Automatic Segmentation of the Thumb Carpometacarpal Joint

M.T.Y. Schneider¹, J. Crisco², A. C. Weiss², A. L. Ladd³, P. Nielsen¹,⁴, T. Besier¹,⁴, J. Zhang¹
¹. Auckland Bioengineering Institute, The University of Auckland, ². Department of Orthopaedics, Brown University, USA, ³. Department of Orthopaedic Surgery, Stanford University, USA, ⁴. Department of Engineering Science, The University of Auckland.

Introduction

The first carpometacarpal (CMC) joint is highly susceptible to osteoarthritis (OA) which affects over 15% of adults over age 30, two-thirds of which are women. We believe that morphology of the CMC joint plays a role in the development of CMC OA. Here we present an automated pipeline for creating parametric meshes of the CMC joint from CT-images, for the purpose of creating statistical models of CMC joint morphology. This method involves the novel combination of random forest regression [1] with a parametric mesh-based statistical shape model (SSM) [2] to automatically create CMC meshes which are correspondent across individuals and are therefore suitable for statistical shape analysis.

Methods

- A training set of 50 CMC joints were manually segmented from CT images of the hand with a resolution of 0.4x0.4x0.625mm (age range: 18 yrs to 67 yrs; 24 females and 26 males).
- A custom piecewise parametric template mesh was fitted to each segmented data cloud, resulting in a set of correspondent meshes of the metacarpal and trapezium which were used to train the SSM.
- 3-D Haar-like features were sampled from the image about each mesh node and used to train a random forest regressor for each node.
- During segmentation, CT image stacks were loaded into image space (A).
- The mean mesh was then initialized near the image-CMC joint via an automatic hierarchical landmark based segmentation algorithm (B).
- Random forest regressors then predicted the best-matching image positions of the mesh nodes (C).
- The mesh was then fitted to the predicted points using deformations permitted by the SSM resulting in a customized mesh of the CMC joint surface (D).
- This segmentation was performed on 35 CT images not a part of the training set and the RMS error between automatically segmented meshes and ground truth was calculated.

Results

- 34 of the 35 data sets not included in the training set were successfully segmented with an average surface-to-surface RMS error of 0.95 mm compared to ground truth.
- The average time taken for the pipeline to segment 1 data set at high accuracy was approximately 10 minutes compared with 5 hours taken to segment 1 data set manually.
- Thus, segmentation time was reduced by ~96%.

Conclusion

- This pipeline shows promise for automatically collecting a large population of CMC joint morphology for statistical analysis.
- Eventually, it may be used in a clinical setting where rapid patient specific mesh generation and analysis would be invaluable.

Acknowledgements

We would like to thank the Auckland Bioengineering Institute, Stanford Orthopaedics, and the NIH for funding.

References


Figure 1 – Automatic Segmentation Pipeline