

WHAT IS THE ACCURACY OF SURFACE MODELS CREATED FROM VISIBLE HUMAN MALE COMPUTED TOMOGRAPHY DATA?

¹Schmidt J, ¹Eng J, ²Viceconti M and ¹Ploeg H

¹University of Wisconsin – Madison, WI, USA

²Rizzoli Orthopedic Institute, Bologna, Italy

e-mail: jschmidt1@wisc.edu, web: <http://www.engr.wisc.edu/groups/BM/>

INTRODUCTION

Three-dimensional (3D) finite element (FE) analysis is used to determine stress and strain distributions in bone in order to predict fracture risk and design orthopaedic implants. Many studies have used computed tomography (CT) data to supply data about geometry and material properties to FE models [1–5]. Both custom-built and commercial segmentation programs have been used to determine the complex bone shape. Yet, few studies have reported the geometric accuracy of the segmentation methods [6-7]. Therefore, the goal of the current study was to determine the accuracy of surfaces created from the visible human (VH) CT data using custom-made and commercial segmentation software programs.

METHODS

The National Library of Medicine's Visible Human (VH) male computed tomography (CT) and cryogenic standardized data sets were used in this study [8]. Two different methods were used to segment both the right (R) and left (L) femurs of the VH CT data. One method uses the custom-made border tracing algorithm, which was developed as part of the HIPCOM project [7], to segment the bones. This method extracts a closed contour as an object, which is an ordered sequence of adjacent pixels. Specifically, once a starting point and direction is located by the user the algorithm searches the eight neighboring points to determine the pixel with intensity greater than or equal to the current pixel. Polygonal surfaces are interpolated from the resulting stack of contour curves. This method is also used to segment the cryogenic VH data.

The second method uses the commercial software Mimics (Materialise, Ann Arbor, MI) to segment the bones. Within this software the primary segmentation command was 'Thresholding'. The 'Thresholding' feature allows the user to specify an upper and lower bound from a range of Hounsfield values, which is known to be related to density. Further processing is uses the 'Edit Masks' commands of 'Draw' and 'Erase'. These commands were only used when needed to fill holes or detach one mask from another.

Polyworks Inspector 8.0.8 software (InnovMetric, Sainte Foye, QC) was used to compare models. The perpendicular distance between points of the CT models and the surface of the cryogenic model was determined. These distances were then used to determine the mean, standard deviation, minimum, and maximum separation distances.

RESULTS

Initial comparisons found no difference between the cryogenic STL and IGS models (L: 0.02 ± 0.11 mm), therefore only the cryogenic STL models were used for the subsequent comparisons. For confidentiality, labels A and B are used to identify the segmentation methods. Method A created models smaller than the cryogenic models (R: -0.29 ± 0.99 mm; L: -0.37 ± 0.62 mm) (Figure 1). Method B created models larger than the cryogenic models (R: 0.46 ± 0.61 mm; L: 0.42 ± 0.60 mm) (Figure 1).

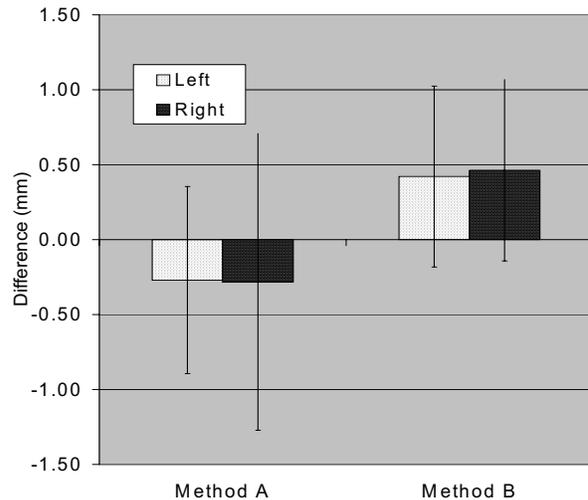


Figure 1: Mean distance and standard deviations between VH cryogenic and CT models created using custom-made and commercial segmentation software.

CONCLUSIONS

The current study reported a smaller mean error (-0.3 – 0.5 mm) compared to a previous study (0.6 – 0.9 mm) [6]. In addition, this study reported a higher range in standard deviation (0.6 – 1.0 mm) than a previous study (± 0.3 mm), which also reported a peak error of 1.5 mm [7].

The current study reported the accuracy of two segmentation methods, while developing a protocol for validation of models created from CT data. This protocol determines the accuracy of a segmentation method using the internationally accessible VH CT data set. This study assumed that the segmented cryogenic VH data set was the gold standard for comparison. A similar method of validation can be used for solid geometry, mesh geometry, and FE deformations and stress. This protocol provides researchers with a method to accurately compare modeling methods created to predict fracture failure or to design orthopaedic implants.

REFERENCES

1. Cattaneo PM, et al. *Proc Instn Mech Engrs* **215**, 203-213, 2001.
2. Donahue TL, et al. *J Biomech Eng* **124**, 273-280, 2002.
3. Keyak JH et al. *J Biomed Eng* **12**, 389-397, 1990.
4. Merz B, et al. *J Biomech Eng* **118**, 387-390, 1996.
5. Prendergast PJ. *Clin Biomech* **12**, 343-366, 1997.
6. Testi D, et al. *Comput Methods Programs Biomed* **65**, 175-82, 2001.
7. Viceconti M. *J Med Eng & Tech* **23**, 77-81, 1999.
8. Spitzer V, et al. *JAMIA* **3**, 118-130, 1996.

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