Impact of a Novel, MRI Based Approach for Ligament Personalization in Knee Modeling

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ABSTRACT

1 Introduction

Several approaches are possible when modeling the knee joint's response to load [1-3]. A common crucial point is how to personalize the model, adapting its parameters so that the model prediction optimally matches the behavior of a specific subject. The model sensitivity may vary considerably depending on the approach [1]. In general, the correct identification of ligament origin, insertion, and resting length have a strong impact on the model response [1,4]. A standard procedure for optimizing ligament properties involves utilizing experimental data, where joint kinematics have been measured under various external loads.[1]. This approach is indeed very effective; however, it generally requires complex and invasive experimental measurements, which reduce its application in standard clinical scenarios, where typically only medical images are available. In this work, we want to present a novel process that uses kinematic prediction of individual joint models based on magnetic resonance images (MRI) to identify the ligament parameters. The results of this method will be compared with those achievable using data directly obtained from MRI, i.e., without an individual model.

2 Methods

We investigated six fresh-frozen lower-limb specimens (one female, five men; age: 67.3±17.2 years; weight: 69.4±13.2 Kg; height: 168.3±8.5 cm). A surgeon declared the legs free from anatomical defects and removed the forefoot and all soft tissues except those at the joint, leaving the knee capsule and ligaments intact. A stereophotogrammetric system (Vicon Motion Systems, Ltd., Oxford, UK) was used to measure the tibia and femur relative motion, employing two trackers directly fixed to the bones, thus introducing no soft-tissue artifacts. The specimen was mounted on a test rig for in vitro analysis of the knee joint motion [5]: the femur was connected to the rig and use to control the knee flexion, while the tibia was free to move according to its passive motion, i.e. without external forces acting on it. Computed tomography (CT) scans and MRI of each knee were acquired. Articular surfaces and ligament insertions were then manually segmented using the free open-source software Medical Imaging Interaction Toolkit. In particular, the origin and insertion areas of the main ligaments of the knee (ACL, PCL, MCL deep and superior bundles, LCL, ALL) were identified, together with their centroid. Anatomical reference systems were defined according to a standardized convention [6], and relative femoro-tibial orientation was expressed according to a YXZ Euler angle sequence [7], while the relative translations were represented as the coordinates of the femur origin in the tibia reference system. For each knee, two deformable multibody models were defined. Both include articular contact modeled with a variation of the mattress of springs and built on cartilage morphology; seven single-fiber ligaments with bilinear elastic characteristic, where the stiffness of ligament and contact was taken from the literature [8], and no viscous effect was introduced. The two models differ only by the location of the ligament insertions and resting length. In particular, one model (MRI-M) simply takes the centroid of the insertion area as identified in the MRI, and the resting length as the linear distance between ligament origin and insertion as measured in the scanning pose. The second model (KIN-M) is instead built on a prediction of knee motion based on the maximization of joint congruence [9] and the reciprocity among joint constraints and helical axis of motion [10]. From the predicted motion, the most isometric fiber of each ligament is identified, providing optimized insertions and resting length. The two models were then compared by computing the passive motion as the envelope of equilibrium position over the flexion range. Mean absolute rotational (MARE) and translational (MATE) errors were computed for each model with respect to the experimental measure.

Table 1: Mean absolute rotational (MARE) and translational (MATE) errors for the two models (MRI-M and KIN-M), computed for each subject and average on the population.

	Subject 1		**Subject 2**		**Subject 3**		**Subject 4**		**Subject 5**		**Subject 6**		**Average**	
	MRI-M	KIN-M	MRI-M	KIN-M	MRI-M	KIN-M	MRI-M	KIN-M	MRI-M	KIN-M	MRI-M	KIN-M	MRI-M	KIN-M
MARE [°]	6.2±1.9	1.8±2.2	12.5±3.2	2.3±0.8	6.7±3.6	4.7±2.9	11.9±6.6	1.5±0.9	7.5±1.2	1.4±1.1	3.2±0.7	1.4±0.7	**8.0±2.8**	**2.2±1.4**
MATE [mm]	4.2±1.1	1.9±0.5	4.7±1.8	3.6±1.0	3.6±2.0	2.6±0.8	6.3±2.8	3.8±1.4	4.6±2.0	2.6±1.2	9.0±2.6	4.1±2.2	**5.4±2.0**	**3.1±1.2**

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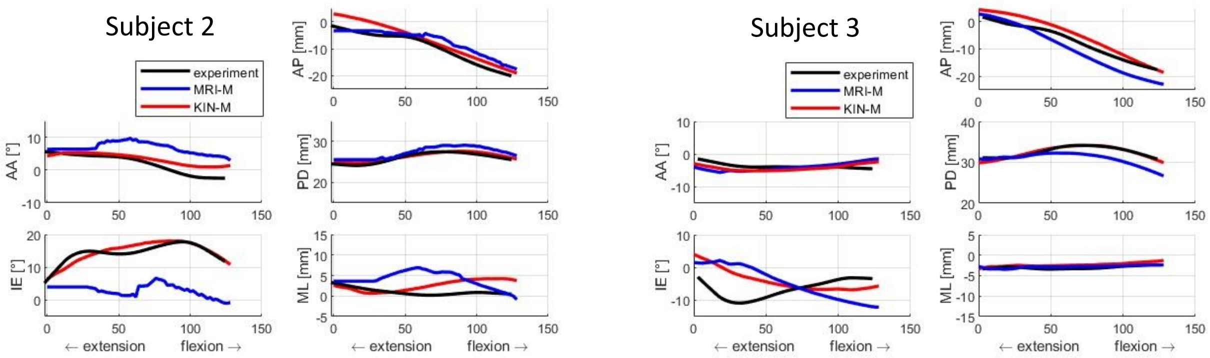

Figure 1: Femoro-tibia kinematics computed with the two models for two subjects: AA is abduction/adduction, IE internal/external rotation, AP anterior/posterior, PD proximal/distal, and ML medial/lateral translations.

3 Results

In Table 1, the MARE and the MATE for each subject are reported for both models. KIN-M always provides a better estimation of knee pose with respect to MRI-M. Interestingly, the discrepancy between the two models is not constant and varies considerably among the subjects. In particular, while MARE never exceeds 4.7° for KIN-M, it may reach up to 12.5° for MRI-M. The resulting passive kinematics reconstructed with the two models are compared to experimental data in Figure 1 for two subjects.

4 Conclusions

The proposed methods for the personalization of ligament properties provide a tool for the personalization of knee joint models based solely on information from MRI, thus making them non-invasive and compatible with clinical practice. The predictions of KIN-M show very good agreement with experimental data, supporting the validity of the approach. Interestingly, MRI-M shows alternate results, in some cases resulting equivalent to KIN-M, while in others, it provides considerable discrepancy with respect to the experimental motion. These results stress the importance of a solid and validated procedure for the definition and personalization of joint models.

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