REPRESENTING MULTI-FIGURE ANATOMICAL OBJECTS

Qiong Han, Conglin Lu, Guodong Liu, Stephen M. Pizer, Sarang Joshi, Andrew Thall

Medical Image Display & Analysis Group, University of North Carolina, Chapel Hill

ABSTRACT

We use multi-figure m-reps to represent anatomical objects, such as human livers, with named components. Each component is represented as a single figure m-rep. These figures of the object are connected via hinge geometry. A smooth object surface is then computed using our technique based on the subdivision method applied to a single figure m-rep. This novel representation allows us to represent and analyze a complex anatomical object by its individual components, by relations among its components, and by the object itself as a whole entity. Using our representation, some preliminary results on statistical analysis of multi-figure anatomical objects are presented.

1. INTRODUCTION

Single figure m-reps (Fig. 1) have been successfully used to represent anatomical objects and the ensembles of them [1, 2]. This representation has also proved to be powerful in deformable model segmentation. M-reps also allow statistical analysis on various kinds of objects [3]. However, many anatomical objects have multiple named components, e.g., livers have left and right lobes, and the first cerebral ventricle has three horns and an atrium. Also, the hand can be modeled as five tube-shaped fingers connected to a slab-shaped palm. Being able to represent not only the overall object but also its components will help us to understand those complex objects.

We use the multi-figure m-rep to represent an object with multiple components. Each object component is geometrically represented by a single figure m-rep, and the figures of the object are connected by the hinge geometry defined in section 3. As with the single figure case, the multi-figure m-rep describes an object at successively smaller scales following a coarse-to-fine hierarchy, from the object, to each individual figure, to medial atoms of each figure, and finally to the boundary of the entire object with a displacements field applied to it. This representation per component enables us to
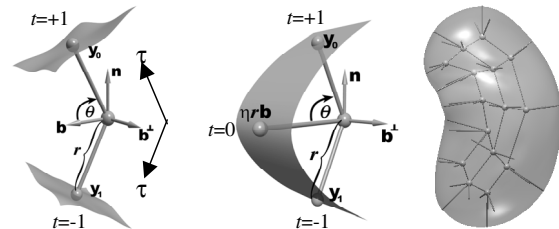

Fig. 1. Left: an internal medial atom. Middle: an end atom. The local implied boundary is incident to and orthogonal to the spoke ends. Right: a single figure m-rep for a kidney and the object boundary implied by it.

analyze efficiently the complex object as a whole. Furthermore, we can talk about component properties, such as shapes and volumes. Statistically, variation of the object within a population can be also measured in a multi-scale fashion. For example, we can investigate the variation of livers as well as of the left liver lobes only. We will describe a segmentation scheme based on m-reps for such a multi-figure representation. Segmentation requires the calculation of the object surface implied by the multi-figure m-rep, by a means we will also discuss.

The rest of this paper is organized as follows. We briefly review the single figure m-rep in section 2. Section 3 develops the technique to represent multi-figure objects by m-reps, and section 4 discusses how we calculate the implied object surface. Section 5 describes image analysis applications based on our multi-figure representation. We show some results on statistical liver analysis using our method in section 6, followed by discussion and concluding remarks in section 7.

2. SINGLE FIGURE M-REP

An *m-rep* [1] is an extension of the medial axis of Blum [4]. The simplest geometric object is represented by a single continuous medial manifold with boundary (Fig. 1, left & middle) at every point on the manifold. A discrete m-rep is formed by sampling the medial manifold over a spatially regular lattice to form a mesh of medial atoms (Fig. 1 right), where each atom consists of a hub x, on the medial sheet, and two equal length spokes. An internal

medial atom is defined as a 4-tuple $m = \{x, r, F, \theta\}$ consisting of the hub position x, the spoke length r, a local frame F including the normal to the medial sheet and the direction along the sheet in which the object narrows most strongly, and the object angle θ between either spoke and the inter-spoke bisector (Fig. 1 left). The medial atoms on the edge of the medial sheet correspond to crests of the object boundary. Such an end atom adds a bisector spoke and a corresponding sharpness parameter (Fig. 1 middle) to control the shape of the crest.

Given an m-rep figure, a smooth object surface is generated to interpolate the boundary positions and normals implied by the atom spokes using Thall's subdivision method [5]. If (u, v) parametrizes the medial sheet, we parametrize the implied boundary by (u, v, t), where t designates the sides of the figure from the top $(t = +1)$ to the bottom $(t = -1)$ across the crests $(t \in (-1, 1))$ (Fig. 1 middle).

Because each medial atom carries an origin, a width, a local frame, and an object angle, we can write any medial atom as a transformation of translation, rotation, magnification, and object angle change from any other medial atom. Thus, an atom can be written in the coordinate system of a neighboring atom. Extending this to the multi-figure m-rep, any atom of a figure can be written in the coordinate system of another.

In [1] a method of multi-scale deformable m-rep segmentation of anatomical objects using a single figure m-rep model was described. In [2] the single figure m-rep segmentation scheme was extended to handle the ensemble of non-overlapping, single figure objects. In this paper we extend the method to multi-figure m-reps.

3. MULTI-FIGURE M-REP GEOMETRY

3.1. Hinge geometry

A multi-figure object is represented by a tree of figures, each represented by a single figure m-rep. For example, a liver can be modeled as a tree with the right lobe as the host figure to the left lobe as a subfigure. The subfigure is attached to its host by a 1D curve of *hinge atoms*, which, when sampled, form an end row or column of the subfigure atom mesh. Each hinge atom rides on the medially implied boundary of the host at a position and an orientation determined by the host's figural coordinate (u, v, t). The host/subfigure arrangement is demonstrated in Fig. 2 left. We recursively attach subfigures to their hosts to form any desired object tree. This allows representation of arbitrarily complex objects, although most anatomical objects are adequately represented by a tree of 2 to 3 levels. The single hinge geometry allows both additive and subtractive subfigures: additive,
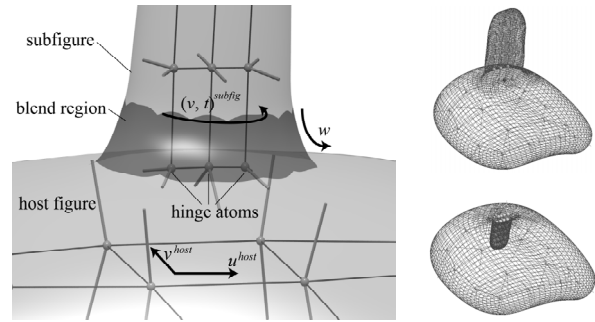

Fig. 2. Left: the host figure/subfigure arrangement, with the subfigure (6 medial atoms appearing) on top, the host figure (4 medial atoms showing) below, and the blend region shown darker. Right: protrusion and indentation subfigures.

forming a protrusion growing out of the host figure; and subtractive, forming an indentation into the host (Fig. 2 right). Subfigures can deform as a consequence of changes in the host figure (section 3.2), or they can transform at the hinge, relative to the host (section 3.3).

Without loss of generality we designate the direction from a subfigure's hinge row to the other end of its medial sheet as parameterized by u.

3.2. Host figure implied subfigure transformation

The hinge geometry implies that as the host figure deforms, the positions and normals of its boundary change and correspondingly each hinge and non-hinge atom of the subfigure must change. The entire subfigure must deform accordingly.

Each subfigure atom can be represented as transformations of its neighboring atoms. Within each chain of atoms from a hinge atom to the other end of the subfigure, each non-hinge atom can be updated to be at an average of the predictions from its already placed immediate neighboring atoms, by maintaining the same transformations between neighbors. This propagation starts from the hinge and is applied to atoms row by successive row. The propagation operates by applying small proportion of the required transformation at a time, followed by regularization, to avoid improper shape changes, such as folding.

3.3. Host-relative subfigure hinge transformations

The subfigure can also translate, rotate, hinge, scale, and elongate on the host figure boundary while the host stays put. In particular, it can translate on the host implied boundary, rotate either on the boundary or about the hinge atoms, widen or shrink, and elongate along the u direction. These basic transformations at the subfigure scale levels form a key component of the coarse-to-fine

hierarchy. All the transformations but elongation change the subfigure hinge atoms. The other atoms are updated by the propagation process described in section 3.2.
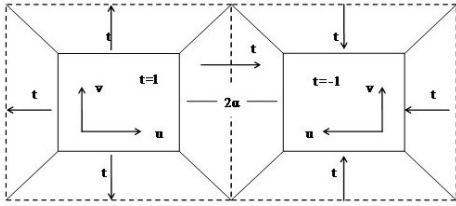

Fig. 3. Planar sheet unfolded from an m-rep figure surface. The two rectangle regions in the middle are the two sides with $t = \pm 1$ and the others are the crests. The parameter α relates distances on the slab faces to distances on the crest.

The four hinge-changing transformations all take place in the host's figural coordinates (Fig. 3), as an unfolded cyclic 2D diagram. Hinge atoms are treated as a discrete curve in the diagram. Hinge-relative subfigure transformations may take the following actions.

- Translate. The hinge atoms are translated in the 2D diagram.
- Rotate. The hinge atoms are rotated by the same amount around the center of the hinge curve in the 2D diagram.
- Hinge. The positions of the hinge atoms stay put. Each hinge atom rotates the same angle about the tangent to the hinge curve in the tangent plane to the host figure boundary.
- Scale. Each hinge atom scales its spoke length r and its relative distance to the center of the hinge curve by the same factor.
- Elongate. The hinge atoms stay put, while each non-hinge atom in the subfigure scales its relative distance to its hinge atom by the same proportion.

With the two types of subfigure transformations, we are able to represent and describe multi-figure objects with variant inter-figure relations. Next, we show how to generate the overall smooth boundary for such objects.

4. INTER-FIGURAL BLENDING

Thall's subdivision method [4] is used to generate the implied boundary of each single figure in a multi-figure object, as a quad-mesh from a quad-mesh of medial atoms. Each host figure and its attached subfigure then meet and merge into each other. In the merging, designated sections from both figures must be removed and replaced by a shared smooth region called the *blend* (Fig. 2 left). The blending algorithm we have developed uses figural coordinates to guide the blend and proceeds in the following steps.

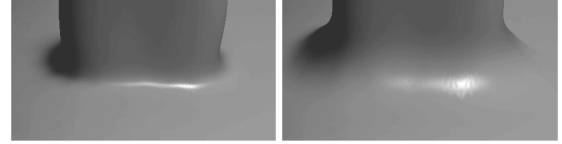1. The intersection curve between the two meshes is calculated and re-sampled.

Fig. 4. Different shape of the blend region controlled by two parameters.

2. The intersection curve is dilated along the host boundary. We convert the curve to a 2D curve in the figural 2D diagram and apply a smoothing flow $F = 1 - \alpha \kappa$, where α is a constant and κ is the local curvature. The dilated curve is converted back to the host boundary. Then the host is cut by the dilated curve and re-meshed.
3. The subfigure is cut by a uniform u value. The part below the cut curve is removed and the rest is re-meshed.
4. The space between the two remaining meshes is meshed together with triangles to form a single mesh, using the Delaunay triangulation criterion. The positions of the vertices are then adjusted according to the initial control meshes of both figures.
5. Catmull-Clark subdivision is used to produce the limit subdivision surface of the adjusted mesh, to the required level of subdivision.
6. The blending region between the two cut curves on the subfigure and host figure is parameterized by (w, v, t), where v and t are the same as the subfigure coordinates and w ranges from $+1$, at the subfigure cut curve, to -1, at the host figure cut curve (Fig. 2 left).

We use two parameters to control the shape of the blend region (Fig. 4): the value of u where the subfigure is cut and the amount of dilation of the intersection curve on the host figure.

5. IMAGE ANALYSIS APPLICATIONS

The segmentation scheme for a multi-figure m-rep extends that for a single figure m-rep. This is a multi-scale, multi-stage process with each stage optimizing the same objective function, composed of a geometric typicality measure plus a geometry-to-image match measure [1].

1. Object stage: the whole object is globally transformed, by a single similarity transform, plus possibly some principal global warps.
2. Main figure stage: the main figure is transformed, by a single similarity transform, plus possibly some principal global warps. The attached subfigures deform accordingly.
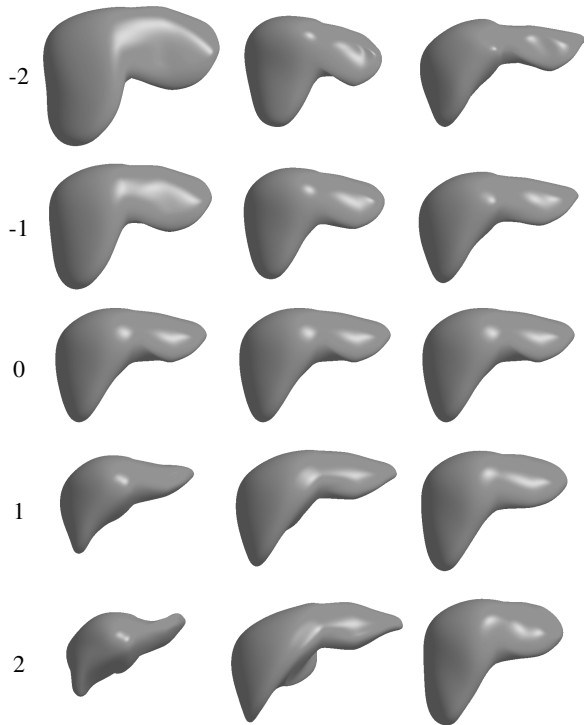3. Main figure atom stage: as with a single figure, the component medial atoms are transformed.

Fig. 5. The first three modes of deformation of two-figure liver models. Each column displays the models corresponding to the indicated # of standard deviations along that principal geodesic.

4. Subfigure stages: in order from hosts to subfigures, each subfigure is transformed by the hinge transformations described in section 3.3.
5. Subfigure atom stage: immediately after the subfigure hinge optimization, the hinge atoms of the subfigure are optimized on the host boundary, while the remaining atoms optimized in their own parameter space.
6. Boundary stage: for the whole blended object, all boundary tile vertices are displaced along the surface normals.

The statistical analysis of m-rep objects proceeds using principal geodesic analysis [3] of the union of the atoms in all figures. We anticipate following this by the statistical analysis on the individual figures of the deformations that form the residue from the full object.

6. PRELIMINARY RESULTS OF STATISTICAL ANALYSIS

To nine manually segmented binary liver images we fit a 2-figure m-rep of 21 and 12 medial atoms, respectively for the right and left lobe. We applied Fletcher's principal geodesic component analysis globally to the resulting m-reps. The modes of variations show not only the shape of both figures, but also the varying relations between the figures. Fig. 5 shows the first three modes of the variations, where the 1st mode roughly corresponds to varying the size of the liver, the 2nd to the varying relations between two lobes, especially the sliding along the hinge, and the 3rd to the varying relative elongation of the left lobe and the right lobe.

7. DISCUSSION & CONCLUSION

With some preliminary results, we have shown that multi-figure m-reps allow representation and analysis of complex anatomical objects by different scales from object to components, and by the inter-relations among components. We developed the geometry and algorithms for multi-figure m-reps representation and segmentation.

We are now extending the multi-figure representation, statistics, and segmentation to multiple levels and applying them to cerebral ventricle segmentation. Also, we are extracting image profiles for multi-figure objects and applying it to gray-level image segmentations. Finally, we are extending multi-object analysis to multi-figure objects.

REFERENCES

[1] S.M. Pizer, P.T. Fletcher, S. Joshi, A. Thall, J.Z. Chen, Y. Fridman, D.S. Fritsch, A.G. Gash, J.M. Glotzer, M.R. Jiroutek, C. Lu, K.E. Muller, G. Tracton, P. Yushkevich and E.L. Chaney. "Deformable M-reps for 3D Medical Image Segmentation", *IJCV*, 55(2/3), Nov. 2003.

[2] P.T. Fletcher, S.M. Pizer, A.G. Gash, S. Joshi. "Deformable M-rep Segmentation of Object Complexes", *Proc. ISBI* 2002, a compact disc, IEEE, 2002.

[3] P.T. Fletcher, C. Lu, S. Joshi. "Statistics of Shape via Principal Geodesic Analysis on Lie Groups", *CVPR* 2003, I: 95-101, 2003.

[4] H. Blum, R. Nagel. "Shape Description Using Weighted Symmetric Axis Features", *Pattern Recognition*, 10(3) 167–180, 1978.

[5] A. Thall. "Fast C_2 interpolating subdivision surfaces using iterative inversion of stationary subdivision rules", Technical report, UNC-CH, Dept. of Computer Science, 2002.