

# Measuring 3D Shape Similarity by Matching the Medial Scaffolds

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## Abstract

We propose to measure 3D shape similarity by matching a medial axis ( $\mathcal{MA}$ ) based representation—the medial scaffold ( $\mathcal{MS}$ ). Shape similarity is measured as the minimum extent of deformation necessary for one shape to match another, guided by the  $\mathcal{MS}$ . This approach is an extension of an approach to match 2D shapes by matching their shock graphs, whereas here in 3D the  $\mathcal{MS}$  is in the form of a hypergraph. The  $\mathcal{MS}$  representation is both hierarchical and complete. Our approach finds the optimal deformation path between two shapes by modelling shape deformations as discrete topological changes (transitions) of the  $\mathcal{MS}$ , with costs associated with each transition. We first regularize the  $\mathcal{MS}$  hypergraphs and use the graduated assignment graph matching scheme to match the hypergraphs. A set of compatibility functions is defined to measure the pairwise similarity between the  $\mathcal{MS}$  nodes, curves, and sheets. Early results on matching carpal bones and other shapes promise its potential in a range of applications.

## 1. Introduction

Measuring 3D shape similarity is an important task in object recognition; applications include shape retrieval and clustering in databases [8], querying industrial parts, matching bio-chemical structures, etc. Central to this task is the issue of shape **representation**. Typically a *descriptor* is extracted from the shape, usually with a great deal of simplification to enable efficient matching. The choice of descriptor is often domain-specific and could vary largely from one application to another, facing the dilemma of either being too coarse (ignoring information) or too complex (redundant and unstable). As the problem of matching *rigid closed* shapes is generalized into matching *partial* or *articulated* shapes, developing a *generic* representation becomes significant and is the key of this paper.

A major branch in shape representation is the symmetry-based **medial axis** ( $\mathcal{MA}$ ). The  $\mathcal{MA}$  is promising for shape recognition [19, 21] in that (i) it organizes the shape information in a *hierarchical, intrinsic* graph-like structure [16], which enables matching parts of deformed shapes naturally,

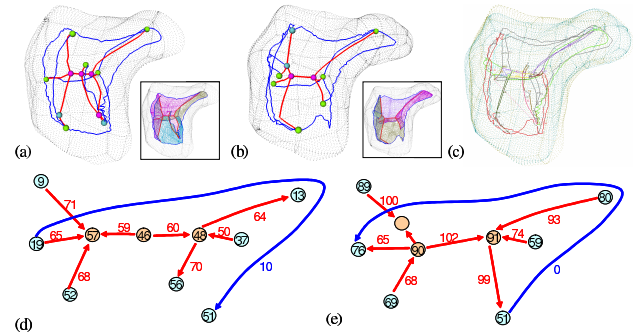


Figure 1. The matching of the  $\mathcal{MS}$  hypergraphs of two carpal bones [17] in (a) and (b) is shown in (c). (d,e) show a manual correspondence, where the graph components are labeled in numbers, serving as the ground truth to validate the automatic matching.

and (ii) such information captured with the  $\mathcal{MA}$  is *complete* in that a full shape reconstruction is always possible [10]. Despite these advantages, the  $\mathcal{MA}$  is generally sensitive to perturbation and difficult to model in the 3D case. Such issues have been recently addressed [12, 11]. We adopt the **Medial Scaffold** ( $\mathcal{MS}$ )—a hierarchical organization of the 3D  $\mathcal{MA}$  into a *hypergraph* form [16] and a *regularization* framework of the  $\mathcal{MS}$  [4] to deal with the above barriers. The  $\mathcal{MA}$  instabilities which induce sudden topological changes are formally classified as a set of *transitions* and thus can be regularized via a set of *transforms*. We propose to match the regularized  $\mathcal{MS}$  such as the ones shown in Fig. 1 to estimate a global similarity between shapes.

Our main contribution is a novel solution to measure 3D shape similarity by matching the  $\mathcal{MS}$  hypergraphs representing the underlying shapes. Following a theoretical framework to measure shape similarity as the *minimum deformation* necessary for one shape to match the other in 2D [19], the matching here is guided by the  $\mathcal{MS}$  as a representation, which retains both key benefits of the  $\mathcal{MA}$  (*hierarchical* and *complete*). The amount of shape deformation can be formulated as an integration of *infinitesimal elastic* changes to optimally match the  $\mathcal{MS}$  branches (sheets and curves). Fig. 2a [3] illustrates an example. We propose to approximate this optimal solution by first regularizing the  $\mathcal{MS}$  [4] and matching the  $\mathcal{MS}$  hypergraphs [5, 13]. Two

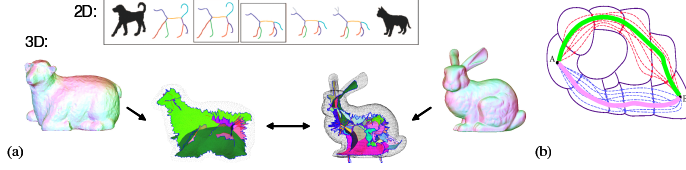


Figure 2. (a) The shock graph in 2D and the  $\mathcal{MS}$  in 3D as the representation for finding the optimal deformation in matching two shapes. (b) Deformation path represented as a sequence of discrete shock transitions. Each blob represents a *shape cell* [19] where all shapes share a common shock/ $\mathcal{MS}$  topology.

improvements are significant: (i) a natural extension of the graph matching scheme to match *hypergraphs* and (ii) a set of similarity measures to reflect the *structural* and *parametric* differences of the  $\mathcal{MS}$  hypergraphs.

The paper is organized as follows. §2 reviews the background in 3D shape similarity matching. §3 describes the  $\mathcal{MS}$  as our representation for 3D shapes. §4 covers our extended graph matching scheme, and §5 elaborates the compatibility measures between the  $\mathcal{MS}$  hypergraph components (nodes, curves, sheets). After the matching is performed, §6 computes the final similarity measure by summing up the compatibility measures weighted by the assignment coefficients. Finally, our approach is examined in §7 on matching medical (carpal bones) and synthetic shapes.

## 2. Background

Measuring shape similarity in recognition is a fundamental problem with an abundant literature; refer to [2] for surveys in the 3D domain. We briefly organize recent approaches into two main categories, namely, the (i) *shape descriptor-based* and (ii) *structural graph-based* methods.

**Descriptor-based** methods are the current mainstream. A shape descriptor (feature, signature) is extracted to describe the shape and distinguish it from others. A large variety of descriptors have been proposed, which are briefly classified into *four* sub-categories: (i) *local feature based*, which relies on local salient geometric features [9, 15] such as the curvature or primitives of flat regions [14]; (ii) *spherical functions*, such as the spherical harmonic, shape histogram, and shape context; (iii) *statistical measure-based*, such as the shape distribution and other generalizations; (iv) *view-based*, by matching 2D views of the 3D objects; and (v) *voxel-based*, assuming the input is a solid volume where a distance transform can be effectively computed. We note that only a few methods are capable of handle *partial*, *non-closed*, and *sampled* shapes (as we do in this paper) such as the *spin-image* [15] and others [14].

**Graph-based** methods employ a graph to represent the connectivity between *parts* of a shape, where the matching of partial or deformed shapes can be carried out naturally. Recent works are organized by the type of graph used in the methods as follows: (i) the *Reeb graph* is a topological graph based on the Morse analysis on a pre-defined

function (such as the geodesic or height functions), where graph edges are not necessarily skeletal/symmetric [1]; (ii) the *skeletal graph* such as [24] encodes topological signature vectors for matching; (iii) the *curve-skeleton* is a one-dimensional centerline roughly central inside the 3D shape. Although it is much simpler than the  $\mathcal{MA}$  (which consists of 2D sheets), a suitable mathematical definition for such “centredness” still needs investigation [7]; (iv) two-dimensional *medial sheets*: Pizer *et al.* pioneer in using fixed-topology medial models for segmentation [23]; Siddiqi *et al.* [21] employ a directed acyclic graph of the *medial sheets* to retrieve articulated 3D models. Our approach belongs to this category. One significance of our method is an explicit exploit of the medial sheet *connectivity* [4] to extract a 3D structure for matching — a direct extension from a simplified 2D analysis in [19, 20].

## 3. Medial Scaffold ( $\mathcal{MS}$ ) as Representation

The 3D medial axis ( $\mathcal{MA}$ ) generally consists of medial sheets ( $A_1^2$ ), curves ( $A_3$ ,  $A_1^3$ ), and nodes ( $A_1A_3$ ,  $A_1^4$ ) [11], where the  $A_k^n$  notation [11] indicates the order ( $k$ ) of contact of a maximal ball with  $n$  surface points used to classify the  $\mathcal{MA}$  points: An  $A_1^3$  curve (red in Fig.1) delimits  $A_1^2$  sheets at an *axis* and ends at  $A_1^4$  or  $A_1A_3$  nodes. An  $A_3$  curve (blue) delimits an  $A_1^2$  sheet at a *rib* and ends at  $A_1A_3$  nodes. We represent the 3D  $\mathcal{MA}$  as the *Medial Scaffold* ( $\mathcal{MS}$ ) [16, 4], which as well organize the abundant information of shape into a hierarchical *hypergraph* form. The  $\mathcal{MS}$  has several advantages in modeling 3D shapes: (i) Shape information is organized *intrinsically* with the  $\mathcal{MS}$  structure and is *complete* (in allowing a full reconstruction of the shape). (ii) Instabilities of the  $\mathcal{MA}$  can be formally handled as *transitions* [12], which are sudden  $\mathcal{MA}$  topological changes corresponding to perturbation of shape. In 3D there are 7 generic *transitions*, which can be regularized case-by-case via 11 *transforms* defined in [4]. The regularized  $\mathcal{MS}$  then captures salient structures of the shape in a simplified form. (iii) The  $\mathcal{MS}$  can be further reduced into a succinct one-dimensional *graph* like structure by keeping the 2D sheet topology at the medial curves (and compress geometry information), which enables to adopt an efficient graph-based algorithm for matching. (iv) Finally, general practical data such as unorganized points or partial meshes can be handled without restrictions [4].

In this paper, we use the  $\mathcal{MS}$  transitions and transforms as a main tool for shape matching, in addition to their use in  $\mathcal{MS}$  regularization in [4]. In 2D, the  $\mathcal{MA}$  transitions are exploited to navigate through the ‘edits’ of  $\mathcal{MA}$  topologies (Fig.2) in exploring candidate deformation paths in matching two shapes [19]. We further extend this idea in 3D. Instead of matching the skeletal graph itself, we define a **dis-similarity** measure to reflect the *optimal* deformation cost between two shapes. The computational cost to explore all

possible edits to match two  $\mathcal{MS}$  hypergraphs is high [3, 19], we thus refer to a *sub-optimal* solution. We first regularize the  $\mathcal{MS}$  hypergraphs to capture the *qualitative structure* of the shape and adopt a graph-matching scheme.

#### 4. Graph Matching the $\mathcal{MS}$ Hypergraphs

Graphs are powerful data structures useful in matching and recognition [6]. The computational intractability of graph matching has led to the development of several classes of sub-optimal algorithms, including *search-oriented* methods using heuristics to explore the state space, and nonlinear optimization methods such as *relaxation labelling*. There are approaches using eigenvalue decomposition, neural networks, and linear programming, *etc.*

The *graduated assignment* ( $\mathcal{GA}$ ) [13] is a relaxation-based energy-minimizing graph matching algorithm suitable to integrate with our approach. We adopt it to match the  $\mathcal{MS}$ 's for several reasons: (i) It enforces a *two-way* assignment via “*softassign*” [22], in contrast to *relaxation labelling* which enforces only an one-way assignment. It is extensible to a *three-way* assignment to match the hypergraphs, a strong fit in our case (§5.3). (ii) It avoids poor local minimum by a *graduated convexity* continuation technique [13]. (iii) It handles missing/extra nodes and links to stabilize the matching under noisy conditions, a factor essential in matching shapes. (iv) The formulation can be adapted to take into account shape deformations represented by continuous variables. (v) Finally, the computational time is comparable to other popular techniques.

##### 4.1. A Review of the $\mathcal{GA}$ Graph Matching Algorithm

The basic setup of the  $\mathcal{GA}$  [13] is to associate the nodes in two graphs  $G$  and  $\bar{G}$  by a *match matrix*  $\mathbf{M}$ , where 1 represents a match of two nodes and 0 otherwise, Fig.3.  $\mathbf{M}$  is a *permutation matrix* if the number of nodes in two graphs are equal. A *slack* row and column are added to  $\mathbf{M}$  to represent missing/extra nodes. We refer to the nodes by  $G_a$  and  $\bar{G}_i$ , and the links by  $G_{ab}$  and  $\bar{G}_{ij}$ , respectively, where  $a, b = 1, \dots, A$ , and  $i, j = 1, \dots, I$ , *i.e.*,

$$\mathbf{M}_{ai} = \begin{cases} 1 & \text{if the node } a \in G \text{ corresponds to node } i \in \bar{G} \\ 0 & \text{otherwise.} \end{cases}$$

An objective *energy function*  $E(\mathbf{M})$  is defined for each possible assignment  $\mathbf{M}$ . For a *quadratic* matching problem:

$$E(\mathbf{M}) = \sum_{i=1}^I \sum_{a=1}^A \sum_{b=1}^A \sum_{j=1}^I \mathbf{M}_{ai} \mathbf{M}_{bj} L_{aibj}, \quad (1)$$

where  $L_{aibj}$  represents the *compatibility* between links  $G_{ab}$  and  $\bar{G}_{ij}$ . Maximizing  $E$  yields the best matching between  $G$  and  $\bar{G}$ . A significant idea in [13] is to extend the above discrete assignment problem to a *continuous* one by embedding it into a large space, where *gradient descent* can be performed to iteratively move from one assignment to another. In this context, the continuous matching matrix  $\mathbf{M}$  takes values between 0 and 1, satisfying the constraint of being a *doubly stochastic* matrix:  $\sum_a \mathbf{M}_{ai} = 1$

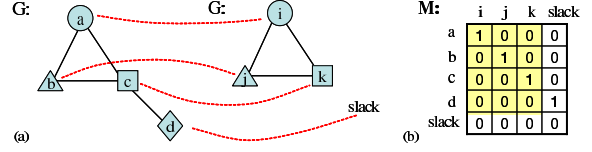


Figure 3. (a) The matching of two synthetic graphs  $G$  and  $\bar{G}$ , where the extra node is matched into the *slack* column of  $\mathbf{M}$ .

and  $\sum_i \mathbf{M}_{ai} = 1$  [22]. The  $\mathcal{GA}$  algorithm then *differentially* moves from one assignment  $\mathbf{M}$  to another, guided by refining the matching energy  $E(\mathbf{M})$  in a *graduated non-convexity* setting [13], which slowly modifies  $\mathbf{M}$  towards a 0 or 1 discretization. The Taylor expansion of  $E$  is:

$$E(\mathbf{M}) = E(\mathbf{M}^0) + \sum_{a=1}^A \sum_{i=1}^I Q_{ai} (\mathbf{M}_{ai} - \mathbf{M}_{ai}^0), \quad (2)$$

where the derivative matrix  $Q$  is:

$$Q = \frac{\partial E}{\partial \mathbf{M}_{ai}} \bigg|_{\mathbf{M}=\mathbf{M}^0} = \sum_{b=1}^A \sum_{j=1}^I \mathbf{M}_{bj}^0 L_{aibj}. \quad (3)$$

The problem of maximizing  $E$  is then turned into maximizing  $\sum_{a=1}^A \sum_{i=1}^I Q_{ai} \mathbf{M}_{ai}$ , which is (again) an *assignment problem* [13] solvable by *softassign*. The  $\mathcal{GA}$  algorithm iteratively (and gradually) modifies an initial  $\mathbf{M}$  toward discretization by decreasing a parameter  $T$  (‘temperature’ in annealing), which controls the convexity of the energy landscape to avoid poor local minima. In each iteration,  $\mathbf{M}$  is best estimated and normalized toward a final assignment.

##### 4.2. Extending $\mathcal{GA}$ to Match $\mathcal{MS}$ Hypergraphs

The original  $\mathcal{GA}$  is shown to be successful in matching two *attributed relational graphs* by combining the energies of node-to-node assignments (1<sup>st</sup>-order term) with link-to-link assignments (2<sup>nd</sup>-order term) [13]. In our case to match the hypergraphs with yet another dimension, we introduce a 3<sup>rd</sup>-order assignment to match the medial sheets (hyperlinks) of the  $\mathcal{MS}$  hypergraph [5]. While the medial sheets could contain complex topology in general, we indirectly match them by matching individual *corners* of the sheet (where medial curves intersect), whose overall effects accumulate to match the sheets.

In defining the energy  $E$  to match the  $\mathcal{MS}$  hypergraphs, ideally  $E$  should reflect the true similarity between two shapes. However it is difficult to model the exact shape variations in practice. Instead, we make  $E$  reflect the *component-wise* compatibility between two hypergraphs  $\mathcal{MS}$  and  $\bar{\mathcal{MS}}$ , which composes of two measures to reflect the *structural* and *parametric* variations. We then optimize the overall similarity by summing up all compatibility measures (§5).

We further exploit two thoughts to improve the  $\mathcal{MS}$  hypergraph matching scheme. First, a *square-root distance*  $d^s = \sqrt{|m_1 - m_2|}$  is used for comparison between two measures  $m_1$  and  $m_2$ , motivated by three reasons [20]: (a)



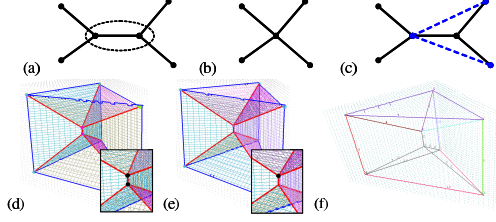


Figure 4. The adding of virtual links correlates a *contracting* edit of (a-c) a graph link in 2D and (d-e) a curve of a hypergraph in 3D. (f) shows the matching of two  $\mathcal{MS}$  hypergraphs across a *contract transform* [4], where the mismatch links are shown in gray.

a re-interpretation of Weber’s law, (b) to maintain sensitivity to variations when two items are close, and (c) to reduce sensitivity when two items are very distant. We found this norm outperforms the weighted distance ( $\frac{|m_1 - m_2|}{\max(m_1, m_2)}$ ) and other metrics [20]. Second, a set of *virtual links* [20] (in addition to the medial curves/links) is introduced which improves the matching robustness in tolerating structural differences (detailed below).

The  $\mathcal{MS}$  matching approach is described as follows. We first regularize the  $\mathcal{MS}$  by applying a set of transforms [4] to simplify it across generic transitions, which bring the two hypergraphs close in structure. The remaining difference is then matched to evaluate similarity. Since the  $\mathcal{GA}$  handles missing and extra nodes (by the slack variables), we can enforce the matching across structural differences by “simulating” them across remaining transitions, *e.g.*, by connecting the nodes that will be brought together in the future transitions by adding *virtual links*, Fig.4, which simulates the effect of applying further  $\mathcal{MS}$  transforms [3]. We only add virtual links to the configurations that warrant high possibility of transitions (with slight shape variations). This helps to explore the better but difficult-to-compute *edit distance* [19] in the candidate spaces to improve the matching as well as its robustness. It essentially complements the one-to-one assignment nature of the  $\mathcal{GA}$  graph-matching scheme in handling structural variations.

## 5. Matching the $\mathcal{MS}$ Hypergraphs: Componentwise Compatibility Measures

This section describes the component-wise node-to-node, curve-to-curve, and sheet-to-sheet compatibility measures to match two hypergraphs  $\mathcal{MS}$  and  $\bar{\mathcal{MS}}$ . The compatibilities are defined for all assignments  $\mathbf{M}$ , such that the  $\mathcal{GA}$  can migrate through the space to produce a final correspondence. The  $\mathcal{MS}$  hypergraphs can be matched **structurally**, *e.g.*, whether a link/hyperlink exists or whether their types are consistent or not. They can also be matched **parametrically**, *i.e.*, by quantitatively comparing the attributes along the medial curves/sheets to define a metric. Consider that a shape can deform via a sequence of (canonical) transformations, dissimilarity between shapes is the amount of *minimum* changes in the space of trans-

Table 1. Compatibility terms used in matching  $\mathcal{MS}$  hypergraphs.

	Structural similarity	Parametric similarity
<b>node</b>	node type, incident curve types	radius $r$ , $\nabla r$ along incident curves, angle of curves at sheet corners
<b>curve</b>	existence, curve type, ending node types, orientation	$\sum r_i$ , edit distance (elastic deformations), Euclidean distance
<b>sheet (corner)</b>	existence, incident curve types, corner node type	corner angle, radius $r$ , $\nabla r$ at the corner, $\sum r_i$ (to approximate volume)

formations. We briefly consider the following measures: (a) *stretching* or *compressing*: the similarity is translated into the length comparison of medial curves; (b) *fattening* or *thinning*: the similarity is measured by the shock acceleration functions; (c) *bending* which affects the curvature along the  $\mathcal{MA}$ . These terms are measured in all hypergraph components (namely, all pairs of nodes, curves, and sheets) in order to compute the compatibility estimate. Table 1 overviews the main terms.

### 5.1. The first-order node compatibility ( $\mathcal{N}$ )

Two shock nodes  $N_a \in \mathcal{MS}$  and  $\bar{N}_i \in \bar{\mathcal{MS}}$  are compared **structurally** on their node types and incident shock curve types. We observe two sets of shock nodes: one from the classification of the 5 generic  $\mathcal{MA}$  nodes in [11] and the other of *high-order* nodes produced by applying  $\mathcal{MS}$  transforms in the regularization process [4]. The above two sets can be re-organized into two categories, namely the  $A_1^m A_3$  and  $A_1^n$ , where  $m, \bar{m} \geq 1$  and  $n, \bar{n} \geq 4$  [3]. We propose to penalize the difference in node types with normalization as:

$$d[A_1^m A_3, A_1^n] = \frac{\max(|n - m|, 3)}{\max(n, m + 3)}, d[A_1^n, A_1^{\bar{n}}] = \frac{|n - \bar{n}|}{\max(n, \bar{n})},$$

$$d[A_1^m A_3, A_1^{\bar{m}} A_3] = \frac{|m - \bar{m}|}{\max(m, \bar{m}) + 3}, \quad (4)$$

where  $d[\cdot, \cdot]$  denotes the *node type difference*. Table 2 lists the values of  $d$  between a few high-order  $\mathcal{MS}$  nodes frequently observed in practice. The structural node compatibility  $\mathcal{N}_s$  is defined as the compliment of node type difference,

$$\mathcal{N}_s[N_a, \bar{N}_i] = 1 - d[N_a, \bar{N}_i], \quad (5)$$

such that  $\mathcal{N}_s = 1$  if the shock types are identical, and  $\mathcal{N}_s = 0$  if the shock types have nothing in common.

We consider three main terms between two shock nodes in the **parametric** compatibility measure: (i) difference of the shock node *radius*  $r$ . (ii) difference of the *gradient* of radius ( $\nabla r$ ) along their incident shock curves. Since there exist numerous incident curves at a shock node (for example, there are four curves at an  $A_1^4$  node), we simply take the maximum and minimum measures ( $\nabla r^+, \nabla r^-$ ) to compute the difference.<sup>1</sup> (iii) the *angles*  $a$  of the incident sheet

<sup>1</sup> Two additional reasons motivate this design: (a) the measures in between the maximum and minimum are less salient and less robust to compare; and (b) the  $A_1 A_3$  node has only two incident curves, thus selecting two distinct curves is most general.

[illegible]
$$\begin{aligned} \mathcal{N}_p[N_a, \bar{N}_i] &= 1 - w_r^- \cdot d^s[r(N_a), r(\bar{N}_i)] \\ &- \frac{w_g^n}{2} d^s[\nabla r^+(N_a), \nabla r^+(\bar{N}_i)] - \frac{w_g^n}{2} d^s[\nabla r^-(N_a), \nabla r^-(\bar{N}_i)] \\ &- \frac{w_a}{2} d^s[a^+(N_a), a^+(\bar{N}_i)] - \frac{w_a}{2} d^s[a^-(N_a), a^-(\bar{N}_i)]. \end{aligned} \quad (6)$$
$$\mathcal{N}_{ai}[N_a, \bar{N}_i] = \mathcal{N}_s \cdot \mathcal{N}_p. \quad (7)$$

## 5.2. The second-order curve compatibility ( $\mathcal{L}$ )

$$\mathcal{L}_s = 1 - w_n^l \cdot d[N_a, \bar{N}_i] - w_n^l \cdot d[N_b, \bar{N}_j], \quad (8)$$

We consider three main terms in the **parametric** compatibility measure between  $C_{ab}$  and  $\bar{C}_{ij}$ : (i) *integration of shock radius* along the curves to reflect corresponding shape volume,

$$V(C) = \int_{s \in C} r \cdot ds \approx \sum_{k=1}^{n_{sample}} r(C_k), \quad (9)$$

Table 3. An example *node compatibility* table ( $\mathcal{N}_{ai}$ ) in matching the  $\mathcal{MS}$  nodes in Fig.1 (value in 1/100). Ground truth pairs with high compatibilities are highlighted in parentheses (boldface in blue). A few *erroneous* matches with value higher than the ground true are underlined in red.

	n51	n59	n69	n76	n80	n83	n89	n90	n91	n92	n94
N00	44	41	41	55	49	53	24	14	16	15	35
N09	57	68	67	68	73	56	(37)	10	12	11	22
N13	68	68	77	54	(72)	57	40	11	12	12	28
N19	54	62	56	(69)	68	49	39	09	10	10	22
N25	59	67	73	45	63	50	34	10	11	10	23
N37	55	58	59	72	66	52	39	09	10	10	23
N46	12	10	13	11	12	12	0	75	69	71	15
N48	14	12	11	12	11	13	0	71	(86)	80	16
N51	20	19	18	20	20	20	37	0	0	0	22
N52	20	18	(17)	22	19	18	34	0	0	0	19
N56	19	14	15	16	14	18	0	44	53	55	14
N57	12	10	10	11	10	11	0	(80)	73	73	14

$$\min \{[ds + dr] + w_a^l \cdot [dt + da]\}, \quad (10)$$
$$\mathcal{L}_p[C_{ab}, \bar{C}_{ij}] = 1 - w_d^l \cdot d_{ed}[C_{ab}, \bar{C}_{ij}] - w_e^l \cdot d_{Eu}[C_{ab}, \bar{C}_{ij}] - w_v^l \cdot |V(C_{ab}) - V(\bar{C}_{ij})|, \quad (11)$$
$$\mathcal{L}_{aibj}[C_{ab}, \bar{C}_{ij}] = \mathcal{L}_s \cdot \mathcal{L}_p. \quad (12)$$

### 5.3. The third-order sheet (corner) compatibility ( $\mathcal{C}$ )

Two shock sheet corners  $S_{abc} \in \mathcal{MS}$  and  $\tilde{S}_{ijk} \in \overline{\mathcal{MS}}$  are compared **structurally** on their boundary shock *curve type* and the shock *node types* at the corner. Specifically, if  $S_{abc}$  or  $\tilde{S}_{ijk}$  is missing or  $(C_{ab}, \tilde{C}_{ij})$  or  $(C_{bc}, \tilde{C}_{jk})$  are of different types,  $C_s = 0$ ; otherwise,

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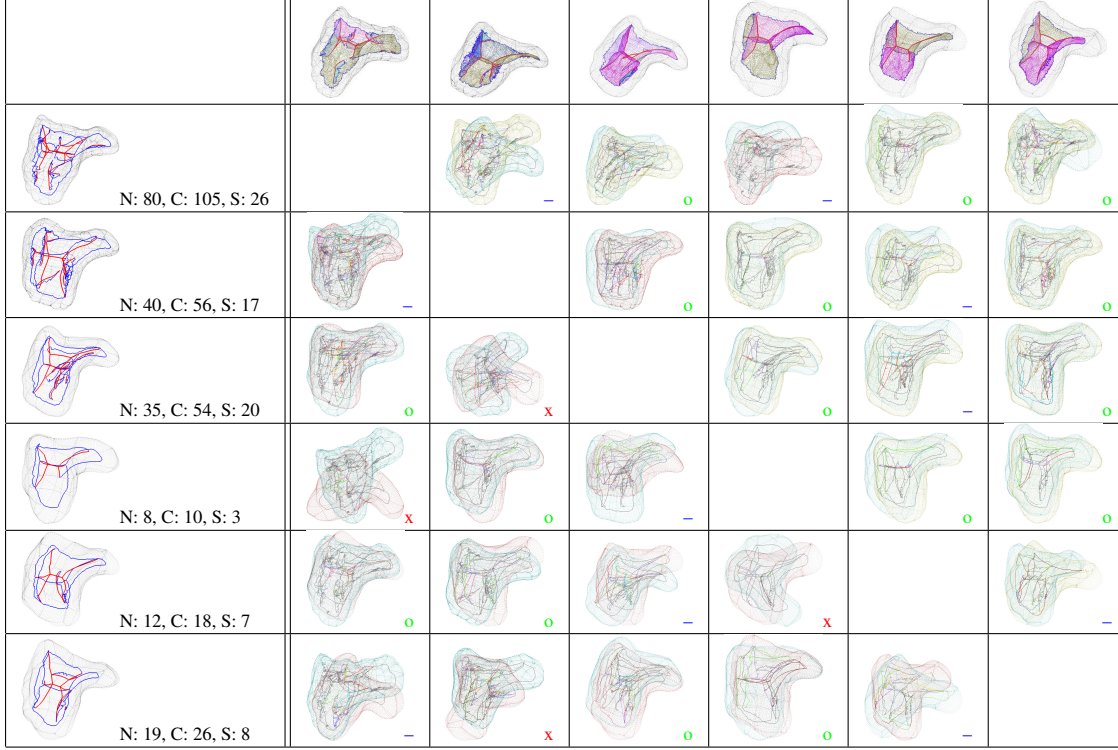


Figure 6. Result in matching the  $\mathcal{MS}$  hypergraphs of the (hamate) carpal bones across 6 patients [17]. Number of medial nodes (N), curves (C), and sheets (S) of the  $\mathcal{MS}$ 's after regularization are labelled on the left. We use the node correspondence to compute a rigid transformation to align the bones for visualization. Closely aligned bones are manually marked with 'o' (16 ones), while roughly aligned ones are marked with '-' (10 ones) and misaligned cases are marked with 'x' (4 ones), out of a visual examination. Since visual misalignment does not necessarily indicate a wrong match, this experiment only evaluates qualitatively how the method performs on matching similar shapes with large skeletal structure variations.

## 7. Results and Discussions

We perform an initial experiment on a human wrist bone dataset (courtesy of Dr. Crisco, RI Hospital [17]) to examine the shape variations of the carpal bones across patients. In Fig. 6, the left-hand *hamates* of 6 females are matched against each other. Note that the graph matching in this case is challenging. The regularized  $\mathcal{MS}$  hypergraphs contain large topological variations: One bone contains only 8 node/10 curves/3 sheets, while another contains 80 nodes/105 curves/26 sheets. The proposed  $\mathcal{GA}$  matching maps most mismatches into the slacks, leading to many correct matches. We observe *asymmetry* matching results due to the rounding of  $\mathbf{M}$  into discrete assignments.

We have also tested our matching approach on a small database (Fig. 7) composed of 20 shapes in 5 categories. The artificial shapes are chosen to examine the matching across particular  $\mathcal{MS}$  transitions in isolation [4], while one hand model is collected online (from Polhemus) and the others are generated from laser scans. Note that similarity measures of within-category shapes are much higher than non-category shapes, indicating the potential in applications such as shape retrieval and recognition.








































The matching of two scaffolds typically takes 5 to 10 minutes to run on a computer with moderate configuration.

The introduction of the  $3^{rd}$ -order energy makes the complexity of Eq. (15) to be  $O(A^3 I^3)$ . However this does not affect the computation time too much due to an efficient encoding of sparsity (Observe the sparsity in Table 5).

**Conclusion:** We have presented a medial axis based graph matching approach to measure 3D shape similarity by matching their  $\mathcal{MS}$  hypergraphs. This is the first attempt exploiting the  $\mathcal{MA}$  transitions [12] integrated with a hypergraph matching framework. We aim to include standard databases in our experiments and compare the result with other skeletal matching methods (*e.g.*, the curve skeleton [7] and medial surfaces [21]) in the future.

## References

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- [3] M.-C. Chang. *The Medial Scaffold for 3D Shape Modeling and Recognition*. Ph.D. dissertation, Division of Engineering, Brown University, Providence RI, 2009. 1, 3, 4

																				
	1.000	0.870	0.710	0.692	0.638	0.535	0.539	0.530	0.479	0.523	0.223	0.202	0.251	0.282	0.385	0.336	0.237	0.163	0.076	0.162
	0.790	1.000	0.700	0.660	0.647	0.545	0.559	0.529	0.519	0.547	0.202	0.206	0.208	0.279	0.460	0.363	0.238	0.234	0.098	0.219
	0.701	0.660	1.000	0.869	0.955	0.612	0.553	0.598	0.555	0.600	0.238	0.082	0.256	0.279	0.444	0.350	0.250	0.217	0.082	0.171
	0.719	0.699	0.843	1.000	0.877	0.484	0.475	0.478	0.589	0.531	0.223	0.225	0.230	0.264	0.348	0.422	0.223	0.188	0.106	0.154
	0.646	0.661	0.953	0.893	1.000	0.591	0.604	0.608	0.565	0.594	0.243	0.138	0.250	0.275	0.421	0.365	0.292	0.197	0.103	0.150
	0.578	0.577	0.615	0.671	0.646	1.000	0.917	0.934	0.862	0.730	0.148	0.108	0.140	0.265	0.247	0.244	0.271	0.147	0.010	0.119
	0.583	0.577	0.624	0.689	0.657	0.908	1.000	0.924	0.899	0.823	0.138	0.199	0.180	0.238	0.263	0.262	0.268	0.147	0.017	0.119
	0.575	0.562	0.619	0.681	0.645	0.925	0.918	1.000	0.885	0.729	0.146	0.178	0.153	0.238	0.256	0.251	0.275	0.141	0.009	0.117
	0.556	0.538	0.594	0.673	0.610	0.867	0.907	0.896	1.000	0.854	0.337	0.200	0.300	0.351	0.343	0.362	0.312	0.176	0.097	0.183
	0.585	0.597	0.645	0.668	0.659	0.734	0.832	0.733	0.818	1.000	0.311	0.261	0.290	0.324	0.404	0.383	0.329	0.260	0.083	0.176
	0.157	0.131	0.169	0.165	0.172	0.133	0.140	0.132	0.327	0.267	1.000	0.613	0.903	0.505	0.220	0.311	0.190	0.012	0.005	0.041
	0.209	0.562	0.085	0.187	0.136	0.277	0.287	0.279	0.160	0.340	0.662	1.000	0.597	0.496	0.179	0.282	0.143	0.038	0.007	0.061
	0.159	0.173	0.188	0.192	0.181	0.146	0.142	0.138	0.334	0.232	0.931	0.596	1.000	0.527	0.208	0.338	0.167	0.013	0.011	0.040
	0.278	0.246	0.266	0.277	0.274	0.278	0.303	0.319	0.370	0.299	0.492	0.192	0.493	1.000	0.236	0.292	0.203	0.036	0.022	0.121
	0.427	0.444	0.420	0.392	0.360	0.243	0.263	0.234	0.292	0.328	0.204	0.016	0.205	0.218	1.000	0.483	0.458	0.118	0.033	0.145
	0.399	0.413	0.245	0.437	0.235	0.306	0.306	0.304	0.370	0.370	0.423	0.283	0.401	0.226	0.513	1.000	0.493	0.125	0.048	0.170
	0.277	0.220	0.341	0.223	0.331	0.241	0.281	0.219	0.296	0.382	0.182	0.138	0.173	0.191	0.528	0.493	1.000	0.018	0.012	0.055
	0.191	0.194	0.196	0.183	0.182	0.065	0.130	0.127	0.142	0.231	0.016	0.046	0.016	0.052	0.100	0.123	0.033	1.000	0.287	0.311
	0.093	0.046	0.087	0.102	0.099	0.008	0.011	0.023	0.019	0.034	0.008	0.012	0.021	0.017	0.032	0.050	0.015	0.274	1.000	0.239
	0.016	0.017	0.015	0.017	0.015	0.012	0.013	0.015	0.013	0.014	0.011	0.012	0.011	0.012	0.114	0.137	0.079	0.217	0.258	1.000