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Organic skeleton correspondence using part arrangements

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Abstract. Shape correspondence between semantically similar organic shapes with large shape variations is a difficult problem in shape analysis. Since part geometries are no longer similar, we claim that the challenge is to extract and compare prominent shape substructures, which are recurring part arrangements among semantically related shapes. Our main premise is that the challenge can be solved more efficiently on curve skeleton graphs of shapes, which provide a concise abstraction of shape geometry and structure. Instead of directly searching exponentially many skeleton subgraphs, our method extracts the intrinsic reflectional symmetry axis of the skeleton to guide the generation of subgraphs as part arrangements. For any two subgraphs from two skeletons, their orientations are aligned and their pose variations are normalized for matching. Finally, the matchings of all subgraph pairs are evaluated and accumulated to the skeletal feature node correspondences. The comparison results with the state-of-the-art work show that our method significantly improves the efficiency and accuracy of the semantic correspondence between a variety of shapes.

§1 Introduction

Humans perform well in perceiving semantics of parts and giving a semantically meaningful part matching across shapes. However, inferring semantics computationally and automatically is very difficult. Thus, shape correspondence methods [8] rarely combine part semantics as prior knowledge and heavily rely on part geometries. In the presence of large pose, geometric and topological variations, geometric similarity becomes unreliable and these methods fail to obtain semantically correct correspondence.

Given a set of semantically related man-made shapes, Zheng et al. [15] observe that although part geometries are quiet different, part spatial *arrangements* (how parts are arranged) are consistent among shapes (e.g., the arrangements of chair legs, seat and back among various chairs in the left of Fig. 1), and thus can be used to reveal semantic correspondence. However,

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Figure 1: Part arrangements among man-made shapes (left) and organic shapes (right). The part arrangements of organic shapes vary under different poses.

the part arrangements of organic shapes vary under different poses [11] (e.g., the arrangements of arms, legs and the body of a monster in the right of Fig. 1), which is beyond the realm of Zheng et al. [15].

In this paper, we focus on the correspondence between two organic shapes with large pose, geometric and topological variations. The challenges to take advantage of part spatial arrangements come from three aspects: Firstly, organic shapes usually come as a whole and segmenting them into parts is difficult and time-consuming in itself. Man-made shapes, by contrast, consist of multi-components and Zheng et al. [15] directly group these components to form candidate parts. Secondly, man-made shapes commonly found online are assumed to have a consistent upright orientation, which makes sure the consistency of part arrangements across shapes. However, the orientations of organic shapes are not aligned. Lastly, the part arrangements of organic shapes vary extrinsically as mentioned.

Our key insight is that it is natural to identify parts and part arrangements on the curve skeleton of a shape. In general, an edge connecting two skeletal feature nodes corresponds to a shape part, and a subgraph with more than one edge corresponds to a part arrangement. Moreover, the skeleton is naturally augmented with geometric properties (e.g., local radius) and distance metrics (e.g., geodesic distance measured along the curve skeleton) from the surface, which are crucial for establishing correspondence. Therefore, we turn to discover part arrangements on the curve skeleton.

Given two organic shapes, we extract their curve skeletons automatically and aim to correspond two sets of skeletal feature nodes (Fig. 2a). Firstly, subgraphs as parts and part arrangements are identified for each skeleton (Fig. 2b). In order to make sure these subgraphs capturing prominent skeleton structures, an intrinsic reflectional symmetry axis is extracted for guidance. Secondly, subgraphs of part arrangements are basic matching units of two skeletons (Fig. 2c). Before matching, the orientation alignment of two skeletons is reduced to the alignment of their symmetry axes. And the pose variations between two skeletons are normalized by a spatial embedding method, which spans out each skeleton. In this way, the orientations between any two subgraphs from two skeletons are consistent and their pose variations are normalized. Lastly, the matchings of all subgraph pairs are evaluated to vote on the skeletal feature node correspondence (Fig. 2d, e).



Figure 2: Algorithm overview. (a) Two input curve skeletons; (b) Symmetry-guided generation of parts and part arrangements. Parts are shown in different colors and the red path is a segment of the symmetry axis; (c) Part arrangement matching. The orientations and pose variation of two skeletons are aligned and normalized for matching and good subgraph matchings are shown in green boxes; (d) The voting matrix; (e) The output feature node correspondence.

We demonstrate the efficiency, effectiveness and robustness of our algorithm on a range of semantically similar shape pairs with large pose, geometric and topological differences. The results of comparison experiments exhibit that the efficiency and accuracy of our method is significantly better than that of the state-of-the-art work Au et al. [1]. Au et al. [1] is the most relevant skeleton correspondence work to ours. They use all subgraph pairs of two skeletons as matching units to vote for skeletal feature node correspondence. By limiting the matching units to subgraphs of part arrangements, which contain significant shape substructures, we dramatically reduce the number of matching units and increase the correctness percentage of node correspondences from matched subgraph pairs.

§2 Related work

Our problem and algorithm pipeline are related to shape intrinsic correspondence and intrinsic symmetry analysis, which are well studied shape analysis problems with extensive previous work. Here we focus our review on the most relevant work.

Curve skeleton correspondence. Since the geometric similarity between two shapes with large variations is not reliable, semantic correspondence calls for global structural information. Various methods have been proposed to construct a graph through curve skeleton extraction,

which provides a robust abstraction of shape geometry and structure. Each graph node corresponds to a shape part and is augmented with geometric descriptors for graph matching. Moreover, recent curve skeleton extraction algorithms perform well for rough shapes [2], even incomplete point clouds [13,5], which makes shape correspondence on skeleton graphs more robust than on noisy surfaces.

Given two skeleton graphs, Bai et al. [3] directly match graph nodes by comparing their geodesic paths. Zhang et al. [16] propose a deformation-driven combinatorial search algorithm for the best node correspondence. The evaluation of the deformation distortion for each possible node correspondence is too costly, which can be dozens of minutes. Au et al. [1] perform a combinatorial search using fast pruning tests to eliminate exponentially many bad correspondences. The passed correspondences vote for a high-quality node correspondence. Our method neither is a direct nor a combinatorial method. By generating and matching subgraphs of part arrangements, our method is a top-to-bottom method, that is from subgraph matchings to node correspondences. Node that the topological structure among internal nodes is sensitive and can be different, Bai et al. [3] and Zhang et al. [16] ignore internal nodes and only match terminal nodes. Au et al. [1] and our work support internal node correspondences. Moreover, Au et al. [1] and our work consider the spatial configuration of symmetric nodes and solve the symmetry switching problem.

Skeleton-intrinsic symmetry analysis. Most intrinsic symmetry analysis works directly search for the best distance-preserving self-mapping on shape surfaces. Some recent works are skeleton-driven or skeleton-intrinsic. Xu et al. [14] compute prominent intrinsic reflectional symmetry axes on shape surfaces by a voting scheme. Jiang et al. [7] apply the voting scheme of Xu et al. [14] to vote for symmetric node pairs of the skeleton, and then the symmetry map of the skeleton is transformed to the input point cloud. Zheng et al. [17] introduce the notion of a backbone, which is a path on the skeleton graph and about which the self-mapping of the skeleton graph is optimal. The backbone can tolerate significant distortions from perfect symmetries and guide the symmetrization of the skeleton, which in turn, guides the symmetrization of the input asymmetric shape. Zheng et al. [17] develop a global search algorithm based genetic programming for backbone searching. Since our input shapes only slightly deviate from perfect symmetries, we simply use the spectral matching method [9] to obtain symmetry axes of skeletons. The orientation alignment of two organic shapes is reduced to the alignment of two 1D symmetry axes, which is significantly easier than on the 2D surfaces according to Liu et al. [10].

§3 Algorithm overview

Given two shapes, we employ the automatic skeleton extraction algorithm [2] to compute their skeletons as the input of our algorithm (Fig. 2a). Then, we take five steps to find a 1-1 semantic correspondence between two sets of skeletal feature nodes. The feature nodes are nodes whose valences are not equal to two, which consist of terminal nodes (equal to one) and



Figure 3: Symmetry-guided generation of part arrangements. (a) Symmetric correspondences of elephant and dog, where a stable symmetric correspondence is shown by a single node and a reflectional symmetric correspondence is shown by a pair of nodes in the same color; (b) Red symmetry axis of each skeleton and two symmetry axes alignment, which is represented by the correspondence of nodes on axes and correspondence are shown in the same color; Parts (c) and part arrangements (d) are extracted under the guidance of the symmetry axis.

internal nodes (larger than two).

First, we perform symmetry analysis on each skeleton to obtain symmetric node pairs, from which the skeleton-intrinsic reflectional symmetry axis is extracted. Second, subgraphs as parts and part arrangements are generated under the guidance of the symmetry axis, as the axis conveys the connections of potential semantic parts (Fig. 2b). Third, we align two symmetry axes and span out skeletons to respectively remove the orientation difference and pose variation between two skeletons for subgraph matching. Fourth, a cascade of pruning tests based on geometry, distance and spatial preservations is designed to filter out bad subgraph matchings (Fig. 2c). At last, the remaining good subgraph matchings vote on individual node correspondences, which results in a voting matrix (Fig. 2d). The final feature node correspondence is synthesized based on the voting matrix, the symmetry map of each skeleton and some other heuristics information (Fig. 2e). The pruning tests and the voting process are similar to those in [1].

§4 Symmetry-guided generation of part arrangements

4.1 Symmetry analysis

Given a skeleton with feature nodes $\mathcal{N} = \{n_1, n_2, ..., n_N\}$, the spectral matching method [9] is applied to construct an adjacency matrix K of an adjacency graph, whose graph nodes are candidate symmetric node correspondences $(n_c, n_{c'})$ in our case, where $c, c' \in \{1, 2, ..., N\}$. The adjacency matrix K encodes graph node affinities and graph edge affinities in the diagonal entries and non-diagonal entries, respectively. Specifically, K(i, i) measures the similarity of the i-th individual correspondence $(n_{c_i}, n_{c'_i})$ and K(i, j), where $i \neq j$, measures the agreement between the i-th correspondence $(n_{c_i}, n_{c'_i})$ and the j-th correspondence $(n_{c_j}, n_{c'_j})$. **Candidate symmetric correspondence.** We pair any two skeletal nodes with the same valence to obtain initial symmetric correspondences. $(n_c, n_{c'})$ is a candidate stable symmetric correspondence when c = c' (single nodes on each skeleton of Fig. 3a). Otherwise, $(n_c, n_{c'})$ is a candidate reflectional symmetric correspondence (pairs of nodes in the same color on each skeleton of Fig. 3a). We further remove candidate reflectional symmetric correspondence between internal skeletal nodes. Because internal skeletal nodes are sensitive during skeleton extraction, while terminal skeletal nodes are robust and the reflectional symmetry among them is prominent.

Graph node affinity. K(i, i) for $(n_{c_i}, n_{c'_i})$ is defined based on the geometric differences of Shape Diameter Function (SDF) [12], Average Geodesic Distance (AGD) [6] and Geodesic Descriptor (GD):

$$K(i,i) = \begin{cases} 0, if \ d_{sdf}(n_{c_i}, n_{c'_i}) > \tau_{sdf}^{sym} \ or \ d_{agd}(n_{c_i}, n_{c'_i}) > \tau_{agd}^{sym} \ or \ d_{gd}(n_{c_i}, n_{c'_i}) > \tau_{gd}^{sym}; \\ exp(-2\frac{d_{sdf}^2(n_{c_i}, n_{c'_i})}{\sigma_{sdf}^2}) * exp(-2\frac{d_{agd}^2(n_{c_i}, n_{c'_i})}{\sigma_{agd}^2}) * exp(-2\frac{d_{gd}^2(n_{c_i}, n_{c'_i})}{\sigma_{gd}^2}), otherwise, \end{cases}$$
(1)

where $\sigma_{sdf} = 2\tau_{sdf}^{sym}$, $\sigma_{agd} = 2\tau_{agd}^{sym}$ and $\sigma_{gd} = 2\tau_{gd}^{sym}$, and τ_{sdf}^{sym} , τ_{agd}^{sym} and τ_{gd}^{sym} are parameters whose concrete values will be introduced in Section 7. Section 7 also gives the values of parameters τ_{iso}^{sym} , τ_{ref}^{sym} , τ_{sdf} , τ_{agd} , τ_{iso} and τ_{rot} , which will appear in the following paper. In order to avoid the trivial identical map and encourage the reflectional symmetry map, the geometric differences of candidate stable correspondences are set to be τ_{sdf}^{sym} , τ_{agd}^{sym} and τ_{gd}^{sym} rather than zeros.

In order to make our work self-contained, we would like to give the definitions and concise explanations of the geometric meanings of SDF, AGD, and GD here. Shape Diameter Function (SDF) [12] is a scalar function defined on a closed manifold surface, measuring the neighborhood diameter of the object at each point. Due to its pose-oblivious property, SDF is widely used in shape analysis, segmentation and retrieval. Average Geodesic Distance (AGD) [6] is also a scalar function, while it is the average value of geodesic distances from current point to the rest points. The smaller AGD is, the closer current point is to the shape center. The maxima of AGD is usually a shape extremity. Geodesic Descriptor (GD) at each point is a vector whose elements are sorted geodesic distances from current point to some specified feature points. In our case, we specify terminal skeletal nodes for GD. A GD vector gives the intrinsic location information of the point.

Graph edge affinity. K(i, j) measures the compatibility between $(n_{c_i}, n_{c'_i})$ and $(n_{c_j}, n_{c'_j})$ based on the deviation from isometry and the inconsistency of spatial configurations. The deviation from isometry is defined as:

 $d_{iso}((n_{c_i}, n_{c'_i}), (n_{c_j}, n_{c'_j})) = max(|d_g(n_{c_i}, n_{c_j}) - d_g(n_{c'_i}, n_{c'_j})|, |d_g(n_{c_i}, n_{c'_j}) - d_g(n_{c'_i}, n_{c_j})|), (2)$ where d_g is the geodesic distance along the skeleton.

When $n_{c_i} \neq n_{c'_i}$ and $n_{c_j} \neq n_{c'_j}$, we further consider the inconsistency between the spatial



Figure 4: Spatial configuration for symmetry analysis and part arrangement matching. Each 3D embedded skeleton with a path are shown in front view (top) and top view (bottom) to be clearer. (a) The non-translational transformation between path $< n_{c_i} \rightarrow o_i \rightarrow o_j \rightarrow n_{c_j} >$ and path $< n_{c'_i} \rightarrow o_i \rightarrow o_j \rightarrow n_{c'_j} >$ is supposed to be a reflection; (b) The case for path $< n_{c_i} \rightarrow o_i \rightarrow o_j \rightarrow n_{c'_j} >$ and path $< n_{c'_i} \rightarrow o_i \rightarrow o_j \rightarrow n_{c'_j} >$ is the same; (c) While the non-translational transformation between source path $< e_1^s \rightarrow o_1^s \rightarrow o_2^s \rightarrow e_2^s >$ and target path $< e_1^t \rightarrow o_1^t \rightarrow o_2^t \rightarrow e_2^t >$ is supposed to be a pure rotation, not including a reflection.

configurations of two paths $\langle n_{c_i} \rightarrow o_i \rightarrow o_j \rightarrow n_{c_j} \rangle$ and $\langle n_{c'_i} \rightarrow o_i \rightarrow o_j \rightarrow n_{c'_j} \rangle$, where o_i and o_j are the closest internal skeletal nodes to $(n_{c_i}, n_{c'_i})$ and $(n_{c_j}, n_{c'_j})$, respectively (Fig. 4a). Throughout this paper, we refer to the shortest path between n_i and n_j when we say path $\langle n_i \rightarrow n_j \rangle$. Note that a spatial embedding using a variant of the least-squares multidimensional scaling (MDS) [4] is performed to span out the skeleton in Fig. 4. After embedding, it is supposed that the non-translational transformation A between two paths is a reflection. Thus, we decompose the rotation component R of A, whose determinant is supposed to be -1, and estimate the deviation of A from R by $||A - R||_F$. If A does not involve a reflection, the determinant of R is 1. We make R = -R to get a large deviation. We also consider the deviation $||A' - R'||_F$ between paths $\langle n_{c_i} \rightarrow o_i \rightarrow o_j \rightarrow n_{c'_j} \rangle$ and $\langle n_{c'_i} \rightarrow o_i \rightarrow o_j \rightarrow n_{c_j} \rangle$ to cover another case in Fig. 4b. The reflection deviation is defined as:

$$d_{ref}((n_{c_i}, n_{c'_i}), (n_{c_j}, n_{c'_j})) = \begin{cases} 0.5, if \ n_{c_i} = n_{c'_i} \ or \ n_{c_j} = n_{c'_j} \ or \ o_i = o_j;\\ min(\|A - R\|_F, \|A' - R'\|_F), otherwise. \end{cases}$$
(3)

The edge affinity is defined as:

W

$$K(i,j) = \begin{cases} 0, if \ d_{iso}((n_{c_i}, n_{c'_i}), (n_{c_j}, n_{c'_j})) > \tau_{iso}^{sym}; \\ exp(-2\frac{d_{iso}^2((n_{c_i}, n_{c'_i}), (n_{c_j}, n_{c'_j}))}{\sigma_{iso}^2}) * exp(-2\frac{d_{ref}^2((n_{c_i}, n_{c'_i}), (n_{c_j}, n_{c'_j}))}{\sigma_{ref}^2}), otherwise, \end{cases}$$

$$(4)$$
here $\sigma_{iso} = 2\tau_{iso}^{sym}$ and $\sigma_{ref} = 2\tau_{ref}^{sym}.$

After obtaining the adjacency matrix K, the principal eigenvector x of K can be computed and interpreted as the confidence values of candidate symmetric correspondences. We rank candidate symmetric correspondences in a descending order based on their confidence values, then greedily accept correspondences one by one from the top of the ranking list. The new added correspondence $(n_{c_j}, n_{c'_i})$ must satisfy three constraints:

- Neither n_{c_i} nor $n_{c'_i}$ is already in accepted correspondences.
- x(j) is larger than zero.
- K(j,i) is larger than zero for any one accepted correspondence $(n_{c_i}, n_{c'_i})$.

The output symmetry map Ω^{sym} consists of all accepted correspondences (Fig. 3a). We define the intrinsic reflective symmetry axis of a skeleton as the longest path, which is stable under the intrinsic reflective symmetry map. In implement, we simply extract the longest path $\mathcal{S} = \langle n_{i_1} \rightarrow n_{i_2} \rightarrow ... \rightarrow n_{i_s} \rangle$ from the stable correspondences of Ω^{sym} (Fig. 3b).

4.2 Part arrangement generation.

Given a skeleton \mathcal{N} and its symmetry axis \mathcal{S} , we extract parts and part arrangements based on the following definitions.

- Parts (p). A part p =< o → e > is a path which starts from an internal node o ∈ S and ends up with a terminal node e ∈ N (Fig. 3c). p has semantics, such as leg, tail and so on. Different parts are connected by the symmetry axis.
- Part arrangements (pa). A part arrangement $pa = \{p_1, s_{12}, p_2, ..., p_{k-1}, s_{k-1k}, p_k\} = \{\langle o_1 \rightarrow e_1 \rangle, \langle o_1 \rightarrow o_2 \rangle, \langle o_2 \rightarrow e_2 \rangle, ..., \langle o_{k-1} \rightarrow e_{k-1} \rangle, \langle o_{k-1} \rightarrow o_k \rangle, \langle o_k \rightarrow e_k \rangle\}$ is a subgraph which consists of $k(\geq 2)$ parts and k-1 paths on S which connect parts. pas encode significant substructures, thus can be useful matching units. In implement, we find that pas with $2 \leq k \leq 3$ parts are enough to reveal potential semantic correspondence (Fig. 3d).

§5 Part arrangement matching

Given the source skeleton $\mathcal{N}^s = \{n_1^s, n_2^s, ..., n_{N^s}^s\}$ and the target skeleton $\mathcal{N}^t = \{n_1^t, n_2^t, ..., n_{N^t}^t\}$, we extract their symmetry axes and part arrangements, respectively. Then, we compute possible node correspondences between any pair of part arrangements (pa^s, pa^t) from two skeletons. A cascade of pruning tests are designed to filter bad correspondences. In order to get better correspondence results, the source symmetry axis \mathcal{S}^s and the target symmetry axis \mathcal{S}^t are aligned before the pruning tests. And only the correspondences, whose matching directions are consistent with the axes alignment direction, are considered.

5.1 Symmetry axes alignment.

We adapt the symmetry axes alignment algorithm of [10] to our work. The goal of [10] is to find the best pair of closed axes from two sets of closed axes, and their optimal alignment to maximize a quality measure. However, as we only have two axes, we directly find their optimal alignment to maximize the quality measure, which considering the length, geometric similarity and structural similarity. Assumed that we have two paths $\mathcal{C}^s = \langle n_{i_1}^s \to n_{i_2}^s \to ... \to n_{i_k}^s \rangle \subseteq \mathcal{S}^s$ and $\mathcal{C}^t = \langle n_{j_1}^t \to n_{j_2}^t \to ... \to n_{j_k}^t \rangle \subseteq \mathcal{S}^t$, and their alignment $c = \{(n_{i_l}^s, n_{j_l}^t)\}_{l=1}^k$, the quality measure is defined as:

$$Q(\mathcal{C}^{s}, \mathcal{C}^{t}, c) = exp(-2\frac{(1-L^{s})^{2}}{\sigma_{L}^{2}}) * exp(-2\frac{(1-L^{t})^{2}}{\sigma_{L}^{2}}) * Q_{align}(\mathcal{C}^{s}, \mathcal{C}^{t}, c),$$
(5)

where L^s and L^t are the geodesic length of path \mathcal{C}^s and \mathcal{C}^t , $\sigma_L = 2\tau_{iso}$, $Q_{align}(\mathcal{C}^s, \mathcal{C}^t, c)$ characterizes the geometric similarity and structural similarity:

$$Q_{align}(\mathcal{C}^s, \mathcal{C}^t, c) = \tag{6}$$

$$\frac{1}{k} \sum_{l=1}^{k} (exp(-2\frac{d_{sdf}^{2}(n_{i_{l}}^{s}, n_{j_{l}}^{t})}{\sigma_{sdf}^{2}}) + exp(-2\frac{d_{agd}^{2}(n_{i_{l}}^{s}, n_{j_{l}}^{t})}{\sigma_{agd}^{2}})) + \frac{1}{k^{2}} \sum_{l=1}^{k} \sum_{r \neq l} exp(-2\frac{d_{iso}^{2}((n_{i_{l}}^{s}, n_{j_{l}}^{t}), (n_{i_{r}}^{s}, n_{j_{r}}^{t}))}{\sigma_{iso}^{2}}),$$
where $d_{iso}((n_{i_{l}}^{s}, n_{j_{l}}^{t}), (n_{i_{r}}^{s}, n_{j_{r}}^{t})) = |d_{g}(n_{i_{l}}^{s}, n_{i_{r}}^{s}) - d_{g}(n_{j_{l}}^{t}, n_{j_{r}}^{t})|, \sigma_{sdf} = 2\tau_{sdf}, \sigma_{agd} = 2\tau_{agd}$ and $\sigma_{iso} = 2\tau_{iso}.$

We search both possible alignment directions and every possible starting node correspondence, then return the best result $\{\mathcal{C}^s, \mathcal{C}^t, c\}$ with the largest $Q(\mathcal{C}^s, \mathcal{C}^t, c)$ (Fig. 3b). For each alignment direction and each starting correspondence $(n_{i_1}^s, n_{j_1}^t)$, the optimal 1-1 solution is computed recursively. The next correspondence $(n_{i_1}^s, n_{j_1}^t)$ must be posterior to aligned correspondences along the alignment direction and have the highest score, which is defined as:

$$s(n_{i_l}^s, n_{j_l}^t) =$$

$$exp(-2\frac{d_{sdf}^2(n_{i_l}^s, n_{j_l}^t)}{\sigma_{sdf}^2}) * exp(-2\frac{d_{agd}^2(n_{i_l}^s, n_{j_l}^t)}{\sigma_{agd}^2}) * \frac{1}{(l-1)} \sum_{r=1}^{l-1} exp(-2\frac{d_{iso}^2((n_{i_l}^s, n_{j_l}^t), (n_{i_r}^s, n_{j_r}^t))}{\sigma_{iso}^2}),$$

$$r_{i_l}^s \text{ corresponds to null node if:}$$

$$(7)$$

 $d_{sdf}(n_{i_{l}}^{s}, n_{j_{l}}^{t}) > \tau_{sdf} \text{ or } d_{aqd}(n_{i_{l}}^{s}, n_{j_{l}}^{t}) > \tau_{aqd} \text{ or } d_{iso}((n_{i_{l}}^{s}, n_{j_{l}}^{t}), (n_{i_{r}}^{s}, n_{j_{r}}^{t})) > \tau_{iso} \text{ for all } n_{j_{l}}^{t}.$

5.2 Part arrangement matching.

The premise of matching a pair of part arrangements (pa^s, pa^t) is that the number of parts in pa^s and pa^t is the same. To match (pa^s, pa^t) is to find the 1-1 match of parts $\{(p_1^s, p_1^t); (p_2^s, p_2^t); ...; (p_k^s, p_k^t)\} = \{(< o_1^s \rightarrow e_1^s >, < o_1^t \rightarrow e_1^t >); (< o_2^s \rightarrow e_2^s >, < o_2^t \rightarrow e_2^t >); ...; (< o_k^s \rightarrow e_k^s >, < o_k^t \rightarrow e_k^t >)\}$. For any one 1-1 match of parts, whose match direction $(< o_1^s \rightarrow o_2^s \rightarrow ... \rightarrow o_k^s >, < o_1^t \rightarrow o_2^t \rightarrow ... \rightarrow o_k^t >)$ is consistent with the alignment direction of symmetry axes, we apply the following three pruning tests to filter bad matches.

Geometric similarity. If the difference of average shape diameter function between a part match (p^s, p^t) or a path match (s^s, s^t) is larger than τ_{sdf} , the match is rejected.

Structure similarity. If the distortion of geodesic distance between a part match (p^s, p^t) or a path match (s^s, s^t) is larger than τ_{iso} , the match is rejected.

Spatial configuration. For any two part matches $(p_1^s, p_1^t) = \{ \langle o_1^s \rightarrow e_1^s \rangle, \langle o_1^t \rightarrow e_1^t \rangle \}, (p_2^s, p_2^t) = \{ \langle o_2^s \rightarrow e_2^s \rangle, \langle o_2^t \rightarrow e_2^t \rangle \}$ from the 1-1 match of parts, it is supposed that

the non-translational transformation A between embedded path $\langle e_1^s \to o_1^s \to o_2^s \to e_2^s \rangle$ and embedded path $\langle e_1^t \to o_1^t \to o_2^t \to e_2^t \rangle$ is a pure rotation, not including a reflection (Fig. 4c). Similar to Section 4, we estimate the difference between A and its rotation component R by $d_{rot} = ||A - R||_F$, which is supposed to be zero. If A involves a reflection and the determinant of R is -1, we make R = -R to get a large deviation. If d_{rot} is larger than a threshold τ_{rot} , the match is reject. With the spatial configuration pruning test, we can not only prune away bad matches, but also avoid the symmetry-switching problem in shape correspondence.

§6 Voting for feature node correspondence

Each node correspondence (n_i^s, n_j^t) in the match of a pair of part arrangement (pa^s, pa^t) contributes one vote to the element t_{ij} of a 2D score table T, which is the total occurrence of this correspondence in all matches of part arrangements. Then, we greedily construct the final correspondence Ω : all correspondences are sorted by their scores in T, and the correspondence (n_i^s, n_i^t) with the highest score is iteratively added to Ω if it satisfies the following conditions:

- Neither n_i^s nor n_i^t is already in Ω .
- The closest internal nodes of n_i^s and n_i^t that are already in Ω must match.
- The symmetric nodes of n_i^s and n_i^t that are already in Ω must match.

§7 Parameters

We use the following default parameter setting for all examples in our paper: $\{\tau_{sdf}^{sym}, \tau_{agd}^{sym}, \tau_{gd}^{sym}, \tau_{ref}^{sym}, \tau_{ref}^{sym}, \tau_{ref}^{sym}\} = \{0.15, 0.15, 0.3, 0.2, 1.0\}$ for symmetry analysis, $\{\tau_{sdf}, \tau_{agd}, \tau_{iso}, \tau_{rot}\} = \{0.3, 0.3, 0.3, 1.0\}$ for part arrangement matching. In contrast to $\tau_{sdf}^{sym}, \tau_{agd}^{sym}, \tau_{iso}^{sym}$, we allow larger values for $\tau_{sdf}, \tau_{agd}, \tau_{iso}$ to tolerate larger geometry and structure variations between two shapes.

§8 Experiments

In this section, we demonstrate and discuss the results of our shape correspondence algorithm on a variety of shape pairs. We also compare our method with the state-of-the-art method.

Time. We implement our algorithm entirely in MATLAB and test it on a 3.4 GHz desktop. Given two input shapes, we pre-compute two skeletons, two embedded skeletons, SDF feature, AGD feature and normalized geodesic distance matrix for each skeleton. Table 1 reports our running time, which excludes the time of pre-computation, for shape pairs in Fig. 5 and Fig. 6. As shown in Table 1, our running time is faster than that of [1], which is implemented by C# language, for all shape pairs. The average time of our algorithm and [1] are 2.19s and 76.84s, respectively. Our performance improvement comes from the small number of part arrangements

Shape pairs	pa1	/pa2	Our/[1](second)			
dog-cat	39	28	1.70	7.11		
dog-feline	39	82	2.46	20.52		
dog-dragon	39	122	2.07	282.1		
dog-cow	39	39	1.23	4.66		
dog-lion	39	44	1.21	4.37		
dog-horse	39	51	1.38	21.36		
dog-elephant1	39	220	5.74	400.12		
ant1-ant2	90	74	4.12	15.21		
Michael-centaur	6	39	0.65	5.01		
horse-centaur	51	39	1.38	7.89		
Avg.	42	73.8	2.19	76.84		
elephant1-elephant2	220	110	8.95	fail		

Table 1: The number of part arrangements and the comparison of running time with Au et al. [1] for shape pairs from Fig. 5 and Fig. 6.

(matching units). Even a elephant with a lot of skeletal nodes only has 220 part arrangements (elephant1 in the table). For shape pairs with the elephant, the performance improvement is obvious. For example, for the dog and elephant1, we take 5.74s while [1] takes 400.12s; for elephant1 with another elephant in a different pose, we take 8.95s while [1] fails.

Visual results. Fig. 5 and Fig. 6 show our semantic correspondence between shape pairs with large pose, geometric and topological variations. As shown, our method produces semantically correct correspondence, even for shape pairs with extra or missing components, such as dog and feline in Fig. 5 and Michael and the centaur in Fig. 6.

However, our algorithm may mismatch nodes, which have different semantics but very similar geometries and structures. For example, the ear of the dog is mismatched to the beard of the dragon, and the ivory of the elephant in Fig. 5; The ears and the nose of the horse are respectively mismatched to the hands and the head of the centaur in Fig. 6. We deem these mismatched nodes as ground-truth correspondences, too.

The mismatch of an internal node pair between the dog and the elephant in Fig. 5 comes from the great structure variation between two shapes. Moreover, the embedded skeletons may not be good enough and lead to mismatches in final results, e.g, the mismatches of Michael's legs and the ears of elephants in Fig. 6.

Part arrangements and general subgraphs. We implement and compare two versions of our method, which respectively employ part arrangements and subgraphs of [1] as matching units. Table 2 reports the number (#) of part arrangement pairs and subgraph pairs, which have passed the pruning tests; the percentage (%) of correct correspondences among all node correspondences from part arrangement pairs or subgraph pairs, compared to manually tagged ground-truth correspondences; the precision $(\frac{a}{b})$ and recall rate $(\frac{a}{c})$ of the final output semantic correspondence, where a is the number of correct output correspondences, b is the total number



Figure 5: The semantic correspondence between the dog in grey box and other animals. Corresponded nodes are shown in the same color. Nodes in small red boxes are mismatched, which have different semantics but very similar geometry and structure with nodes of the dog.

of output correspondences and c is the number of ground-truth correspondences.

We can observe from the table that the number of part arrangement pairs is significantly smaller than the number of subgraph pairs, while the percentage of correct correspondences for voting is significantly larger. The observation indicates that the increase of subgraph pairs has little contribution to the positive votes. The precision and recall rate of final semantic correspondences are comparable for most shape pairs in the table. But, using part arrangements stands out when shapes have a lot of skeletal nodes, such as a dog and an elephant.

§9 Conclusion and limitation

In this paper, we propose an automatic and efficient algorithm of finding semantic correspondence between shape skeletons with large variations. By extracting and matching part arrangements from two skeletons, our algorithm largely reduces the number of matching units while increasing the accuracy of node correspondences for further voting. Experimental results on a variety of shape pairs exhibit the improved performance and accuracy over the state-ofthe-art method. Although our method performs well, it still has some limitations. Firstly, the input skeletons are assumed to have global intrinsic reflectional symmetry. It is more desirable that we can handle partial symmetry and more symmetry types, such as rotational symmetry. Secondly, the spatial embedding of skeletons are not robust enough for simple shapes, such as Michael in Fig. 6, and shapes with large pose distortion, such as elephant2 in Fig. 6.



Figure 6: The semantic correspondence between four more shape pairs. Corresponded nodes are shown in the same color. Nodes in red solid boxes are mismatched, which have different semantics but very similar geometry and structure with nodes of the horse. Nodes in dashed boxes are exchanged, because they are too closed to each other after embedding (ant1 and elephant2) or the embedding is not reasonable (Michael).

Shape pairs	#(pa-pa/sg-sg)		%(pa-pa/sg-sg)		$rac{a}{b}(ext{pa-pa/sg-sg})$		$\frac{a}{c}$ (pa-pa/sg-sg)	
dog-cat	44	19082	66.5	32.5	$\frac{10}{10}$	$\frac{10}{10}$	$\frac{10}{10}$	$\frac{10}{10}$
dog-feline	66	60401	66.0	31.3	$\frac{10}{10}$	$\frac{10}{10}$	$\frac{10}{10}$	$\frac{10}{10}$
dog-dragon	91	61379	75.3	44.4	$\frac{11}{11}$	$\frac{11}{11}$	$\frac{11}{11}$	$\frac{11}{11}$
dog-cow	51	33585	79.5	44.1	$\frac{11}{11}$	$\frac{11}{11}$	$\frac{11}{11}$	$\frac{11}{11}$
dog-lion	61	24486	74.5	37.4	$\frac{10}{10}$	$\frac{10}{10}$	$\frac{10}{10}$	$\frac{10}{10}$
dog-horse	64	39815	81.9	39.6	$\frac{11}{11}$	$\frac{11}{11}$	$\frac{11}{11}$	$\frac{11}{11}$
dog-elephant1	168	276022	52.1	25.0	$\frac{10}{11}$	$\frac{9}{11}$	$\frac{10}{11}$	$\frac{9}{11}$
Avg.	77.9	73539	70.8	36.3	98.7%	97.4%	98.7%	97.4%

Table 2: The comparison of two versions of our method, which respectively employ part arrangements (pa) and subgraphs (sg) of [4] as matching units. The shape pairs are from Fig. 5.

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