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# Surface Reconstruction From Non-parallel Curve Networks

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**Abstract**

*Building surfaces from cross-section curves has wide applications including bio-medical modeling. Previous work in this area has mostly focused on connecting simple closed curves on parallel cross-sections. Here we consider the more general problem where input data may lie on non-parallel cross-sections and consist of curve networks that represent the segmentation of the underlying object by different material or tissue types (e.g., skin, muscle, bone, etc.) on each cross-section. The desired output is a surface network that models both the exterior surface and the internal partitioning of the object. We introduce an algorithm that is capable of handling curve networks of arbitrary shape and topology on cross-section planes with arbitrary orientations. Our algorithm is simple to implement and is guaranteed to produce a closed surface network that interpolates the curve network on each cross-section. Our method is demonstrated on both synthetic and bio-medical examples.*

## 1. Introduction

Reconstructing a complete surface from incomplete data is a topic of wide interest in geometry processing. A common case of this is planar curves that represent cross-sections of a complete surface. In bio-medical modeling, for instance, contours of an anatomical structure are drawn by physicians on 2D images (such as in freehand ultrasound) or on slices of a 3D volume (such as MRI and CT scans), and a surface connecting these contours is sought which represents the structure in 3D. An example is shown in Figure 1 (a) for a human Parotid gland obtained from a CT volume.

Surface reconstruction from cross-section curves has been extensively studied for the past three decades. Previous work mostly considers connecting curves on parallel cross-sections (e.g., Figure 1 (a)), where many solutions exist (see a brief review in Section 2). Here we are interested in the more difficult problem of surface reconstruction from non-parallel cross-sections (e.g., Figure 1 (b)). The need for handling curves on non-parallel planes arises in multiple applications. In freehand 2D ultrasound, for example, both the location and orientation of each individual image plane can be freely changed through an input device that has 6 degrees of freedom. Additionally, when selecting planar slices of a 3D MRI or CT scan to specify contours, a physician often wishes to customize the orientation of each slice to better align to the imaged object. For example, the contours in Figure 1 (b) delineate the same subject as in (a) but are drawn on a set of non-parallel slices chosen by a physician to more accurately capture anatomically meaningful features.

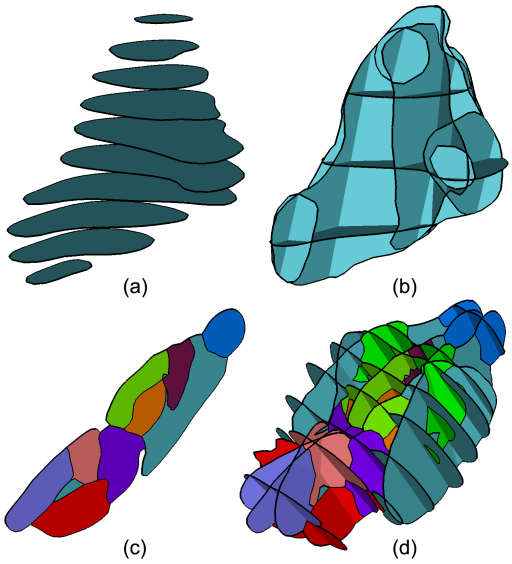


**Figure 1:** *Types of cross-section curves we consider in this paper: simple closed curves on parallel (a) and non-parallel (b) planes, and curve networks (c,d).*

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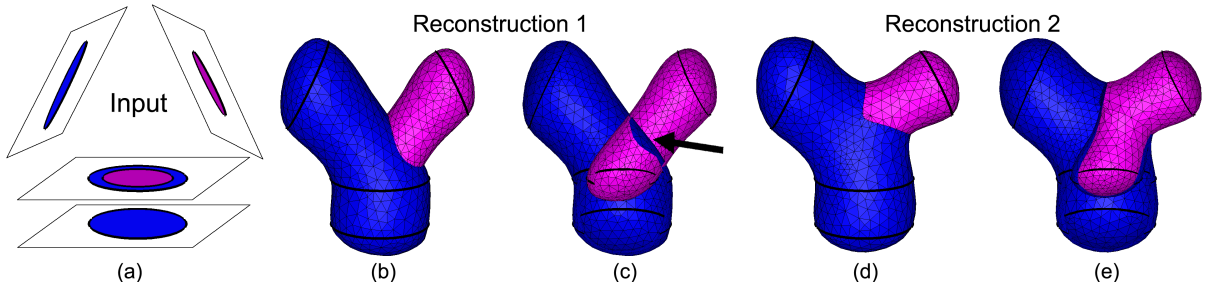


**Figure 2:** *Surface reconstruction from curve networks: the input with 3 region labels: blue, red and white (a), surfaces independently constructed from simple closed curves bounding the blue or red regions (b) resulting in a non-closed partitioning of space as seen in the cut-away view (c), and a closed surface network generated by our method (d) with a cut-away view (e).*

Another demand that increasingly arises in engineering and medical applications is reconstructing objects that are segmented by different material or tissue types. This leads to *curve networks* that partition each cross-section plane into regions associated with *multiple* labels (e.g., air, muscle, bone, etc.). Figure 1 (c) shows an example curve network that represents the segmentation of the mouse brain into various anatomical structures on a single cross-section, and Figure 1 (d) shows a set of these cross-sections from which a surface representing the segmented mouse brain needs to be reconstructed. In particular, we desire the reconstruction to be a *surface network* that partitions the space into labelled 3D regions. Note that the simple closed curves in Figure 1 (a,b) are also a curve network where the regions labels are simply inside and outside.

### 1.1. Problem statement

We consider the general problem of surface reconstruction from curve networks on possibly non-parallel cross-sections. Specifically, given a set of planes partitioned by curve networks into labelled 2D regions, we desire a surface network with the following properties:

- **Closed:** The surface network partitions the space into labelled 3D regions, so that two regions sharing common boundary have different labels (e.g., inside and outside).
- **Interpolating:** The surface network interpolates the curve networks, and the labels of partitioned 3D regions are consistent with those of 2D regions on each cross-section.

To the best of our knowledge, the reconstruction problem has never been tackled at this level of generality. While a few methods were proposed for handling non-parallel cross-sections, including the very recent work of Boissonnat and Memari [BM07], these methods are restricted to simple closed curves on each cross-section. To handle multiply-labelled curve networks, one may apply these methods to reconstruct one surface for each label, by considering only the simple closed curves bounding regions of that label on each cross-section, and combine these surfaces together. However, the resulting surface may easily violate the closedness criteria, as illustrated in Figure 2: while surfaces can be constructed each for the blue and red label of the input curve networks (a), their combination in (b) inevitably leads to a non-closed surface as a portion of surface (pointed by the arrow in (c)) is shared by two 3D regions of a same label (red). Similar observations were made by Weinstein [Wei00] and Ju *et al.* [JWC*05], who proposed different methods capable of generating closed surface networks from inputs containing curve networks. However, both of these methods are restricted to parallel cross-sections.

### 1.2. Method overview

We present a novel algorithm for surface reconstruction from non-parallel curve networks. We follow the divide-and-conquer strategy of Boissonnat and Memari [BM07] and consider the partitioning of space into cells by all cross-section planes (known as an *arrangement*). The core of our algorithm is the construction of a closed surface network within each partitioned cell, which generalizes the projection-based approach of [JWC*05] from between two parallel planes to within an arbitrary convex space. Unlike [BM07] or [JWC*05], our algorithm handles both parallel and non-parallel planes as well as curve networks on each plane.

The result of our algorithm, while satisfying the closedness and interpolation criteria, may exhibit a jagged appearance unsuitable for applications where smooth surfaces are desired. We next utilize existing techniques to improve the surface quality, in particular, for modelling smooth anatomical structures in bio-medical applications. We considered mesh fairing based on surface-diffusion flow [SK01, YB02, XPB06] and mesh refinement via edge-swapping and triangle splitting [PS96]. An example result is shown in Figure 2 (d,e).

**Contribution** We introduce a simple and robust algorithm that is guaranteed to produce a closed surface network interpolating arbitrary curve networks on cross-sections with arbitrary (parallel or non-parallel) orientations. The method is demonstrated on both synthetic and medical examples.

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## 2. Previous work

We start by briefly reviewing representative work on surface reconstruction from planar curves (also known as *contour interpolation* or *contour stitching*), with an emphasis on the limitation of these methods in handling complex inputs. Note that a closely related area is the interpolation or approximation of spatial curves with smooth algebraic surfaces [BI92, BIW93] or spline representations [XBE02, BCX95], where the resulting surface is either limited to simple topologies or based on an initial polyhedral surface.

### 2.1. Simple closed curves

**Parallel cross-sections** The majority of surface reconstruction methods are developed for connecting simple closed curves lying on parallel planes. Early approaches attempted to find a polygonal tiling that connected curve loops on two neighboring planes while optimizing a quality measure [Kep75, FKU77, CS78, MSS92]. Unfortunately, these tiling methods may fail to generate closed surfaces between planes containing multiple and nested curve loops. Robust handling of these more complex cases has become the focus of recent work. Among them, Boissonnat [Boi88] pioneered the method based on Delaunay-meshing, which has been refined and improved in later work [Gei93, CD99]. The methods of Herman *et al.* [HZB92] and Csebfalvi *et al.* [CNKG02] represent the 2D curves on each plane using implicit functions and extract the 3D surface by interpolating these functions. The two steps of building and interpolating the implicit functions are combined in the variational framework of Turk et al. [TO99]. Also, a number of methods [BS96, BCL96, OPC96, KSS00, BGLSS04] have been developed based on computing orthogonal projections of curves from two neighboring planes onto a common plane. For example, the method of Barequet *et al.* [BGLSS04] obtains intersections of projections from inside and outside regions on different planes, triangulates the intersected regions using Straight Skeletons [AA96], and lifts the triangulations in 3D to form the final surface. In a more recent work [BV07], the authors utilized the projection to find the matching between neighboring planes and constructed the geometry by performing non-linear interpolation across multiple planes.

**Non-parallel cross-sections** Very few methods have been developed for connecting curves on non-parallel planes. Several attempts have been made [RU90, WMT*95, BTS04] to extend implicit interpolation onto non-parallel planes. These methods are limited to the special case of serial planes so that the surface can be built from pieces, each of which bounded between two neighboring planes. More general approaches have been proposed by Payne and Toga [PT94], by Dance and Prager [DP97], and very recently by Boissonnat and Memari [BM07], who extended the original Delaunay-meshing method from parallel cross-sections [Boi88]. A common strategy adopted in these methods is to consider a partitioning of space by all cross-section planes. Within each partitioned cell, a closed triangular mesh is extracted as the exterior of a 3D tetrahedral mesh connecting the cell boundary. In particular, Boissonnat and Memari [BM07] introduced the *branching diagram* to characterize the surface topology within each cell.

### 2.2. Curve networks

While many of the above-mentioned methods can handle curves with arbitrarily complex shape and topology, they are designed for simple closed curves that bi-partition each plane into inside and outside regions. Few attempts have been made so far to extend these approaches to handle curve networks. Weinstein [Wei00] extended implicit interpolation by representing the curve network on each plane as a multi-labelled implicit function. More recently, Ju *et al.* [JWC*05] extended the contour projection approach of [BGLSS04] from simple closed curves to curve networks by considering intersections of projections from regions with different labels on different planes. Note that both methods rely heavily on the fact that the curve networks reside on parallel planes, so that there is a well-defined direction (i.e., the plane normal) for implicit interpolation [Wei00] and for projection [JWC*05].

## 3. The algorithm

We now describe our algorithm for reconstructing a surface network from non-parallel curve networks. To handle non-parallel cross-sections, we follow the general divide-and-conquer strategy adopted in previous works [DP97, BM07]. In particular, we consider the partitioning of space into *cells* by the set of all cross-section planes (known as the *arrangement* in Computational Geometry). The complete surface is built by first constructing a piece of surface within each partitioned cell, followed by stitching together pieces from neighboring cells. Note that if each surface piece is closed within the cell and interpolates the curves on the cell boundary, the result after stitching will remain closed and interpolating.

The remaining problem is how to construct a closed surface network within each cell that interpolates the curve networks on the cell boundary. To this end, we generalize the projection-based approach of [JWC*05] from a cell bounded by two parallel planes to an arbitrary cell bounded by multiple intersecting planes. We will describe the basic ideas in 2D before presenting the full algorithm in 3D.

### 3.1. The idea in 2D

We begin by considering a simpler, lower-dimensional problem in 2D. Here the input is a set of cross-section *lines*, each divided by a set of *points* into labelled 1D regions. Two examples are shown in Figure 3 for two parallel cross-sections (a) and three non-parallel cross-sections (e). In this paper, we assume that the inputs are valid cross-sections, in that the region labelling on two intersecting cross-sections are consistent at their intersection. In this 2D setting, our goal

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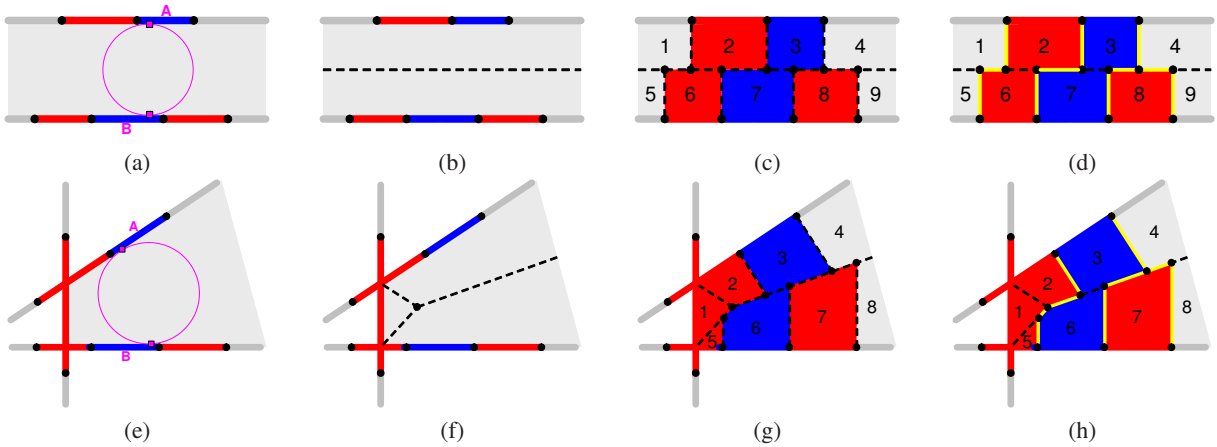


**Figure 3:** *2D illustration of our algorithm for parallel (top) and non-parallel (bottom) cross-sections (see Section 3.1).*

is to reconstruct a closed *curve network* that interpolates the points on the cross-section lines.

Following the divide-and-conquer strategy, we consider the partitioning of the plane by all the lines into cells, such as the shaded regions in Figure 3 (a,e). Note that each cell is necessarily convex. Our task is to construct a closed curve network within each cell that interpolates the points on the cell boundary.

A simple algorithm exists [JWC*05] for the case of a cell bounded by two parallel lines, like that in Figure 3 (a). The idea is to partition the cell into smaller *compartments*, each attached to, and labelled by, a 1D region on the cell boundary. Specifically, the cell is first divided into two compartments by the *medial line* between the two lines (dashed in (b)), then broken into smaller compartments by the segments that connect each point on the cell boundary to its orthogonal projection on the medial line (shown in (c)). The key observation is that the curve network separating neighboring compartments with *different* labels (e.g., yellow lines in (d)) is closed and interpolates the points on the cell boundary.

We extend this simple idea to cells bounded by multiple lines. The key modification we make is replacing the medial line between two parallel lines by the more general *medial axes* (MA) of a cell. The MA is the loci of points that are closest to two or more points on the cell boundary. Because the cell is convex, the MA consists of a set of lines or line segments (e.g., dashed lines in Figure 3 (b,f)). Note that the medial line is a special case of the MA when the cell is bounded by two parallel lines.

Using the MA, we can apply the above medial line projection algorithm to an arbitrary cell, which we will illustrate using the example in Figure 3 (e). First, the cell is partitioned into compartments by the MA (dashed in (f)) as well as the segments that connect each point on a cell boundary to its orthogonal projection on the MA (shown in (g)). Next, the curve network is extracted as the boundaries between neighboring compartments with different labels (e.g., yellow lines in (h)). As in the original algorithm [JWC*05], this curve network is closed and interpolates the points on the cell boundary.

**Why medial axes:** Note that the use of orthogonal projection and the MA in the algorithm is not a necessary condition for producing a closed curve network. In particular, picking other projection directions or other shapes to project onto may yield curve networks with a different topology. One advantage of using the MA and orthogonal projection is that the correlation between topology of the resulting curve networks with the configuration of cross-section planes can be mathematically characterized. Formally, let A and B be two 1D regions with a common label on different boundary lines of a cell (see Figure 3 (a,e)). By the definition of the MA, A and B will both belong to the same 2D region partitioned by the resulting curve network (e.g., the blue regions in Figure 3 (d,h)) if there exists a circle inscribing the cell at a point in A and a point in B (see Figure 3 (a,e)).

### 3.2. The algorithm in 3D

The 2D idea can be easily extended to 3D. Our algorithm takes as its input a set of cross-section planes, each containing a curve network with partitioned 2D regions labelled. The curves are represented as piece-wise linear polylines. The algorithm first computes a partitioning of the space by all planes. Within each partitioned cell bounded by a subset of planes (like that in Figure 4 (a)), the algorithm closely follows the 2D approach to build a closed surface network interpolating the curve networks on the cell boundary:

- **Step 1: Obtaining MA.** Compute the MA of the cell. Since a cell is always convex, the 3D MA consists of planar pieces called *sheets* (dashed in Figure 4 (a)).
- **Step 2: Forming compartments.** The cell is partitioned into compartments by the MA sheets and polygons connecting the curve networks to their orthogonal projections

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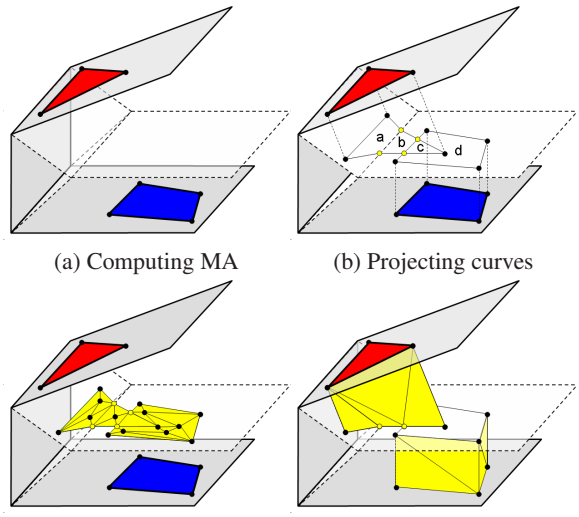


(a) Computing MA (b) Projecting curves

(c) Surface extraction I (d) Surface extraction II

**Figure 4:** *3D illustration of our algorithm within a cell.*

on the MA. Note that new vertices may be created when projecting the curve networks onto the MA if the projections from different planes intersect with each other or with the border of a MA sheet (yellow dots in Figure 4 (b)). Each compartment is attached to, and labelled by, a 2D region on the cell boundary.

- **Step 3: Extracting surfaces.** The surface network is extracted as the boundaries between neighboring compartments associated with different labels. Specifically, this network has two parts: triangulated portions of the MA sheets that are projected from a single region on the cell boundary (e.g., a,b,d in Figure 4 (b)) or from two regions with different labels (e.g., c in Figure 4 (b)), shown in Figure 4 (c), and triangulated polygons connecting curve network edges to their projections on the MA, shown in Figure 4 (d).

Finally, the complete surface network is formed by stitching together surfaces constructed in neighboring cells. As in 2D, the topology of the resulting surface network correlates with the spatial configuration of the cross-sections in a well-defined manner. Specifically, two 2D regions with a same label on the cell boundary will belong to one 3D region partitioned by the surface network if there exists a sphere inscribing the cell at one point in each 2D region.

**Implementation** We follow the classical tracing algorithm of Sherbrooke *et al.* [SPB96] to compute the MA and the Straight Skeleton method [AA96] for triangulation on the MA sheets (Figure 4 (c)). Note that, depending on the shape of the cell, the projection of curve networks on the MA may lie far away from the original data (e.g., when the dihedral angle between two planes is close to $\pi$). To prevent numerical issues, in practice we place a virtual bounding box (we used 2 times the size of the tightest bounding box of the input) around the curve networks and treat each wall of the bounding box as a new cross-section containing no curves. Note that the addition does not affect the closedness or interpolation of the result.

**Complexity analysis** Here we briefly analyze the time complexity of each part of the algorithm. Computing the partitioning of the space by $k$ planes can be done in $O(k^3)$ time as in [BM07]. Within each convex cell bounded by $n$ planes containing $m$ curve-network vertices, computing the MA using [SPB96] takes $O(n_s n)$ time where $n_s$ is the number of seams between the MA sheets, while Straight Skeleton triangulation costs $O(m_i^2 log(m_i))$ time for a region on the MA with $m_i$ vertices projected from the cell boundary, amounting to $O(m^2 log(m))$ time for all regions in the worse case.

## 4. Mesh improvement

The result of our algorithm presented in the previous section, while being closed and interpolating, exhibits a jagged and unnatural appearance. An example output is shown in Figure 5(a) for the input in Figure 2(a). Observe that all triangles are either orthogonal to the cross-section planes or aligned with the medial axes within each cell partitioned by the planes. In addition, the surface contains triangles with widely varying sizes and shapes, in part due to the sparse, non-uniform spacing between points on different cross-sections.

The surface network as it is cannot be directly used in applications where smooth surfaces are desired, such as modeling anatomical structures in bio-medicine. We next resort to existing mesh fairing and refinement techniques to improve the visual appearance. In essence, we improve a piecewise constant interpolation among the input curve networks

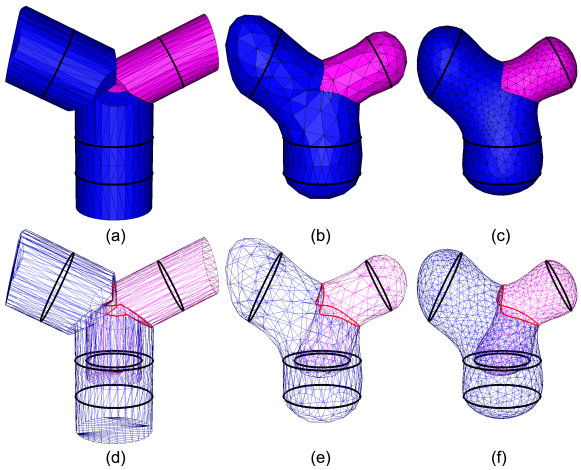


**Figure 5:** *Improving the initial surface network (a) using iterative refinement and fairing at 5 (b) and 10 (c) iterations. The bottom row shows the tessellation where the non-manifold edges are highlighted.*

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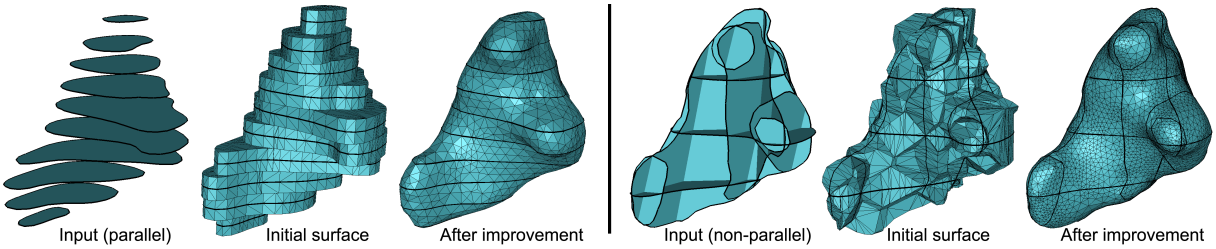


**Figure 6:** *Reconstruction from parallel and non-parallel contours of a human Parotid gland.*

(resulted from Section 3) by exerting minimum energy constraints.

**Fairing:** A constraint imposed by our reconstruction goal is the interpolation of input curve networks. In particular, we demand that the resulting surface network smoothly interpolate these curves so as to exhibit a fair overall appearance. As a result, we consider a class of fairing approaches based on surface-diffusion flow [SK01, YB02, XPB06], which allows surface fairing with $G^1$ continuity at the constrained boundaries. Surface diffusion evolves an initial surface by moving each vertex in the surface normal direction to minimize local curvature differences. To impose the curve constraints, we follow the iterative vertex update formulation of Yoshizawa and Belyaev [YB02] while restricting vertex updates to only mesh vertices that do not lie on input curves. Additionally, to handle surface networks with a non-manifold topology, we apply Bi-Laplacian flow [KCVS98] instead of surface diffusion to the network of non-manifold vertices, where a meaningful surface normal fails to exist.

**Refinement:** The effect of fairing can be limited by the presence of large triangles. To this end, we adopt the multi-scale, coarse-to-fine fairing procedure similar to [KCVS98, WDSB00, Ber04]. Specifically, we adopt the refinement method of Pfeifle and Seidel [PS96], which produces a Delaunay-like triangulation via edge-swapping and triangle splitting. To preserve the input curve networks, edge-swapping is restricted to non-curve-network edges. The refinement is controlled by a user-defined factor $\alpha$ that relates the density of triangles to the lengths of constraint edges. Liepa [Lie03] showed that $\alpha = \sqrt{2}$ yields a mesh that visually matches the density of the constrained vertices. Refinement and fairing are alternated in an iterative manner, with refinement performed on an increasing density factor at each iteration. Starting with $\alpha = 0$, the iterations terminate when $\alpha = \sqrt{2}$. In this paper, we used 10 iterations for all models. Figure 5 shows the result of refining and fairing an initial surface network at 0, 5 and 10 iterations. It is important to note that the improved mesh still interpolates the original curve networks.

## 5. Examples

We test our method on both synthetic examples and biomedical data, such as those in Figure 1, where the contours are provided by physicians and neuroscientists at the Medical School of Washington University and Pacific Northwest National Lab. The complexity of each example and the performance of our method is summarized in Table 1.

We begin with examples containing simple closed curves on each cross-section. Figure 6 shows the initial surface network produced by our algorithm as well as the result after mesh improvement for the Parotid gland contours in Figure 1 (a,b). Another example is shown in Figure 7, where the input curves are obtained by synthetically slicing the Stanford Horse model on a selected set of planes (in this and later examples, the results are shown after mesh improvement).

Next we present examples containing more complex curve networks. Figure 8 shows a synthetic example where a "sapphire ring" is reconstructed from curve networks on 4 planes. Note that the stone and the ring shares a common boundary outlined by non-manifold edges. Figure 9 shows the reconstruction of 3 abutting anatomical structures in the mouse brain from curve networks on 4 cross-sections. Observe that the surface network interpolates the input curve networks and partitions the space into 3D regions sharing common boundaries. Finally, Figure 10 shows the reconstruction of the whole mouse brain with 10 internal anatomical structures from 14 cross-sections.

## 6. Conclusion

We present a simple and robust algorithm for surface reconstruction from multi-partitioning curve networks on non-parallel cross-sections. The algorithm guarantees to produce a closed surface network that interpolates curve networks

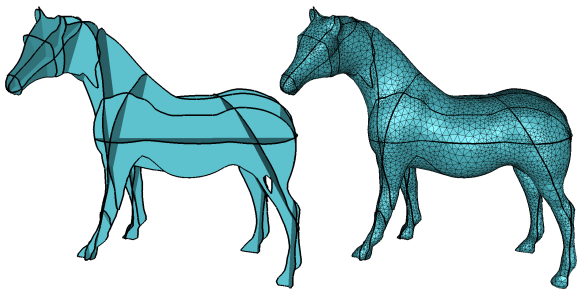

**Figure 7:** *Reconstruction from synthetic slices of the Stanford Horse.*

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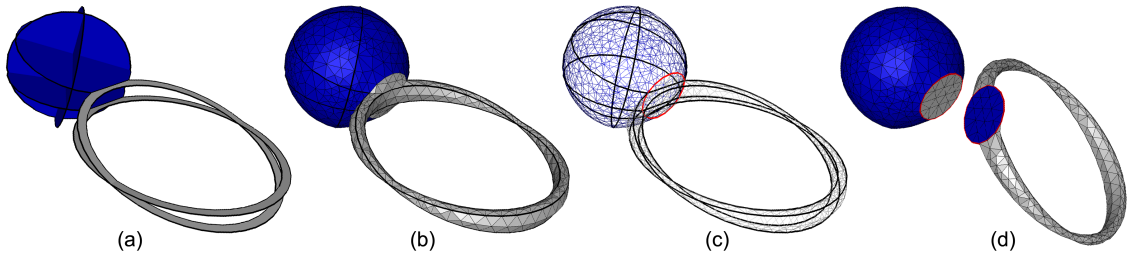


**Figure 8:** *Reconstruction of a two-material sapphire ring from curve networks on four non-parallel cross-sections(a), shown as shaded surfaces (b), wireframe (c) highlighting the non-manifold edges (red), and surfaces bounding each material (d) where the ring is rotated towards the viewer to show the common boundary between the two materials.*

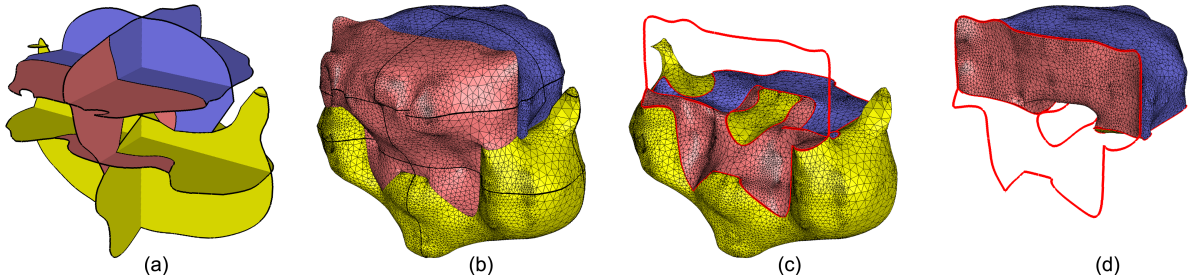


**Figure 9:** *Reconstruction of 3 anatomical structures from contour curve networks on four non-parallel planes (a), shown as shaded surfaces (b), and surfaces bounding individual anatomical structures (c,d) and colored by neighboring structures.*

| Model | Region Labels | Curve Edges | Output Triangles | Surface Construction | Mesh Improvement |
|---|---|---|---|---|---|
| Parotid (parallel) | 2 | 327 | 2188 | 47 ms | 671 ms |
| Parotid (non-para.) | 2 | 620 | 6272 | 203 ms | 1655 ms |
| Horse | 2 | 1668 | 16364 | 535 ms | 4028 ms |
| Ring | 3 | 282 | 1768 | 47 ms | 438 ms |
| Brain | 11 | 2251 | 23747 | 3588 ms | 7122 ms |

**Table 1:** *Performance on a 3GHz PC with 2GB memory.*

with arbitrary shape and topology on cross-sections with arbitrary orientations. In addition, the topology of the surface network correlates to the density of planes in a well-characterized manner.

The current method has a number of limitations that we wish to address in the future. First, as an extension of the projection-based approaches [BGLSS04, JWC*05], our method suffers from the same drawback as the topology of the final surface heavily depends on the configuration of the cross-section planes in addition to the relative location of the curve networks. In particular, it may result in disconnected geometry when the projections of the curves do not overlap on the MA between the planes. On the other hand, Delaunay-based methods [Boi88, BM07] offer more robust determination of topology as they are less reliant on the plane orientations. In the future, we would like to investigate convenient means for the user to adjust the surface topology computed by our method to his or her need, similar to that proposed in [JWC*05]. Second, while the initial surface generated by our algorithm is free of self-intersecting geometry, the surface after mesh improvement may lose this property. We plan to consider intersection-free alternatives for improved geometric accuracy. Third, we would like to explore domain-specific mesh improvement techniques that customize the result to particular applications. For example, in medical imaging, the grayscale 3D volume from where the contour curves are obtained, if available, would be a valuable piece of information to guide mesh fairing.

**Acknowledgement** We thank Stanford 3D Scanning repository for providing the Horse model. This work is supported in part by NSF grant (CCF-0702662).

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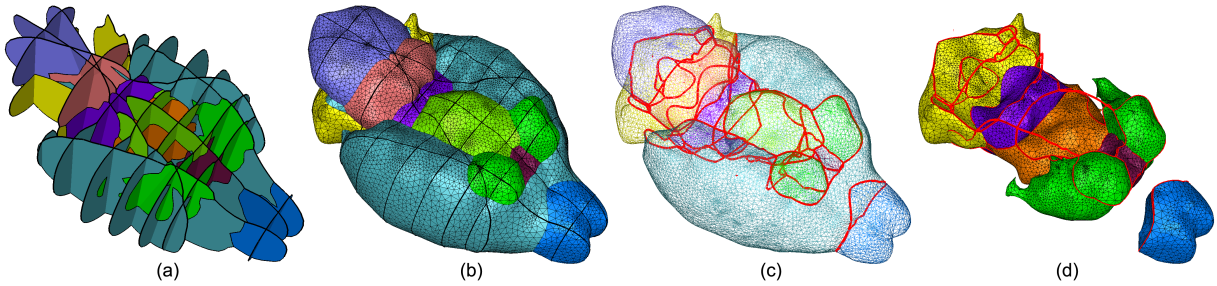


**Figure 10:** *Reconstruction of 10 anatomical structures from contour curve networks on 14 non-parallel planes (a), shown as shaded surfaces (b), wireframe (c) highlighting the non-manifold edges, and surfaces bounding a subset of the structures (d).*

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