Rapid and Brief Communication

Graph matching for object recognition and recovery

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Abstract

A robust skeleton-based graph matching method for object recognition and recovery applications is presented. The object model uses both a skeleton model and contour segment models, for object recognition and recovery. The presented skeleton-based shape matching method uses a combination of both structural and statistical methods that are applied in a sequential manner, which largely reduce the matching space when compared with previous works. This also provides a good alternate means to alleviate difficulties encountered in segmentation problems. Experiments of object recovery using real biomedical image samples have shown satisfactory results.
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1. Introduction

Image understanding includes two key interrelated components: image segmentation and object recognition. Image segmentation yields contours, either exact or approximate, of objects of interest in images for recognition. Object recognition performs shape matching and the results can be fedback into the image segmentation to increase the accuracy of the segmentation results. This is normally referred to as object recovery. The object recognition in the object recovery is the focus in the paper, which is realized through shape matching, by matching the skeleton graph of the input contour from a deformable contour method (DCM) with those of the models. Skeleton is selected as the object shape descriptor due to its significant features on the desired representational properties, such as invariance to object geometric transformations (translation, rotation and scaling) and reversibility to the original shape. Moreover, skeleton is the only representation method providing object structural information, such as location of convex-parts, width and length of each part, which is important for the object recognition applications.

The "best" matching skeleton pair determines the correct model and constructs the contours' feature point (landmark) correspondences. The correspondences of the contours' segments follow automatically. Then, for the contour segments with a large error compared with the matched model segments, a fine-tuning process, which is formulated as a maximization of a posteriori probability [2], is performed for final result.

The objective of this paper is to present a new skeleton-based object shape matching approach to yield a robust and efficient model-based object recovery. Previous skeleton-based works for object recognition [3,4] are not suitable for this object recovery application since correspondences on contour landmarks cannot be determined from their skeleton edges correspondences. The notation for skeleton entities is presented in Section 2. Section 3 gives the algorithm description. Experimental results on matching animal profiles for recognition and recovering shapes in biomedical images are provided in Section 4.

2. Skeleton structure notation

The skeleton representation consists of the locus of centers of maximal disks (CMD) that can be inscribed within

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Fig. 1. A skeleton graph (a), its tree representation (b) and SE string (c).

the object and a maximal disk is not completely contained in any other disk in the object. The notation used for the major skeleton entities is illustrated in Fig. 1(a) with a skeleton example of a side view of a quadruped animal. The curve segments of actual skeleton edges are simplified as line segments in a *skeleton graph*. The attributes of a skeletal point on the derived skeleton graph are its distance value and if it is a CMD or not. A skeletal point having only one skeletal point in its eight neighbors is defined as an *ending node* (E-node) (e.g. A, B) and a skeletal point having at least three skeletal points in its eight neighbors is defined as a *bifurcation node* (B-node) (e.g. C, D). All others are normal nodes. After the skeleton computation, skeletal points can be linked to form skeleton edges (SE). A SE that has two B-nodes is defined as a *primary* SE (e.g. CD, DJ), otherwise it is a *normal* SE (e.g. AC, BC).

3. Proposed approach

This skeleton-based shape matching and recovery approach can be described in four major steps: (I) skeleton processing, (II) skeleton model construction, (III) skeleton matching and model detection, and (IV) contour segment correction, as shown in Fig. 2.

3.1. Skeleton processing

The first step consists of determining the skeleton, removing SEs produced by shape noise, and representing the skeleton. After the skeleton computation [1] for input and model shapes, the skeletons can then be pruned based on the importance of the SEs, which are measured by the number of the object points to produce the SEs. Then a B-node tracing algorithm to generate a skeleton tree is applied by recording SEs sequentially, starting from the B-node connected with the shortest normal SE. The tree nodes are the B-nodes and the tree edges are the primary SEs, as shown in Fig. 1(b). Finally, the skeleton tree can be represented as a SE string grouped by the B-nodes, and each group consists of a set of normal SEs connected by the common B-node, as shown in Fig. 1(c).

3.2. Skeleton model construction

The following specifies a skeleton model: (1) rigid transformations, (2) nonrigid deformations, and (3) model

Fig. 2. Proposed approach flowchart.

specific rules. The first includes the admissible connectivity relationship among the skeleton edges, parameterized by the bifurcation angles between adjacent SEs and the variations of skeleton edges caused by the bifurcation delay/splitting phenomena (BDP/BSP) [3] (e.g. the B-node D will split to two B-nodes as FD shifts left along DJ in Fig. 1(b)). The second includes the object shape variations, described as the Gaussian distribution on the distance values of skeletal points. A typical example of the model specific rules would be that the limbs should be the protrusions on the same side of body for any side-view of quadruped mammals and birds.

3.3. Skeleton matching and model detection

The skeleton matching and model detection algorithm encompasses three major steps: searching for possible matches or correspondences between the SEs of the input skeleton and the skeleton models; checking the validity of identified matches based on the model information; and computing similarity measure to determine the correct model and SE correspondences.

A branch-and-bound string matching algorithm is used in our application. The algorithm searches over all possible matches between the two strings for the same number and

connectivity relationship of B-nodes, and the same numbers of primary and normal SEs in each matched B-node group pair. For each match found, several validity checks based on the rules and information collected in Section 3.2 can be used to take out the invalid matches, thus reduce the searching space for following steps.

The last task is to detect the correct model from a set of models passed above checking and to determine the correct SE correspondences based on a similarity function between the input and a model. Given an input shape skeleton string $D = (d_1, d_2, \ldots, d_R)$ and its corresponding model skeleton string $M = (m_1, m_2, \ldots, m_R)$, their similarity function is defined as: $S(D, M) = e^P/(E_1 E_2 E_3)$, where P is the thickness similarity of the input shape D and a model M, weighted by the shape error weight E_1, the thickness error weight E_2, and the length error weight E_3. Here

$$P = \frac{1}{R} \sum_{i=1}^{R} p(d_i, m_i),$$

$$\text{with} \quad p(d_i, m_i) = \prod_{j=1}^{N} \frac{1}{\sigma_j \sqrt{2\pi}} e^{-(rd_{ij} - rm_{ij})^2/2\sigma_j^2},$$

where rd_{ij} and rm_{ij} are the normalized distance values of the jth corresponding points on the skeleton edges d_i and m_i, respectively, after normalizing the skeleton edges d_i and m_i to be the same length N. rd_{ij} and rm_{ij} are normalized with respect to the largest distance value on d_i and m_i. σ_j is the variance of the normalized rm_{ij}. In the experiments, we use $\ln(p(d_i, m_i))$ instead of $p(d_i, m_i)$ to avoid a very small P. The E_1 is to measure the shape difference between D and M. After transforming the input SE d_i to the coordinate system of its corresponding model SE m_i and normalized to the same length as d_i', E_1 can be computed as

$$E_1 = \frac{1}{R} \sum_{i=1}^{R} e_1(d_i, m_i), \quad \text{with} \quad e_1(d_i, m_i)$$

$$= \frac{1}{N} \sum_{j=1}^{N} \sqrt{(xd_{ij}' - xm_{ij}')^2 + (yd_{ij} - ym_{ij})^2},$$

where (xd_{ij}', yd_{ij}') and (xm_{ij}, ym_{ij}) are the coordinates of the jth corresponding points on d_i' and m_i, respectively. The E_2 is to measure the difference of the average thickness ratio between D and M, and it is formulated as

$$E_2 = \frac{1}{R} \sum_{i=1}^{R} e_2(d_i, m_i), \quad \text{with} \quad e_2(d_i, m_i)$$

$$= \frac{|\overline{rd_i}/\overline{rd} - \overline{rm_i}/\overline{rm}|}{\overline{rm_i}/\overline{rm}},$$

where $\overline{rd_i}$ and $\overline{rm_i}$ are the average distance values of d_i and m_i, $\overline{rd}$ and $\overline{rm}$ are the average distance values of all the skeletal points on D and M. Likewise, the length error weight E_3 is to measure the difference of the length ratio between D and M. The model has the largest similarity

with the input is selected as the correct one, together with the correct skeleton edge correspondences. When the input skeleton has additional or missing SEs, only the similarity between the matched SEs is computed.

3.4. Contour segment correction

The contour landmarks are determined by the E-nodes of its SEs. These landmarks are then used to determine the contour segment correspondences. Contour segments are compared for errors. A fine-tuning process, which is formulated as a maximization of a posteriori probability [2], given the contour segments model and image features, is performed on the segments with large errors for final result.

4. Experiments

In this section, two experiments are used to illustrate our algorithm: the first experiment uses a set of animal silhouette shapes to demonstrating the graph matching algorithm for object recognition; the second uses biomedical image samples, MRI corpus callosum images to show the object recovery process.

Skeleton-based graph matching for model detection are demonstrated by selecting the most similar shape for the input test shapes, shown in Fig. 3, from a set of animal model shapes shown in Fig. 4. Both the input and the model shapes include several quadruped mammals and birds, which were obtained from some
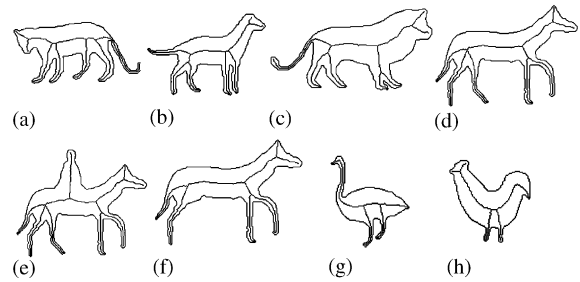

(a)　　　(b)　　　(c)　　　(d)

(e)　　　(f)　　　(g)　　　(h)

Fig. 3. The input animal shapes and skeletons.

(1) cat　　(2) dog　　(3) horse　　(4) lion
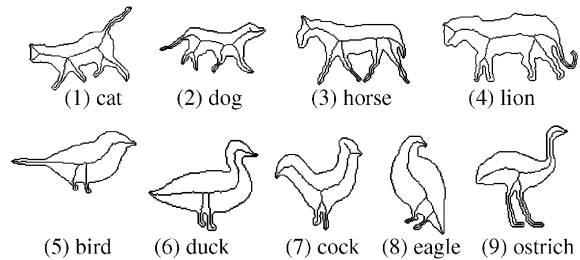
(5) bird　　(6) duck　　(7) cock　(8) eagle　(9) ostrich

Fig. 4. The model animal shapes and skeletons.

Table 1
Similarities between input and model shapes

	(a)	(b)	(c)	(d)	(e)	(f)	(g)	(h)
1	**8.90**	2.79	0.18	0.65	0.64	**3.81**	—	—
2	0.01	**4.66**	0.01	0.22	1.98	2.05	—	—
3	4.45	3.27	0.55	**3.70**	**3.61**	0.97	—	—
4	5.12	0.28	**5.12**	0.08	0.06	0.88	—	—
5	—	—	—	—	—	—	0.44	2.49
6	—	—	—	—	—	—	1.74	0.86
7	—	—	—	—	—	—	3.94	**3.53**
8	—	—	—	—	—	—	3.17	3.30
9	—	—	—	—	—	—	**4.08**	1.70
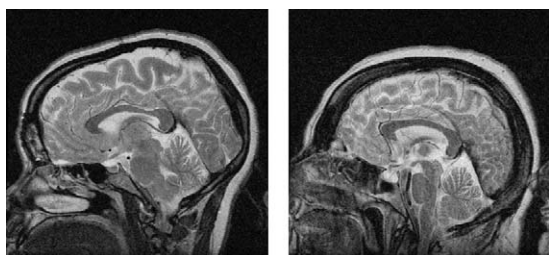
Fig. 5. Two examples of the original MRI brain image.

Fig. 7. The resulting corpus callosum contour after contour segments correction (a) Brain 1 final result, (b) Brain 2 final result.

Fig. 6. The corpus callosum model and input shapes obtained by a DCM; (a) Model, (b) Brain 1 input, (c) Brain 2 input.

biology books, and the Brown University Stimuli (http://www.cog.brown.edu/~tarr/stimuli.html). After skeleton matching is used to locate the corresponding skeleton edges between the input and all the possible models, the similarity functions are computed for all valid matches. Table 1 shows the linearly normalized similarity values (0–10), with the highest values being shown in boldface. The quadruped mammals do not match with birds because their skeleton structures are not the same.

Two experiments on MRI corpus callosum images (Fig. 5) are used to illustrate how to apply the skeleton-based graph matching algorithm for object recovery. The two input corpus callosum shapes (Fig. 6(b), (c)) obtained by
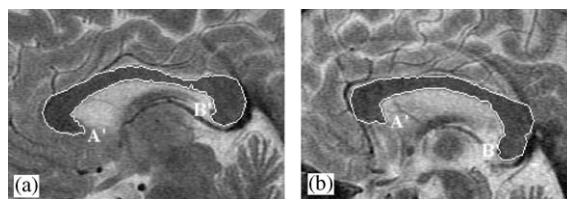
a DCM are used to match with the corpus callosum model (Fig. 6(a)). The landmarks are determined from the skeleton E-nodes and the skeleton matching algorithm is applied to construct the correspondence, as shown in Fig. 6(A–A, B–B). Compared with the corresponding model contour segments, the contour segments AB (top segments) in both input contours have large error. The contour segment correction approach is then applied to search the final result, as shown in Fig. 7.

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