

Semi-Automatic Segmentation of Mouse Embryo MRIs

L. Baghdadi¹, J. G. Sled^{1,2}, J. E. Schneider³, R. M. Henkelman^{1,2}, and J. P. Lerch^{1,2}

¹Mouse Imaging Center, Toronto, Ontario, Canada, ²University of Toronto, Toronto, Ontario, Canada, ³University of Oxford, Department of Cardiovascular Medicine, United Kingdom

Introduction:

There is new interest in prospectively knocking out each of the approximately 25000 genes of the adult mouse. Imaging, and in particular MRI, is becoming recognized as a valuable tool for phenotyping the resulting adult mouse lines. As a complement to the adult mouse, there is also a need to phenotype mouse embryos in order to analyze normal embryonic development as well as embryonic lethal mutations. Schneider et al have developed a method to stack 32 embryos embedded in gel and have imaged them within a single RF coil at 9.4 Tesla [1]. The large number of embryos grouped within a single MRI field-of-view (see Fig 1 a) indicates that a significant segmentation challenge must be solved before further automated image processing can take place. Here we describe a semi-automatic technique to segment individual embryos from the 32 in the MRI dataset using a deformable model algorithm.

Methods:

Our method uses a modified deformable model algorithm to correctly segment the boundaries of an embryo [2][3]. A confounding challenge to the successful use of deformable models is their sensitivity to incorrect initialization of the algorithm. We overcome this problem by feeding a binary classification of the background gel to the initial stage of the deformable model. The classified image is generated by first creating a local variance map from the MRI, and then using a Bayesian classifier [4] with the variance as well as the original MRI as input. The user then places the starting sphere within the embryo. Using the classified image, the simplex mesh sphere [3] is then expanded to the initial embryo using balloon forces [2]. This embryo along with original MRI is then used as the initial state for the deformable model for the final deformation [3]. The position of vertices evolves iteratively under the influence of gradient forces and an elastic constraint on the shape regularity. The deformation stops when the sum of the distances between the mesh and the image edge is below a user specified threshold. Finally, we create a mask using a rasterization algorithm from the mesh. To keep the results consistent, the parameters that control the deformable model algorithm are constant for all embryos.

Results:

Figure 1 shows one slice of the 3D segmentation on one embryo. We have tested our method on three individual embryos from different tubes and compared the results to manual segmentations of the same embryos. Our algorithm was able to reproduce the manual segmentation quite accurately, with a mean Kappa value (measure of similarity between two binary images which ranges from 0 meaning no alignment and 1 meaning perfect alignment) across the three embryos of 0.9 ranging from 0.89 to 0.91.

Discussion and Conclusion:

We have demonstrated the ability to segment multiple embryos using a modified deformable model algorithm with constant parameters using a separate initial model for each embryo. This approach is conditional on having embryos not in direct contact with each other in the image as the model may leak should the embryos touch each other. We anticipate that we will be able to correct for touching embryos using a mesh collision-detection algorithm to stop the deformation at collision point.

References:

1. Schneider JE, et al, "Identification of cardiac malformation in mice lacking Ptdrs using a novel high-throughput magnetic resonance imaging technique", *BMC Developmental Biology*, 4:16, 2004.
2. Park JY, et al, "A non-self-intersecting adaptive deformable surface for complex boundary extraction from volumetric images", *Computers & Graphics* 25 (2001) 421-440.
3. Delingette H, "General Object Reconstruction based on Simplex Meshes", *Int. Journal of Computer Vision* 32, 111-142, 1999.
4. Zijdenbos AP, et al, "Automatic pipeline analysis of 3-D MRI data for clinical trials: application to multiple sclerosis", *IEEE Transactions on Medical Imaging* 21, 1280-1291, 2002.

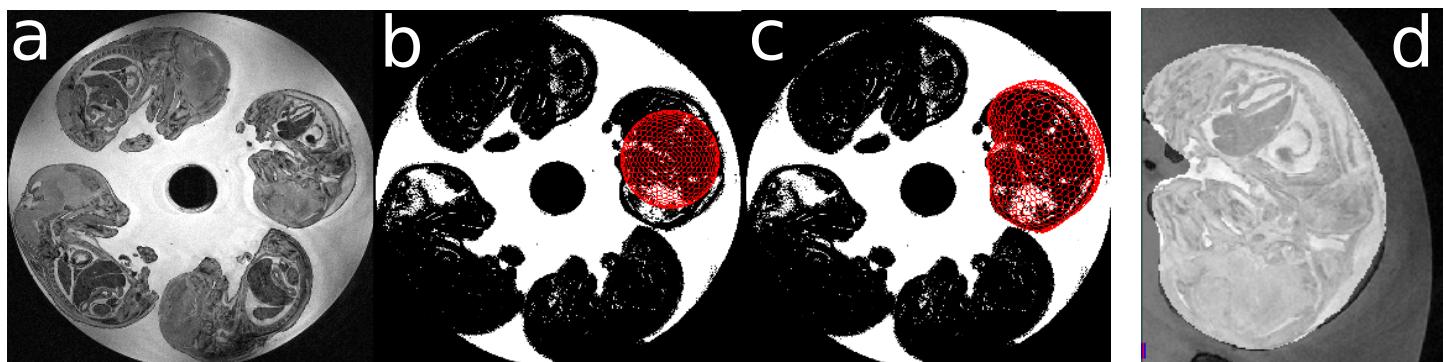


Figure 1: Segmentation Procedure a) original image b) classified image with initialized sphere c) deformed sphere to embryo d) final mask over original image