SCAMP: A Solid Modeling Program Using Slice-Constrained Medial Primitives for Modeling 3D Anatomical Objects

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1. Introduction

*M-reps (medial representations)*, as developed here at UNC\(^1\), give a 3D representation for solid objects with width-proportional boundary tolerances. SCAMP provides a modeling tool for creating and visualizing m-rep based models, allowing users to interactively create m-reps matching structures in 3D medical images. SCAMP also includes features for segmentation and registration of image data using these medial models. (Registration issues will be addressed in a separate report.)

2. Technical details

2.1 Basic Concepts

The Blum symmetric axis was developed to represent binary objects; M-Reps are based on multi-scale medial axes, extensions of the Blum idea to non-binary images, as a way of dealing with objects which have uncertainty in their boundary locations. M-Reps are composed of a set of medial atoms, which are linked together to describe an object. A medial atom can be thought of as a function of eight parameters in a three-dimensional Euclidean space: \(M(x, r, \mathbf{F}, \theta)\). In this representation, \(x\) is a 3-vector which gives the position of the medial atom, \(r\) is the distance from \(x\) to the object’s boundary (i.e., the radius of the medial atom), \(\mathbf{F}\) is a frame describing the orientation of the medial atom, and \(\theta\) is half the angle between the medial atom’s arms. The axes of \(\mathbf{F}\) are denoted as \((\mathbf{b, n, b})\), with the arms of the medial atom lying in the \(\mathbf{b-n}\) plane. The implied surface of the medial atom touches the ends of the arms such that the arms are normal to the surface.

2.2 Internal data structures

SCAMP uses an internal hierarchy to combine medial atoms into a model. A number of atoms are linked end to end to form a chain, or a slice of the model; the boundary indicating vectors from the medial atom are constrained to lie within the plane of this slice. Multiple slices with equal numbers of atoms are then connected—with correspondences between the homologous atoms of each slice—to form a mesh of atoms representing a figure. Finally, multiple figures can be combined into an object. For example, a hand can be composed of six figures – a palm and five fingers – each of which is represented by a mesh of medial atoms.

There were a number of reasons that a slice-constrained medial structure was chosen over a more general quad-mesh or triangular lattice of medial atoms:

- foremost, having a slice-based structure allows the simultaneous display of the medial primitives and slice data from a 3D data-set, allowing simple, 2D manipulations of the primitives to model the objects in the data;
- techniques exist to smoothly interpolate boundaries and medial loci given a chain of medial atoms in 2D.\(^2\)\(^3\) SCAMP does not currently use these, but was built with the capability in mind;

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\(^3\) Yushkevich, P, SM Pizer, T Culver (1999). Statistical object shape via a medial representation. Internal report, Dept. of Comp. Sci., Univ. of NC at Chapel Hill.
• slice-based medial figures are easily manipulated, and are a natural fit to many anatomical objects, particularly those with tubular or extruded structures or substructures;
• the constrained quad-mesh structure allows easy interpolation of the boundary using Bezier spline patches and preserving the surface normals where indicated by the medial atoms.

3. Using the Modeler

![Image](image_url)

**Figure 2. A view of SCAMP with a pelvis model.**

### 3.1 Building models

Each figure in a model is initially created as a generic rectangular grid of equally spaced medial atoms. Figures, slices, or individual atoms can be selected using the mouse, and operations are performed on this working set of selected atoms. General operations on a set of atoms include scaling, rotation, and translation and can be performed either with sliders or by dragging the mouse in the viewing window. Operations on individual atoms
include changing the object angle theta and the radius r, and are only available through sliders.

3.2 Visualizations

A model can be viewed simultaneously in four different windows. In the primary window the model can be placed at an arbitrary viewing angle. The three other windows provide orthogonal views of the model along the x, y, and z axes. The view of the model can be both translated and scaled in all four windows independently.

A single figure consists of the medial atoms defining it and the links between the atoms; either or both can be displayed in the four viewing windows. The surface of the model can be displayed either as a wire frame or as a filled surface (both interpolated by Bezier patches), or as a polygonal tile set which can be included in the model’s definition. In addition, SCAMP can load a 3D grayscale image and display it as three orthogonal 2D projections. The planes of these projections can be adjusted using sliders.

Figure 3. A pelvis model consisting of four figures with a total of 72 medial atoms. Only medial atoms and connectors are displayed on the left. The right image shows the wireframe view of the implied surface.

4. Conclusions and Future Directions

Ongoing work using SCAMP involves the use of m-rep models for image registration tasks; once a model is built from a 3D reference image, SCAMP can be used to register this model to a target image using landmark-based rigid transformations, and work is
underway to implement non-rigid deformations as well. Semi-automatic techniques for the non-rigid deformation of medial models into data, given a rough placement of an initial model, will be useful in model-creation as well as in registration.

Further development of SCAMP-like design tools will depend on more sophisticated methods to visualize the 3D data-sets and better paradigms for positioning the medially-defined primitives in the volumes.