Shape Modeling Using Automatic Landmarking

Jun Xie and Pheng-Ann Heng

Department of Computer Science and Engineering
and
Shun Hing Institute of Advanced Engineering,
Chinese University of Hong Kong, Shatin, Hong Kong
{jxie, pheng}@cse.cuhk.edu.hk

Abstract. This paper describes a novel approach to automatically recover accurate correspondence over various shapes. In order to detect the features points with the capability in capturing the characteristics of an individual shape, we propose to calculate the skeletal representation for the shape curve through the medial axis transform. Employing this shape descriptor, mathematical landmarks are automatically identified based on the local feature size function, which embodies the geometric and topological information of the boundary. Before matching the resulting landmarks, shape correspondence is first approached by matching the major components of the shape curves using skeleton features. This helps in keeping the consecutive order and reducing the search space during the matching process. Point matching is then performed within each pair of corresponding components by solving a consecutive assignment problem. The effectiveness of this approach is demonstrated through experimental results on several different training sets of biomedical object shapes.

1 Introduction

Deformable models in medical imaging have a variety of applications including anatomical registration, segmentation and morphological analysis. Since shape information is a crucial visual cue for human perception, one of the most promising class of deformable models, the statistical model of shape [1], has been proposed to capture the patterns of variation in the shapes and spatial relationships in a class of objects. In this approach, a shape is commonly described by locating a finite number of points, the landmarks, on the boundary. Landmarks are well-defined points which are supposedly homologous from one instance to the next.

Although manual landmarking is an intuitive way to obtain those discernable points in practice, it is subjective and labor intensive and studies have shown that the precision of manual landmarking drifts with time and the accuracy varies among the landmarkers. There are also some semi-automatic and automatic landmarking approaches [2]. The mathematical landmarks are located according to some mathematical or geometric properties such as curvature, angle and arc length. One of the problem with curvature-defined landmarks is that in some applications (e.g. biological imaging), these points are not always born out clearly or uniquely by the individual shape, and in this case the landmarks must be inferred from a more global context.

Davies *et al.* [3] proposed to use the Minimum Description Length (MDL), as a quantitative measure of “simplicity”, to achieve a dense correspondence across a set of

shapes. However, like other global shape correspondence methods [4], the MDL-based approach constructs a very complicated and highly nonlinear cost function. Belongie *et al.* [5] introduced a shape matching scheme using roughly uniform samplings. Based on the proposed descriptor, this approach has produced encouraging results on a wide variety of data sets [6]. However, as shown by many researchers (e.g. [3]), the equally spaced landmarks can result in poor models, which indicates unit-length sampling cannot capture the shape's crucial characteristics if the sampling is not dense enough. Another weakness of this approach is the absence of any consecutive constraint. This leads to more erroneous matches. Recently, a continuity constraint was incorporated into the shape context matching scheme by Thayananthan [7] and the cost function was optimized using a dynamic programming.

In this paper, we present a simple and fast algorithm to obtain shape correspondence via an automatic landmarking scheme. Given a shape, we first re-sample the shape curve in an optimal way based on the Medial Axis Transform (MAT) proposed by Blum [8]. Landmarks along the shape curve are located using the Local Feature Size (LFS) function, which is determined by the geometric and topological features around the curve points. The major contribution of the paper is a fast and robust approach to match those non-uniformly samplings. It consists of two steps. First, the characteristic points on the medial axis are matched. This leads to an initial correspondence of different major components of the shapes. Then point correspondences are obtained within each pair of corresponding curve segments.

2 Optimal Shape Sampling

2.1 Medial Axis Transform

Let $F(u) = (x(u), y(u))$ be a smooth curve representing a shape. A point is on the medial axis (or skeleton) of the shape if it is equidistant from two or more points on the shape curve as shown in Fig. 1(a).

There are three kinds of points on a medial axis, including the endings, the midpoints and the junctions. In the continuous case, the distinction between an ending, a

Fig. 1. An illustration of the shape sampling rule. (Left) A curve (light) and its medial axis (heavy). The circle indicates a maximal disk. (Middle) The sampling result using the γ -sampling rule. There are totally 85 samples with $\gamma = 0.4$. (Right) The sampling result using curvature maxima (top 85 points).

midpoint and a junction of the skeleton follows from the number of times a disc centered at the point intersects the skeleton. The endings and midpoints are equidistant from exactly two boundary points while the junctions are equidistant from three or more points on the boundary. The maximal disk associated with the singular medial location osculates the object's boundary, meaning that the curvature radius (CR) of the boundary at the location of tangency is equal to the radius of the maximal disk. The two involutes necessarily converge at this location of tangency.

Based on the medial axis directly, many approaches [9,10] have been developed for shape matching. However, comparing shapes via exact matching of medial axes is not trivial since the internal structure of medial axis may change greatly due to minute deformation or occlusion of shape curves as shown in Fig. 3.

2.2 Shape Sampling

Given a shape, we seek a method to sample the shape curve with a compact set of points, which can characterize the inherent feature of this shape uniquely. In other words, this set of samplings can lead to only one possible smoothed curve, the original shape. Our sampling condition is based on a geometric length scale, local feature size, which was first proposed by Ruppert [11] for mesh generation. The local feature size for a shape F is a continuous function: $LFS : F \rightarrow R^2$ defined as distance of $p \in F$ to the medial axis of F , see Fig. 1(a). Because it is defined on the medial axis, the local feature size function is dominated by both the geometric features (e.g. curvature and orientation) and the topological features (e.g. symmetry and width).

Using this detail descriptor, we sample a curve under the following γ -sampling condition. Let $S \in R^2$ be a set of points on a shape F . Set S is defined as a γ -sample of F if for each point $p \in F$, there is a sample point $q \in S$ so that $\|p - q\| \leq \gamma LFS(q)$. This condition makes sampling density vary with the local feature size on the curve, so that areas of less detail will be sampled less densely. Two sampling results using γ -sampling condition and curvature maxima are shown in Fig. 1(b) and Fig. 1(c), respectively. We can see that γ -sampling can produce a more representative and full descriptor for the shape than the curvature maxima based sampling method.

It has been observed that for $\gamma \geq 1$, the sample set may produce more than one curve that is the polygonal reconstruction of a smooth curve γ -sampled by S . This indicates the sampling is not dense enough for the unique reconstruction of the original shape. In this case, there are some small features on the shape that are sampled inadequately. Therefore, such a undersampling will block the success of point distribution based shape matching. On the other hand, for considerably smaller γ (e.g. $\gamma < 1$), Amenta [12] and Dey [13] have shown that there is only one possible reconstruction of the curve. Typically, in our approach, $\gamma = 1/3$ gives a good performance for all experiments.

3 Shape Correspondence

After the optimal sampling process, each shape is represented by a set of sampling points $S = \{s_1, s_2, \dots, s_n\}$, $s_i \in R^2$. Because our sampling rule is an adaptive strategy based on the medial axis, the number of resulting samplings at each shape may not equal. Given two shapes and their sampling sets, S_1 and S_2 , we wish to match one point

in S_1 to another point in S_2 , in an optimal scheme. One way to achieve this purpose is to check all possible matchings of the two sets of points and choose the assignment with maximal similarity as the result [5]. However, this is computationally expensive and prone to produce erroneous matches. It would be desirable to obtain a good correspondence in the first step. We thus propose the following two-stage matching scheme.

3.1 Initial Matching

In the first step, we match the two shapes using only the topological principle points on the medial axis. The skeleton is a nice shape descriptor because it captures the notion of parts and components, while the skeleton's principle points are important features to describe the topological information embedded in the skeleton.

We assume that different shapes of a certain object usually compose of the similar significant components. Because each ending on the medial axis generally locates in a major component or part of the shape, these endings have a good capability in indexing the major parts. On the other hand, we observe that the junctions and midpoints on medial axis are too sensitive to the changes of the shape curve. Therefore, we choose only the endings for the coarse matching. A point on the medial axis can be identified as an ending if there is only one skeleton point in its eight neighbors.

To match two sets of endings, we use the shape context matching method [5]. Given a set of samplings $S = \{s_i\}_{i=1}^L$ of a shape F and the endings $E = \{e_k\}_{k=1}^K$ of its medial axis, the shape context of each ending $e_k \in E$ is a log-polar histogram h_k , which records the relative locations of the sampling points referring to e_k .

The optimal matching of two sets of endings is achieved by minimizing the total matching cost $\sum_1^K C(k, \pi_k)$, where π_k is the index of correspondence of e_k and $C(k, \pi_k)$ denotes the cost of matching e_k with e_{π_k} , measured using the χ^2 statistic of their shape contexts. When the two sets of endings have difference sizes, dummy points will be added to each set. The resulting square cost matrix is then input to an assignment problem (AP) and the optimal matching between the two sets of endings is obtained by solving this AP problem using the algorithm in [14].

Fig. 2. An example of ending matching. (a) and (b) are two shapes of a hand. Because the two shapes have the same significant components, the ending correspondence is very intuitive. (c) A pair of corresponding segments in (a) and (b). The two arcs direct the corresponding ending tangents.

Fig. 3. An example of shape matching. (a) and (b) are two hand outlines with corresponding segments. The same colors indicate the corresponding segments. The point matching results of the shape context method and our method are shown in (c) and (d), respectively.

Recall that each point on the medial axis has two or more tangents on the shape. Particularly, each ending has exactly two tangents. We can imagine the ending tangents as hinges between a sequence of segments of the shape curve. Each segment consists of an opened curve and two ending tangents (see Fig. 2).

To find the point correspondence across two shapes, we want to match these segments first. This can be done easily with the matching of the medial axis endings. Consider a pair of corresponding endings of two shapes. There are only two possible mapping of their ending tangents from one shape to another. For an ending tangent t_i on the first shape, we choose as its correspondence the candidate t_j on the second shape with the smaller matching cost $C(t_i, t_j)$. Because each segment of the shape can be identified by two neighboring ending tangents, the correspondence of ending tangents on the two shapes leads to a unique matching of these segments. See Fig. 3(a-b) for an example of the initial matching result.

3.2 Point Correspondence Within Segments

After obtaining the segment correspondence, the point correspondence problem can be restricted to searching the optimal matching within only each pair of corresponding segments. This provides a significant gain to increasing the robustness of shape matching, for the mismatch from one component to others is avoided. Moreover, this matching strategy can improve the speed of the matching process greatly since, for each point on one shape, only several points on the corresponding segment will be considered.

Now, we consider the point correspondence problem within a pair of corresponding segments. Recall each segment has two terminals, i.e. two ending tangents. Given two segments $\Gamma_1 = \{t_{11}, s_{11}, \dots, s_{1i}, \dots, s_{1m}, t_{12}\}$ and $\Gamma_2 = \{t_{21}, s_{21}, \dots, s_{2j}, \dots, s_{2n}, t_{22}\}$, we want to find the best match across the two sets of points. Without loss of generality, we suppose the points on each segment are in the following order $t_{11} < s_{11} < \dots < s_{1i} < \dots < s_{1m} < t_{12}$, $t_{21} < s_{21} < \dots < s_{2j} < \dots < s_{2n} < t_{22}$ and $m \leq n$. Because those samplings are selected in an optimal way, all of them are useful for describing the input shapes. Therefore, we wish to find the largest match between the pair of segments. In other words, we want to find $\min(n, m)$ pairs of corresponding points across the two segments.

Note that the points on each segment are arranged in a string order. We constrain our method to preserve this ordering in the matching. Meanwhile, since Γ_1 and Γ_2 are corresponding segments, their terminals should also be corresponding to each other, i.e. $t_{11} \leftrightarrow t_{21}$ and $t_{12} \leftrightarrow t_{22}$. Fig.2(c) gives an illustration of this matching problem, which we define as Consecutive Assignment Problem (CAP). This problem can be solved by the following optimal combination scheme.

Because Γ_1 contains fewer samplings than Γ_2 ($m \leq n$), for each sampling $s_{1i} \in \Gamma_1$, we need to find one sampling from Γ_2 . Thus, finding one-to-one point matching between two segments is equivalent to removing $(n - m)$ samplings from Γ_2 so that the remaining set of samplings on Γ_2 have the same size as that on Γ_1 . Because each set of samplings is in a string order and the terminals of the two strings are already matched, there is a unique matching between the two sets of samplings. To measure the similarity of points, the shape context of each point is calculated using all the samplings obtained through the re-sample process introduced in previous sections. The point correspondence is found by minimizing the sum of cost $\sum_{i=1}^m C(i, \pi_i)$.

The search space for this consecutive assignment problem is $C_n^{(n-m)}$, which is much smaller than that for the assignment problem in [5]. Moreover, the points to be considered in this step are restricted in the curve segment. Therefore, the number of points in this case is only a small set of the total samplings of the whole shape. Those greatly improve the matching speed. A matching example of two outlines of a hand is shown in Fig. 3.

4 Experiments

To demonstrate the performance of our approach for statistical shape modeling, we apply it on several training sets of biomedical objects. For an object, each shape in the training set is matched to all others with the minimal sum of matching cost, which is defined as the difference of each pair of shapes. The shape with the minimal total difference is selected to find the overall correspondence of the whole set, by selecting the same corresponding points among the matching results of it with other shapes.

Fig. 4 shows two of our experimental results. The hand training set contains 15 hand outlines extracted from the Jochen Triesch Static Hand Posture Database [15] and the

Fig. 4. Two models automatically generated using the proposed approach

Fig. 5. Three kidney models generated using the proposed method, manual landmarks and even-space samplings

Table 1. Evaluation of The Three Kidney Models

Kidney Model	Number of Points	Variance			
		Mode 1	Mode 2	Mode 3	Total
Automatic Landmarking	81	46.89	34.92	13.08	94.89
Manual Landmarking	54	60.13	34.91	14.58	109.62
Even-space Sampling	81	172.86	35.44	30.82	239.12

callosum set contains 14 callosum shapes extracted from 14 MRI brain slices. Using the proposed automatic landmarking algorithm, we obtained 128 landmarks on each shape for the hand data set and 112 for the callosum data set. Each three rows of the two experiments show the first three modes of each model varied by $\pm 2\sigma$, where σ refers to the standard deviation along principal directions.

To evaluate our method quantitatively, we compared the automatic model (Fig. 5) with those built using manual landmarks and equally spaced samplings, in terms of variance of the three largest modes of the models. The training data is the kidney data set from [16] which contains 20 2D left kidney shapes from different patients. The quanlity results in Table 1 show that the automatically generated model has the smallest variances in all three principal directions.

5 Conclusions

In this paper we have presented a novel approach for automatic landmarking of shapes. To capture the crucial characteristic of a shape, we sample the shape curve based on the local geometric and topological features. Then the shape correspondence is obtained through a two-stage matching approach, which stands for the major contribution of this paper. The course mapping of the skeleton endings provides an initial correspondence of the major components of the shapes, yet allows the following local point matching so that the computation complex is considerably reduced. Meanwhile, because the consecutive enforcement included in the point matching process, our approach enables better correspondences. We evaluated the proposed approach using the statistical shape modeling on various shapes of biomedical objects and the results are excellent in terms of both compact and speed.

Acknowledgments

The work described in this paper was supported by a grant (Project No. CUHK4223/04E) from the Research Grants Council of the Hong Kong Special Administrative Region, China and CUHK Shun Hing Institute of Advanced Engineering.

References

1. T. Cootes, C. Taylor, D. Cooper, and J. Graham, "Active shape models-their training and application," *Computer Vision and Image Understanding*, vol. 61, pp. 38–59, 1995.
2. F. Mokhtarian and R. Suomela, "Robust image corner detection through curvature scale space," *IEEE Trans. Pattern Anal. Machine Intell.*, vol. 20, no. 12, pp. 1376–1381, 1998.
3. R. Davies, C. Twining, T. Cootes, J. Waterton, and C. Taylor, "A minimum description length approach to statistical shape modeling," *IEEE Trans. Med. Imag.*, vol. 21, no. 5, pp. 525–537, 2002.
4. A. Hill, C. Taylor, and A. Brett, "A framework for automatic landmark identification using a new method of nonrigid correspondence," *IEEE Trans. Pattern Anal. Machine Intell.*, vol. 22, no. 3, pp. 241–251, 2000.
5. S. Belongie, J. Malik, and J. Puzicha, "Matching shapes," in *Proc. IEEE Int. Conf. on Computer Vision*, Vancouver, Canada, 2001, pp. 454–463.
6. ———, "Shape matching and object recognition using shape contexts," *IEEE Trans. Pattern Anal. Machine Intell.*, vol. 24, pp. 509–522, 2002.
7. A. Thayananthan, B. Stenger, P. H. S. Torr, and R. Cipolla, "Shape context and chamfer matching in cluttered scenes," in *Proc. IEEE Computer Vision and Pattern Recognition*, vol. I, Madison, USA, June 2003, pp. 127–133.
8. H. Blum, "A transformation for extracting new descriptors of shape," in *Proc. Models for the Perception of Speech and Visual Form*, W. Wathen-Dunn, Ed. Cambridge, MA: MIT Press, Nov. 1967, pp. 362–380.
9. D. Sharvit, J. Chan, H. Tek, and B. B. Kimia, "Symmetry-based indexing of image databases," *Journal of Visual Communication and Image Representation*, vol. 9, no. 4, pp. 366–380, Dec. 1998.
10. T. B. Sebastian, P. N. Klein, and B. B. Kimia, "Recognition of shapes by editing shock graphs," in *Proc. IEEE Int. Conf. on Computer Vision*, 2001, pp. 755–762.
11. J. Ruppert, "A new and simple algorithm for quality 2-dimensional mesh generation," in *Proc. ACM-SIAM Symposium on Discrete algorithms*, 1993, pp. 83–92.
12. D. E. N. Amenta, M. Bern, "The crust and the β -skeleton: Combinatorial curve reconstruction," *Graphical Models and Image Processing*, vol. 60, no. 2, pp. 125–135, 1998.
13. T. Dey, J. Giesen, S. Goswami, J. Hudson, R. Wenger, and W. Zhao, "Undersampling and oversampling in sample based shape modeling," in *Proc. IEEE Visualization*, vol. I, San Diego, California, Oct. 2001, pp. 83–90.
14. R. Jonker and A. Volgenant, "A shortest augmenting path algorithm for dense and sparse linear assignment problems," *Computing*, vol. 38, no. 4, pp. 325–340, 1987.
15. J. Triesch and C. Malsburg, "A system for person-independent hand posture recognition against complex backgrounds," *IEEE Trans. Pattern Anal. Machine Intell.*, vol. 23, no. 12, pp. 1449–1453, 2001.
16. J. Xie, Y. Jiang, and H. Tsui, "Segmentation of kidney from ultrasound images based on texture and shape priors," *IEEE Trans. Med. Imag.*, vol. 24, no. 1, pp. 45–57, Jan. 2005.