Deformable Surface Models
for Segmenting 3D MR Images of Mice

G. Hamarneh[*], N. Kovacevic, J. Sled, M. Henkelman

Overview

We apply image analysis screening techniques to three dimensional (3D) Magnetic Resonance (MR) images as part of an effort to eventually identify mutant mice carrying traits of human disease.

A key task towards this goal is the detection of organ anomalies in images of randomly mutagenized mice, which in turn necessitates quantifying typical variations of organ shape in a normal (un-mutagenized) population.

Image segmentation is a crucial step for identifying the boundaries of mouse organs allowing such quantification.
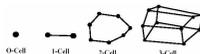
In particular, we demonstrate the use of deformable surface models for segmenting anatomical mouse structures from 3D MR images.

Deformable Simplex Meshes

The underlying geometry of the model used is a simplex mesh [1]:

A k-simplex mesh is a union of k-cells.

Examples of k-cells: Generic 2-simplex meshes:

0-Cell 1-Cell 2-Cell 3-Cell

A simplex mesh is topologically dual to triangulation.

Two types of local forces are calculated and applied at each vertex (V_i) of the mesh: Internal forces (f_{int}) derived from surface smoothness energy terms, and external forces (f_{ext}) along surface normals and proportional to the distance from a vertex to high gradient image voxels (analogous to Active Contour Models or Snakes [2]).

Deformable Simplex Meshes apply the Newtonian law of motion to update the positions of the mesh vertices:

$$m\frac{d^2V_i}{dt^2} + \delta\frac{dV_i}{dt} = \alpha f_{int} + \beta f_{ext}$$

m : mass, δ : damping coefficient, α, β : weights

Global transformations are obtained through the application of global forces (f_{global}) resulting in a deformation field with lower degrees of freedom [3].

A parameter λ is used to weight the influence of global and local forces to update the vertices' positions:

$$V_i^{t+1} = V_i^t + (1-\delta)\left(V_i^t - V_i^{t-1}\right) + \lambda\left(\alpha f_i^{int} + \beta f_i^{ext}\right) + (1-\lambda) f_i^{global}$$

Notes

Implementation:
- The segmentation algorithm was realized through the use of TCL scripts written to interact with the YAV++ software, which is a generic platform of C++ libraries for processing and visualization of volumetric images, developed at INRIA's research group Epidaure, France.
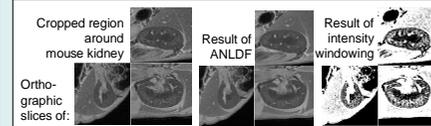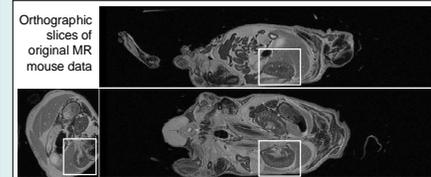
Challenges and Future directions:
- Identifying robust segmentation parameters.
- Segmentation of objects of varying topology (e.g. vessel structures and liver lobes).
- Modeling inter- and intra- mice strain shape variation of segmented organs.
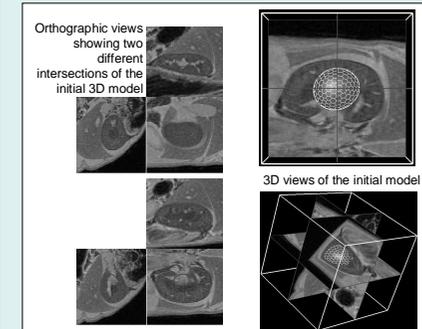
References

[1] H. Delingette. "General Object Reconstruction based on Simplex Meshes". International Journal of Computer Vision, vol. 32(2), pp. 111-146, 1999.

[2] M. Kass, A Witkin, D. Terzopoulos. "Snakes: Active Contour Models". International Journal of Computer Vision, vol. 1(4), pp. 321-331, 1987.

[3] J. Montagnat, H. Delingette. "Globally constrained deformable models for 3D object reconstruction". Signal Processing, vol. 71(2), pp. 173-186, 1998.

[*] e-mail: ghassan@cs.toronto.edu
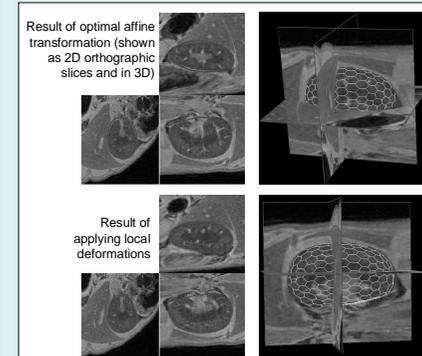
Segmentation Procedure

Prior to deformable model segmentation, the 3D image data is pre-processed by cropping the region of the target organ, applying anisotropic nonlinear diffusion filtering (ANLDF) to reduce noise and enhance edges, and applying image intensity windowing:

Orthographic slices of original MR mouse data

Cropped region around mouse kidney

Result of ANLDF

Result of intensity windowing

Orthographic slices of:

The deformable model is initialized in the vicinity of the target structure:

Orthographic views showing two different intersections of the initial 3D model

3D views of the initial model

The model is then iteratively deformed to latch to the structure boundary while progressively allowing more localized deformations:

Result of optimal affine transformation (shown as 2D orthographic slices and in 3D)

Result of applying local deformations

Results

Segmenting mouse bladder in MR. 1st & 3rd rows: Orthographic slices, white boxes surround regions of interest. 2nd & 4th rows: Initialization (left), 2D sections and 3D view of final result (right).
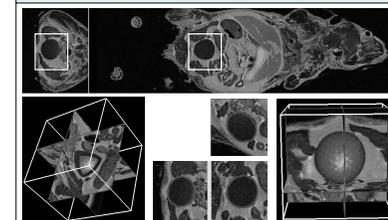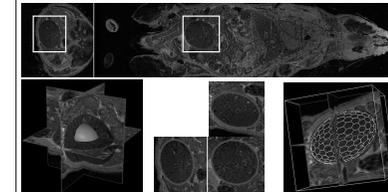
Segmenting mouse kidney. 1st row: Orthographic slices. 2nd row: Initialization, 2D sections, and 3D view of final result (left to right).
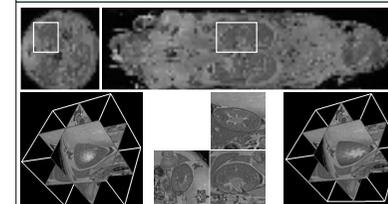
Segmenting mouse brain. 1st & 4th rows: Orthographic slices. 2nd & 5th rows: Initialization, model deformation, and final result (left to right). 3rd row: Consecutive 2D sections of final results. 6th row: 2D sections of segmentation progress.