Statistical Shape Models for Age Prediction: Evaluating the Impact of Modeling Software in ACL-Injured Youth

Zachary A. Flahaut[1], Elese J. St Louis[1], Daniel L. Benoit[2], Sasha Carsen[3], Allison L. Clouthier[1,4]
[1]Ottawa-Carleton Institute for Biomedical Engineering, University of Ottawa, Ottawa, Canada
[2]Department of Health Sciences, Faculty of Medicine, Lund University, Lund, Sweden
[3]Children's Hospital of Eastern Ontario Research Institute, Ottawa, Canada
[4]School of Human Kinetics, University of Ottawa, Ottawa, Canada
Email: zflah021@uottawa.ca

Summary

Statistical shape models (SSMs) can be used to characterize age-related morphological changes in pediatric patients with ACL injuries and explore how these changes might influence biomechanics and injury risk. It is unclear if the choice of MRI segmentation software might affect SSM development. To address this, we compared the Elucis and Medical Imaging Interaction Toolkit (MITK) segmentation platforms. We found that segmentation software selection affects the percent variance explained, the generalizability of model predictions but not model specificity. Correlations between principal components (PCs) and developmental markers such as age and Tanner stage, are also affected.

Introduction

Understanding how skeletal morphology evolves with age is crucial for tailoring treatments, improving rehabilitation strategies, and assessing biomechanics in pediatric patients. SSMs, created with principal component analysis (PCA), are a promising tool to understand skeletal morphology and its relationship to age and growth stages. Previous studies highlight the dynamic nature of bone growth during adolescence [1-2], emphasizing the need for tailored computational tools to assess age-related variations effectively. However, limited research addresses how preprocessing software affects SSM accuracy and interpretation. This study investigates the role of segmentation software in shaping predictive capabilities, focusing on ACL-injured youth.

Methods

MRI scans of 36 female pediatric patients (age = 15.32 ± 1.27 years, height = 165.22 ± 5.51 cm, mass = 65.49 ± 10.39 kg, BMI = 23.68 ± 3.51) with ACL-injured knees were analyzed. These scans were segmented by a single rater using two platforms: Elucis (v.1.5.1, RealizeMedical, Canada), a virtual reality-based segmentation tool, and MITK (MITK, Germany), a standard 2D segmentation software. Statistical shape models (SSMs) were constructed using a custom Python pipeline (Python 3.11.5). Metrics such as percent variance explained, model generalizability, and model specificity were evaluated [3]. To assess the model's specificity, 500 virtual samples were generated and compared with real training samples to measure their deviation. Correlations between PC scores and developmental markers (age, Tanner stage) were assessed using Pearson's r. ANOVA and Tukey's HSD tests were performed to analyze PC distributions across developmental stages. Both platforms utilized identical datasets to ensure comparability.

Results and Discussion

MITK demonstrated superior performance compared to Elucis across multiple metrics. Specifically, MITK explained a higher percent variance in PC1, which predominantly represents size (30.45%), compared to Elucis (18.99%). The total variance explained by the included PCs was slightly higher in MITK (90.95%) compared to Elucis (90.35%), with MITK requiring fewer PCs (17 vs. 19) to achieve this, indicating a more compact and efficient model. MITK also achieved better model generalization with a lower RMSE (0.596±0.154 mm) compared to Elucis (0.659 ±0.201 mm). There were no difference for model specificity between MITK and Elucis.

Age and Tanner stage generally exhibited weak or very weak correlations with PCs, apart from PC3, which showed moderate correlations with Elucis for age and MITK for Tanner stage. Visual analysis of PC1 highlights variability, demonstrating how the choice of preprocessing software can impact the interpretability and predictive accuracy of SSMs.

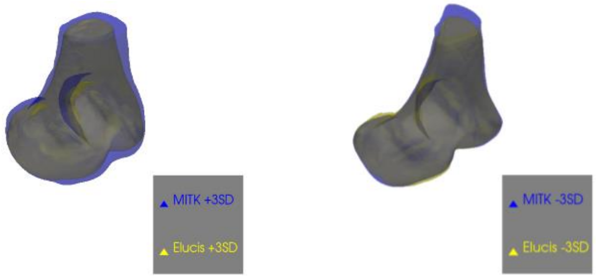

Figure 1. Left: +3SD PC1 morphologies generated by MITK (blue) and Elucis (yellow). Right: -3SD PC1 morphologies generated by MITK (blue) and Elucis (yellow).

A higher variability was observed in PC scores in younger participants reflecting ongoing growth processes, while older participants exhibited more clustered scores, indicating stabilization of skeletal morphology. This trend was more pronounced and consistently captured by MITK, possibly due to its ability to handle size-related variance and morphological subtleties.

Conclusions

This study highlights that large shape features are similar between segmentation software, however subtle features may differ. SSM metrics were better for the model generated from MITK segmentations than Elucis and the MITK model may have been better able to identify age-related shape differences. These results indicate that consideration should be given to the choice of segmentation software when using SSMs to study variation in bone morphology.

References

[1] Baroni F. et al., (2022). *Front. Endocrino*., **13**:1101403.
[2] Connie W. (2002). *Endocrine*, **1**:43-48.
[3] Audenaert E. A. et al., (2019) *Front. Bioeng. Biotech.*, **7**:302