An Efficient Virtual Dissection Tool to Create Generic Models for Anatomical Atlases

Mei XIAO^{1a}, Jung SOH^a, Oscar MERUVIA-PASTOR^a, David OSBORN^b, Nathan LAM^a, Benedikt HALLGRÍMSSON^b, Christoph W. SENSEN^a

^aSun Center of Excellence for Visual Genomics, Department of Biochemistry and Molecular Biology, Faculty of Medicine, University of Calgary ^bMorphometrics Laboratory, Department of Cell Biology & Anatomy Faculty of Medicine, University of Calgary

Abstract. We have developed an efficient virtual dissection tool to create generic 3D models for anatomical atlases without the need for artistic drawings. Our custom-developed tool can be used to extract 3D models from 2D medical image stacks, cut the models and align the sub-models. Corresponding 2D medical image portions of the sub-models can then be registered and averaged. In the end, a generic model can be obtained from the averaged 2D images of several subjects. The technique optimizes the functionalities of existing toolkits and the resulting software package will allow biologists to build their atlases more quickly and accurately.

Keywords. generic anatomical model, virtual dissection, virtual anatomical atlas, 3D alignment, 3D reconstruction

1. Introduction

Generic human anatomical digital 3D atlases have been used in a variety of fields such as medical education, virtual crash testing, therapy planning and customizing replacement body parts [1, 2]. Furthermore, generic 3D atlases of some species have been used to study relationships between genetic perturbations and shape developments [3]. Generic models also have been used for object recognition and reconstruction [4, 5]. There is a high demand for building generic anatomical atlas models of various species. However, building generic anatomical models generally requires a graphic designer to study shapes of real objects intensively and design polygon meshes using modeling software. This process is very time-consuming and labor-intensive. In order to satisfy the high demand for generic atlas models, we have developed a virtual dissection tool that biologists can use to create generic 3D models for their atlases without the need for artistic drawings.

¹ Corresponding Author: Mei Xiao, Email: mxiao@ucalgary.ca

2. Methods

To illustrate our method we chose to build an atlas of mice. Five male and five female laboratory mice from the same strain were used as subjects to validate our tool. Female mice were 54 to 61 days old and weighed 16 to 21 grams; male mice were 61 days old and weighed 20 to 25 grams. Models of the skeleton components were built first.

For each subject the following steps were applied to produce the model for a specific bone: Produce 2D computed tomography (CT) images of the mouse; Use the marching cubes algorithm in VTK [6] to extract the 3D model of the skeleton from the image stack; Use the custom-developed cutting tool to continuously cut the skeleton model until the separation of the desired bone model is achieved (see Figure 1 and Figure 2 (a)); Calculate the bounding box of the bone model; Generate the bone model's corresponding 2D CT image portions. Then all the bone models and their respective bounding boxes were displayed in the same 3D coordinate system.

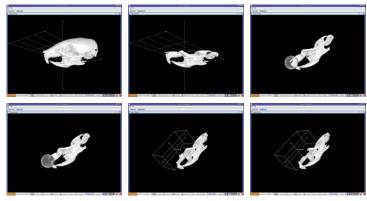


Figure 1: Model cutting.

At this point users can scale, rotate and transform a model within its bounding box and are allowed to align the models in any configuration they choose (see Figure 2 (b)). Once users are satisfied with the 3D alignment, they may create generalized shape images (GSIs) [3] by scaling and registering corresponding 2D images that contain those models according to that configuration and then averaging the intensities of the pixels. At the end, the marching cubes algorithm is applied to the resulting GSIs to extract the generic bone model which represent the average shape of the bones across all the subjects (see Figure 2 (c)).

The production and averaging of 2D CT image portions are done using functionalities in ImageJ [7]. The scaling of 2D CT image portions is done using VTK. An intensity-based rigid 3D registration algorithm which uses a mean square metric, a linear interpolator, a versor rigid 3D transform and a versor rigid 3D transform optimizer inside ITK [8] is used to register the images automatically. An initial transform that is generated through the model alignment is utilized in order to make the registration process work robustly. Our software is written in Java. Open source toolkits such as VTK, ITK and ImageJ are integrated in a creative combination.

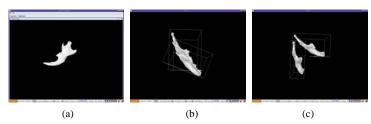


Figure 2: (a) A left mandible model created by continuously cutting a skeleton model. (b) Manual alignment of models. (c) Generic models for the left mandible (female mice and male mice).

3. Results

In order to automatically or semi-automatically create generic 3D models, different approaches have been proposed. However, those generic model building tools will either need perfect individual models or require costly human computer interactions to register corresponding images. Our approach can be used to create desired models very quickly and automatically register images. Therefore, this method significantly shortens the generic model building time by eliminating a large amount of human computer interactions. Using a plane to separate a 3D polygon mesh has been used to refine a model created from CT or MRI image stacks [9]. Our approach can use not only a plane, a box or a sphere to cut 3D models, but also is open to adding more cutting algorithms. The technique we developed optimizes the functionalities and technologies of existing toolkits and the resulting software package will allow biologists to build their atlases more quickly and accurately.

This work has been supported by Genome Canada through Genome Alberta; Alberta Science and Research Authority; Western Economic Diversification; the Governments of Canada and of Alberta through the WEPA Partnership Agreement; the iCORE/Sun Microsystems IR Chair program; the Alberta Network for Proteomics Innovation; and the Canada Foundation for Innovation.

References

- [1] Schmutz, B., Reynolds, K.J. and Slavotinek, J.P. Development and validation of a generic 3D model of the distal femur. Computer Methods in Biomechanics and Biomedical Engineering. Issue 5. 2006.
- [2] Zachow, S., Zilske, M. and Hege, H.C. 3D reconstruction of individual anatomy from medical image data: segmentation and geometry processing. CADFEM User's Meeting. 2007.
- [3] Kristensen, E., Parsons, T.E., Hallgrímsson, B. and Boyd, S.K. A novel 3D image-based morphological method for phenotypic analysis. To appear in IEEE transactions on Biomedical Engineering. 2008.
- [4] A-Nasser, A., Mohamed, A. 3-D face modeling using two views and a generic face model with application to 3-D face recognition. AVSS'03.
- [5] Chowdhury, A.R., Chellappa, R., Krishnamurthy, S. and Vo, T. 3D face reconstruction from video using a generic model. ICME '02. Proceedings.
- [6] Schroeder, W., Martin, K. and Lorensen, B. The Visualization Toolkit. Prentice-Hall, Inc. 2006.
- [7] Rasband, W.S., ImageJ, U. S. National Institutes of Health, Bethesda, Maryland, USA, http://rsb.info.nih.gov/ij/, 1997-2005.
- [8] Yoo, T (ed.) Insight into Images. A.K.Peters, 2004.
- [9] Yushkevich, P.A., Piven, J., Hazlett, H.C., Smith, R.G., Ho, S., Gee, J.C., and Gerig, G. User-guided 3D active contour segmentation of anatomical structures: Significantly improved efficiency and reliability. Neuroimage. 2006.