider the Relative Angles around a vertex, what we RAC, as a random variable. The probability mass function (pmf) of the variable can be expressed as:

![Fig. 2. PCA frame and Relative Angles of 3D graphic model.](image)
\[ p_k(v_i) = \frac{1}{N} \sum_{j=1}^{N} \phi_j^k(v_i) \quad \text{where} \quad \phi_j^k(v_i) \]
\[
= \begin{cases} 
1 & \text{if } |(|\text{RAng}_{ij} - k)| \leq \delta & k \in [0, 2\pi] \\
0 & \text{otherwise}
\end{cases}
\] (6)

Here, \( \delta \) is the sample interval of the angles. We call this distribution curve, Relative Angle-Context Distribution (RACD). Obviously, RACD contains the full set \((N-1)\) Relative Angles of the spoke vectors, and gives detailed and compact description of the global shape context of a vertex. Furthermore, as the number of the sample points selected from the model increases the global shape is increasingly better approximated, and the representation of the shape becomes more exact. An example of RACD curve is shown in Fig. 1(b) and (c).

Similarly, we can further investigate the distribution of the Relative Angles using different ranges of the vertex’s neighborhood to capture successive local structures around the vertex as well as its global structure. Formally, let’s define the concept of “neighbor” for a 3D graphical model. We first define the first order neighborhood layer of vertex \( v_i \) as its immediate neighbors. That is, vertex \( v_i \) is in the set of its first order neighbors \( \text{nbr}_{1}(v_i) \) if and only if these two vertices share the same patch in the patches-set \( P \) of the model. In the same way, the vertices on the second neighborhood layer are the immediate neighbors of the immediate neighbors (i.e. 2nd order neighbors), and so forth. Please note that the neighborhood layers are constructed in a way that no vertex is repeated twice in the neighborhood of another vertex. From the definition of \( \text{nbr}_{1}(v_i) \), we can further define the \( j \)th neighborhood field \( \text{nbr}_{j}(v_i) \) for a given vertex \( v_i \) as:
\[
\text{nbr}_{j}(v_i) = \cup \text{nbr}_{l}(v_i) \quad (1 \leq t \leq j)
\] (7)

Suppose \( v_i \) has \( R(v_i) \) neighborhood fields, and its \( j \)th neighborhood field, \( \text{nbr}_{j}(v_i) \) contains \( S_j(v_i) \) vertices, we can construct \( R \) different Relative Angle-Context distributions for the different neighborhood fields. The \( j \)th neighborhood field distribution can be formulated as:
\[
p_j^k(v_i) = \frac{\sum_{\text{nbr}_{j}(v_i)} \phi_j^k(v_i)}{S_j(v_i)}
\]
\[
\phi_j^k(v_i) = \begin{cases} 
1 & \text{if } |\text{RAng}_{ij} - k| \leq \delta & v_j \in \text{nbr}_{j}(v_i) & k \in [0, 2\pi] \\
0 & \text{otherwise}
\end{cases}
\] (8)

The distributions based on the different neighborhood fields can be further concatenated to form a Neighborhood Relative Angle-Context Distribution (NRACD) curve for every vertex. That is, \( p_j(v_i) = \int_{R(v_i)\setminus(v_i)\cup R(v_i)} p_k(v_i), \) where \( r \leq l \leq R \) is the selected range of neighborhood fields and \( k \in [0, 2\pi, (R-r)] \).

It can be seen that NRACD expresses the local feature of a model surface as the value of \( k \) is small, and represents the global feature of the model when the value of \( k \) becomes large. When \( l = R(v_i) \), the curve describes the same global structure as RACD. Therefore, NRACD captures the local to global spatial information of the vertices around a given vertex. Hence NRACD is able provide a more accurate and robust basis for detecting point correspondence between 3D models, from the local to the global layers, in a hierarchical paradigm.

4. Point correspondence matching and model similarity measuring based on Relative Angle-Context distributions

Having defined the probability mass functions of the vertices, the next issue is to compute and provide a representation of these distributions. Since an analytical evaluation of the distribution is not feasible for each of the vertices, we employ stochastic methods to evaluate samples from the RACD and NRACD and construct a histogram by counting how many samples fall into certain sized bins. Suppose \( \Phi \) is the number of the histogram bins and all of the RACD and NRACD are rounded. For example, for RACD, if \( \Phi = 36 \), the Relative Angles will be rounded to the nearest 10 degree, e.g. 72° will be rounded down to 70° and 79° will be rounded up to 80°. If we select \( \rho \) possible histograms in NRACD and if the layer \( l \) in \( \text{nbr}_{l}(v_i) \) ranges from \( r \) to \( R \), in \( \Delta \) intervals, \( \rho = \frac{R-r}{\Delta} \) and the number of bins will be \( \rho*\Phi \).

4.1. Constructing point correspondence between 3D models

Once the RACD and NRACD of each vertex has been calculated, we compare them and produce a dissimilarity measure between the selected vertices belonging to two different models. Our hypothesis is that the distribution curves of the correspondence points of the same type of 3D objects should be similar and therefore the best matching distributions lead us to the most suitable point correspondence. In other words, we postulate that the distributions associated with a pair of corresponding points in the same class of 3D objects possess the same form of probability mass function, even though the random variables may be subjected to some forms of distortion and noise.

Formally, the dissimilarity between the RAC distributions of two vertices of the investigating models could be expressed as:
\[
d_k(v_i, v'_i) = ||p_k(v_i) - p'_k(v'_i)||, \]
(9)
where \( v_i \in V \) of model \( \mathcal{R} \) and \( v'_i \in V' \) of model \( \mathcal{R}' \). As RAC and NRAC are distributions represented as bins, it is natural to use Goodness-Of-Fit \( \chi^2 \) test statistics, i.e.
\[
df(v_i, v'_i) = \sum_{k=0}^{2\pi} \frac{\left[ (p_k(v_i) * S(v_i) - p'_k(v'_i) * S'(v'_i))^2 \right]}{p_k(v_i) * S(v_i)} . \]
(10)

We can further add a weight series \( \Omega \) into the discrepancy factor of NRACD, such that \( df \) is modified to
\[
df(v_i, v'_i) = \sum_{k=0}^{2\pi} \alpha_k \left[ (p_k(v_i) * S(v_i) - p'_k(v'_i) * S'(v'_i))^2 \right] / p_k(v_i) * S(v_i) \]
(11)
One of the examples of $o_k$ could be defined by a half Gaussian function which monotonically increases with the number of neighborhood fields, i.e.

$$o_k = \frac{1}{\sqrt{2\pi\sigma}} e^{-\frac{(x_i - 1)^2}{2\sigma^2}}.$$ 

The reason for selecting this definition is that the global features should be more important than the local features for establishing the robust point correspondence in most cases. This approach will make the correspondence detection algorithm insensitive to noise and subtle local deformations. In general, since the number of feature points for a given surface is not too large, and also since the histogram calculation and comparison are very computationally efficient, it is feasible to exhaustively search through all of the vertices in the target model to obtain the optimal solution without resorting to iterative optimization techniques.

Fig. 3. Typical head model and liver model: (a) a head model, (b) a slice of segmented liver images, (c) reconstructed liver model.

Fig. 4. (a) The correspondence matching in head models and (b) the plot of RACD curve for point A (blue solid lines) and point B (green dashed lines) on the left and right ears.
4.2. Similarity measure for 3D surfaces

Measuring the similarity between 3D shapes is a fundamental problem in many fields including computer vision, molecular biology and computer graphics. In our algorithm, after the point correspondence has been established, the surfaces of the two models can be compared easily and the similarity between two models can be quantified by the Similarity Factor $sf$ defined as:

$$sf_{R,W} = \frac{\sum_{i=1}^{N} 1 - df(v_i, cp(v_i))}{N},$$

(12)

### Table: Point Correspondence

<table>
<thead>
<tr>
<th>Point No.</th>
<th>Description</th>
<th>Ab.</th>
<th>Point No.</th>
<th>Description</th>
<th>Ab.</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Eye-Left Corner</td>
<td>Eye-LC</td>
<td>9</td>
<td>Ear-Right Lobule</td>
<td>Ear-RL</td>
</tr>
<tr>
<td>2</td>
<td>Eye-Right Corner</td>
<td>Eye-RC</td>
<td>10</td>
<td>Ear-Left Rim</td>
<td>Ear-LR</td>
</tr>
<tr>
<td>3</td>
<td>Nose-Tip</td>
<td>Nos-T</td>
<td>11</td>
<td>Brain-Hind</td>
<td>Bra-H</td>
</tr>
<tr>
<td>4</td>
<td>Nose-Bridge</td>
<td>Nos-R</td>
<td>12</td>
<td>Brain-Top</td>
<td>Bra-T</td>
</tr>
<tr>
<td>5</td>
<td>Nose-Base</td>
<td>Nos-B</td>
<td>13</td>
<td>Brain-Left Middle</td>
<td>Bra-LM</td>
</tr>
<tr>
<td>6</td>
<td>Lip-Upper Middle</td>
<td>Lip-M</td>
<td>14</td>
<td>Neck-Back Middle</td>
<td>Nec-BM</td>
</tr>
<tr>
<td>7</td>
<td>Lip-Right Corner</td>
<td>Lip-RC</td>
<td>15</td>
<td>Larynx-Middle</td>
<td>Lar-M</td>
</tr>
<tr>
<td>8</td>
<td>Ear-Left Helix</td>
<td>Ear-LH</td>
<td>16</td>
<td>Face-Right Middle</td>
<td>Fac-RM</td>
</tr>
</tbody>
</table>

Fig. 5. Correctness in correspondence matching of head models using iterative closest point (ICP) and our RACD approach.
where \( cp(v_i) \) is the corresponding vertex of \( v_i \) on the surface model \( W' \). Furthermore, the vertices that have high discrepancy factors (i.e. the most dissimilar corresponding points) could be identified through the similarity comparison and more interestingly, the most mismatched neighborhood fields of these vertices could also be detected using NRACD for further investigation. Undoubtedly, since the proposed approach provides a detailed similarity and morphological analysis for 3D models of human organs will potentially be invaluable for medical diagnosis and will also be very useful for other model-based applications such as 3D model classification, retrieval and object recognition.

5. Experiments and results

The methods described in the preceding sections have been implemented in C++ and incorporated into a 3D model matching system that runs on PC/Windows computers. The experiments were run on a PC with an 1,800 MHz Pentium 4 processor and 1GB of memory. We focus our experiments on human anatomical organs (such as the head and the liver) with well defined shape and have non-linearly deformation among patients. Frequently, it is often very difficult to define or to obtain a ground-truth correspondence point set for such models (especially for soft-tissue organs). This approach provides a feasible method of detecting point correspondence for such models.

5.1. Evaluation of the correctness of point correspondence in head models

We attempt to evaluate our Relative Angle-Context Distribution based matching algorithm in a systematic way. First, we test the correctness of our point corresponding algorithm in the human head database as shown in Fig. 3(a). Heads are roundish, approximate symmetric organ, but have some well-defined feature vertices. The head models employed in the experiments have been obtained from a 3D digital scanner. The number of vertices in a head model is around 6000, and the size of the patch-sets is 6000–7000. We use \( \Phi = 18, r = 40, R = 160, A = 40 \). The results show that our algorithm is very fast, the system takes around five seconds to construct a global correspondence map for two typical head models containing thousands of triangles, and it computes the dissimilarity measure for any pair of vertices in less than a millisecond. The time complexity of RACD is \( N \times \Phi \) and when the neighborhood relationship of NRACD is pre-computed, its time complexity is \( N \times \frac{\Phi}{2} \times \Phi \). The resultant corresponding point-sets between two head models are shown in Fig. 4(a). Interestingly, in this figure, we find that the vertex A, located on the edge of the right ear of the left model is correctly matched to the edge of the right ear of right model. Note that the Relative Angle-Context Distribution of vertex A on right ear and vertex B on the left ear have almost symmetrically mirrored distribution profiles, as shown in Fig. 4(b).

![Fig. 6. The comparison chart of the hit rates for RACD and NRACD.](image_url)

Furthermore, we select 16 feature points on the head model as shown in Fig. 5(a) and (b) to test the correctness of our RACD correspondence matching algorithm. However, hitting the exact vertex on the transformed version of the model would be too restrictive in the experiment, especially when the sample rate is very high, i.e. the surface points are very dense. So we consider the correspondence matching is acceptable if the resulting corresponding point is within the first order neighbor layer of the vertex, i.e.

\[
\text{hit-rate} = \frac{\sum_{i=1}^{N} \Psi(v_i)}{100}.
\]

where

\[
\Psi(v_i) = \begin{cases} 
1 & \text{if } cp(v_i) \in nbI_1(v_i) \cup v_i \\
0 & \text{otherwise}
\end{cases}
\]

Fig. 5(c) compares the correctness of correspondence matching using RACD and the Iterative Closest Point (ICP) algorithm [36]. In this evaluation, we use 100 human subjects with 100 different expressions each, altogether 10,000 models. We found that the performance of ICP was particularly good for some of the feature points, especially for points that lie on relatively flat surface such as points on the top of the head (e.g. points 11 to 13 in Fig. 15(b)), neck and cheek. That is because those surfaces are relatively rigid and do not deform very much across individuals and hence allow for more accurate surface matching using ICP. However, for most of the points that lie on high curvature or highly deformed surfaces, the correctness of correspondence matching are very low. Comparatively, in RACD, the correctness of matching for most of the feature points exceeds 90%. It can be also seen that the correspondence matching of a few feature points is not so good for various reasons. For example, the percentage of correct matches for the lip corner is 80% due to the different expressions of the models (for example, laughing); points on the top of head are around 73% due to differences in the global
head shape of the different subjects. Since the head model we used in the experiments are very dense, some of the surface points are located very close to each others. If we extend the acceptance region to the second or the third neighborhood layer, almost all of the feature points could find their correct correspondence region. Although we had not counted this kind of correct matches into the resultant hit-rates, the advantage of our approach can still be clearly demonstrated.

5.2. Evaluation of the correctness of point correspondence in affine transformed liver models

We also tested our proposed correspondence-matching algorithm in a liver model database. Liver models are particularly challenging for medical imaging and analysis due to potentially significant deformations of the liver obtained from individuals and the lack of a well defined boundary of the liver in CT or X-Ray liver images. Livers are roundish

![Fig. 7. Correspondence points matching between liver models. (a) The resulting matching of some selected vertices. (b) The RACD curve for vertex A. (c) The RACD curve for vertex B. (d) Superimposed RACD curves of the corresponding points of A for 10 liver models.](image-url)
and approximately symmetric which has caused other local feature based correspondence matching techniques to fail (such as local normal orientation statistics in [16] and local invariants such as corners or curvature in [9] and [18]). A rendered liver model is shown in Fig. 3(c). The liver models used in our experiments have been reconstructed from a Computerized Tomography image series provided by the Department of Diagnostic Radiology, Caritas Medical Centre in Hong Kong (as shown in Fig. 3(b)). Sample points on the liver contours were generated from the detected edges, and a triangular mesh representation of 3D liver surfaces was automatically constructed based on nearest neighborhood rules. In all of the following experiments on liver models, the cardinality of vertices-set in the liver model is $N = 1400–1,600$. The size of the patch-sets are $P = 2000–4000$. We use $\varphi = 72$ for RACD and $\varphi = 18$, $r = 10$, $R = 47$, $\Delta = 12$ in the NRACD based point corresponding algorithm.

In the following experiment, we define the hit-rate by finding the correspondence points between a model and its transformed versions of the same model (multiplied by a $3 \times 3$ matrix) with random perturbing noise (perturbing each vertex of every triangle randomly with a 1% position movement). Since the affine transform should not change the topological relationship between vertices, the ground truth for the point coupling is maintained after the transformation and can serve as our ground-truth. The comparison chart and resulting hit rates of RACD and NRACD have been shown in Fig. 6, 10 liver models have been tested in this experiment. The results of this experiment demonstrate our point correspondence algorithm is robust to the affine transformation, as well as noise and shape deformations.

5.3. Establishing point correspondence in a liver model database

Fig. 7(a) shows the established point correspondences between a number of selected vertices of two liver models, using the RACD approach. The first and second principal axes of the models are shown as in pink and yellow respectively. It can be observed that the resulting point correspondence is visually correct. The RACD curve of

![Image](https://example.com/image)

Fig. 8. (a) The comparison between two corresponding points (white dot in the left model and pink dot in the right model). (b) NRACD curves for four successive neighborhood sizes of these two points (blue solid line for white dot and green dash line for pink dot).
vertex A on the model on the left and its corresponding vertex \(A_0\) on the model on the right are plotted in Fig. 7(b) and (c), respectively. However, the true point correspondence is very difficult to define and evaluate on livers from a group of individuals. Typically, only a small number of vertices on a liver model could be accurately identified as landmark points by specialists. Even though, it is not difficult to discover that the profiles of the two distributions are very similar except the spectrum of Fig. 7(b) is wider than in Fig. 7(c). This is because at vertex A the surface of the left model has a lower curvature contour than that of the right one at vertex \(A_0\). The resulting RACD curves of 10 livers for the corresponding points of A are superimposed and plotted in Fig. 7(d). It can be seen that they matched very well even though some of the liver models were significantly different from each other (reference to Fig. 11).

One advantage of the Relative Angle-Context Distributions is that they contain the relative location information of a vertex in addition to its shape description. This can be achieved because differently located vertices have very different RACDs with respect to the principal axes. This characteristic is indispensable for matching vertices lying on symmetric surfaces, particularly for the vertices on roundish surfaces. Fig. 1(b) and (c) show the very different RACD curves of two vertices on the base part of the liver, which is an approximate half-sphere surface. The resulting curves are almost symmetric therefore induce a large discrepancy factor.

Fig. 9. A vertex (white dot in left model) and its top 10 candidate corresponding points (pink dots in right model) (a) using RACD (b) using NRACD.

Fig. 10. The chart for discrepancy factors of the verticex’s top 10 candidate corresponding points using RACD and NRACD respectively. (x: 1–10 candidate points in Fig. 9, y: the discrepancy factors of these 10 candidate points.)
5.4. **Performance comparison between RACD and NRACD**

To investigate the performances of NRACD and RACD, the Neighborhood Relative Angle-Context Distribution curves which include four successive neighborhood fields have been constructed and comparison of one of the corresponding points is shown in Fig. 8(b). Compared with RACD, NRACD is able to further reveal that the two vertices on the surfaces in Fig. 8(a) have a higher discrepancy in the first and second local neighborhood fields and basically match well on global structures.

In Fig. 9, we show the top ten potential corresponding points (pink dots in the model on the right) for a given vertex (white dot in the model on the left) by choosing the vertices on the model on the right which have the smallest 10 discrepancy factors based on RACD and NRACD respectively. The related $\text{dfs}$ are compared in Fig. 10. We found that the top 10 corresponding points converged very well in the corresponding region, which demonstrates that the algorithm does have a good ability to discriminate between the locations of the vertices. It is also easily seen that NRACDs have more discriminating power since the top ranked corresponding points using NRACDs have a much smaller $\text{df}$ than that of RACD while the other top 9 discrepancy factors increase significantly.

5.5. **Similarity measurement between liver models**

We also calculate the similarity factors between a reference liver model (Fig. 3(c)) and other nine liver samples using RACD, as shown in Fig. 11. Interestingly, if we plot the discrepancy factors for each vertex and its homologue as a discrepancy function between models (Fig. 12(b)), the points that have larger differences from their homologues can be easily identified. Fig. 12(a) shows the points in which $\text{df} > 0.1$ with red dots and it can be seen that these “dissimilar” points conform to what might be expected from simple observation. Undoubtedly, these kinds of sim-
ilarity measurements will prove valuable for clinical procedures and will also be useful for other 3D model retrieval or classification applications.

6. Conclusion and discussion

We have proposed a point correspondence-matching algorithm for polygonal free-form 3D surface models. The relative angles of the spoke vectors derived from a vertex have been defined and the probability mass function of the relative angles are used to describe the shape context in the neighborhood of the vertex. Two kinds of relative angle based distributions RACD and NRACD have been designed as the signatures of the vertices on similar 3D surfaces to build point correspondences between models. The experiments conducted have shown that both kinds of distributions are sensitive to global structures but that the NRACD is likely to produce more robust correspondence. Our experiments have also demonstrated that our algorithm produces correct results in terms of the similarity measurement and could be directly adopted in many model retrieval and classification applications, and image based medical applications.

There are many point correspondence matching algorithms have been proposed as we have reviewed in the first part of the paper. Each one has advantages and disadvantages. We admit that our algorithm could not achieve the “Best Correspondence” in some sense, as claimed in [31,32]. However, besides the high efficiency and robust, another important advantage of our method is no matter the surface points do or do not have truly ‘accurate’ correspondences, it can always locate into the correspondence region within a small neighborhood around correspondence. Sometimes this is very good performance for the medical images, since more accurate correspondence could be achieved by investigating some other features of the anatomical structure such as intensity or texture.

Acknowledgements

The authors would like to thank the Department of Diagnostic Radiology, Caritas Medical Centre, Hong Kong, for providing the liver CT images used in this work. This work is jointly supported by Competitive Earmarked Research Grant of the Research Grant Council, Grant No: CityU1150/01E, CityU1210/03E and CityU1137/06 of the Hong Kong SAR. Finally, we wish to thank the reviewers’ comments which have greatly helped to improve the presentation of this paper.

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