

Automatic Segmentation of the Thumb Carpometacarpal Joint

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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.

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%.

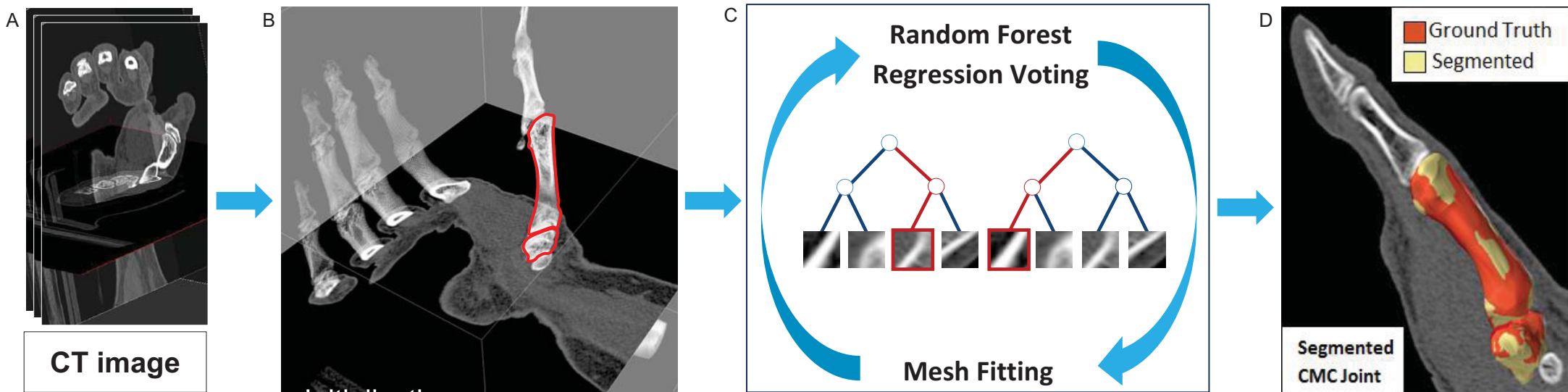


Figure 1 – Automatic Segmentation Pipeline

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.

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

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References

1. Cootes, T.F., et al., *Robust and accurate shape model fitting using random forest regression voting*, in *Computer Vision—ECCV 2012*. 012, Springer. p. 278-291.
2. Zhang, J., Malcolm, D., Hislop-Jambrich, J., Thomas, C. D. L., & Nielsen, P. M. F. (2014). An anatomical region-based statistical shape model of the human femur. *Computer Methods in Biomechanics and Biomedical Engineering: Imaging & Visualization*, 1–10. doi:10.1080/21681163.2013.878668