Pipeline for Specimen Specific Bone-Ligament-Cartilage Finite Element Models

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Abstract

In recent decades, computational human body models (HBM) have improved dramatically and have been utilized in order to understand, quantify, and predict human injury. However, the time necessary to create a new model can be extreme. There have been previous efforts aimed at rapid HBM development which utilized statistical anthropometric data to generate target models with given stature, weight, and age; however, these do not reflect the specific geometry of any particular human or surrogate.[6] Consequently, the large majority of models in use today have either a single or limited number of representative geometries. From these examples, it has been shown that without geometric fidelity, these generalized models struggle to predict biomechanical response for testing scenarios where the surrogate is not similar to the representative model. Therefore, the objective of this study was to develop a pipeline to rapidly and algorithmically generate specimen-specific finite element models that are fidelic in their bony, ligamentous, and collagenous structures, so that biomechanical influence of geometric variation can be represented in the model.

Prior work elastically deforming, or "morphing," a template finite element human femur model to specimen-specific geometries was adapted and expanded to the lower extremity[2,3]. The lower extremity was considered for its numerous bones and soft tissues. First, an algorithm was created that allows for the input of multiple bony structures while still preserving fidelic joint spacing. In this case, bony structures from the template model were morphed to the specimen-specific shape of the respective STL using an adapted surface-registration process[3,4]. Second, the bony topology underlying the ligaments and cartilage (soft-tissues) are extracted as distinct features after which each is realigned to the target geometry using an iterative-closest-point (ICP) method. In this way, the soft-tissue attachments can be accurately transferred from template to target. Additionally, this methodology incorporates dynamic ligament wrapping around bony surfaces[5]. Cartilage thickness was further assessed by checking for penetration between cartilage pairs. Next, material properties and contact definition were transferred from the template to the new model. Finally, these three steps were implemented as subroutines to a single automated wrapper function.

Using this methodology, an existing lower extremity finite element model, including 28 bones, 111 ligaments, and 30 cartilage pairs, is able to be rapidly and automatically morphed into any new specimen-specific geometry, typically in 5-18 hours. This quick process from acquisition of target geometry, e.g. from CT, to HBM creation enables use of the specimen-specific model in parallel with traditional experimental methods. This capability has the potential to leverage the strengths of parametric computation simulation in concert with experimental test setups to a degree not previously possible.

References

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