

A MESH MORPHING BASED METHOD TO ESTIMATE CRUCIATE LIGAMENT ATTACHMENTS BASED ON CT-DATA

M. Asseln^{1,3*}, C. Haenisch^{1*}, G. AlHares¹, V. Quack², K. Radermacher^{1,3}

1* Chair of Medical Engineering, Helmholtz-Institute for Biomedical Engineering, RWTH Aachen University, Germany, asseln@hia.rwth-aachen.de

2 Dept. of Orthopaedics, Aachen University Clinic, RWTH Aachen University, Germany

3 Pauwels Center Aachen, Aachen, Germany

INTRODUCTION

For a proper rehabilitation of the knee following knee arthroplasty, a comprehensive understanding of bony and soft tissue structures and their effects on biomechanics of the individual patient is essential. Musculoskeletal models have the potential to predict dynamic interactions of the knee joint and provide basic knowledge to the understanding of knee biomechanics [Heller2007]. Investigating complex biomechanical problems and local joint phenomena, such as forces and strains on the knee structures or implant, require subject-specific models [Asseln2014, Chen2014]. In this context, the implementation of the major ligaments should be considered as one important aspect for individualised dynamic modelling of the knee [Nolte2013]. However, the information regarding the patient specific attachments which may be obtained from high resolution MRI, is not available in the clinical routine e.g. in knee arthroplasty.

Erhardt et al. used a registration atlas based procedure to estimate anatomical landmarks on pelvic bone [Erhardt2003]. A similar approach was recently presented by Ascani et al., who assessed origins and insertions of the knee ligaments using a set of 16 bone landmarks. [Ascani2014]. However, the landmarks need to be manually defined and subsequently a manual adjustment is required (snap to surface). Pellikaan et al. proposed a morphing based method to estimate muscle attachment sites of the lower extremity [Pellikaan2014].

The goal of this study was to evaluate the accuracy of a fully automatic and robust mesh morphing method that estimates locations of cruciate ligament attachments on the basis of training data (Fig. 1).

MATERIALS AND METHODS

The cruciate ligament attachments from 6 (n=6) different healthy male subjects (BH 184±6cm, BW 90±10kg) were identified in MRI-datasets by a clinical expert in the medical image software Osiris [Ligier1994]. The insertion areas were exported as point clouds (sampling points of the curves). Due to the inhomogeneous point distributions, the point sets had to be uniformly resampled to compute the geometric centers which served as approximations of the attachments. These insertion points were used to annotate the mean shapes of femur and tibia.

The mean shapes were built up from 332 training data sets, which were available in the form of IGES surface data. The surface data were obtained from CT scans by performing an automatic segmentation followed by manual cleaning steps (e.g. osteophyte removal). Subsequently, the IGES data were converted to triangle mesh data (STL-format). The mean shapes were computed as follows. First, a data set was selected randomly. Small gaps from the conversion procedure were closed and the surface was minimally smoothed employing a non-shrinkable smoothing filter [Taubin1995] available in the mesh processing software MeshLab (Visual Computing Lab ISTI-CNR). Then, this reference was rigidly aligned to each of the remaining data sets and fitted using the non-rigid ICP variant (N-ICP-A) of

[Amberg2007]. Due to this morphing step, point correspondences were established. That is, for each vertex point on the reference geometry, say, a point on the epicondyle, the spatial distribution was known. The mean location of each vertex point was computed and a mean shape obtained. To reduce the bias of the reference shape, the procedure was repeated twice, each time taking the hitherto estimated mean shape as the reference shape.

By morphing a mean shape to a particular target geometry, landmark points of the target can be determined on the fitted reference geometry by simply searching for the nearest vertex points. Doing this for the cruciate ligament attachments for all data sets, the distribution of the insertions on the original mean shape was obtained. Subsequently, a statistical mean was computed (annotated mean).

The annotated mean shape was again morphed to the target data sets and the deviations of the respective predicted insertion points from the measured insertion points were computed.

RESULTS AND DISCUSSION

The training data was successfully morphed to all 6 subjects in an automatic manner. As expected, the morphing algorithm used was able to fit the target geometries with virtually no distance error (the mean distance error was about 10^{-5} mm). The morphing results are presented in Table 1. The mean distance between the measured and morphed ligament attachments was highest for the ACL in the femur (4.26 ± 1.48 mm) and lowest for PCL in the tibia (1.63 ± 0.36 mm). The highest deviation was observed for femoral ACL for subject S01 with a value of 6.93 mm.

Subject	Femur		Tibia	
	ACL [mm]	PCL [mm]	ACL [mm]	PCL [mm]
S01	6,93	5,30	1,48	1,76
S02	4,16	1,24	3,64	1,14
S03	4,55	1,07	1,55	1,27
S04	2,65	1,57	3,59	1,94
S05	4,05	2,32	2,96	2,03
S06	3,25	2,74	2,82	1,63
Mean	4,26	2,37	2,67	1,63
SD	1,48	1,57	0,96	0,36

Table 1: Results

Comparing to the registration atlas based approach from Asceni et al. the mean deviations were in the same range, however, the maximum value in our study was lower (6.93 vs 11.3 mm). Pellikaan et al., who also used a morphing based approach, reported mean distances smaller than 15 mm for about 70% of the muscle attachment sites.

CONCLUSION

In this study, a morphing based approach was presented to predict origins and insertions of the knee ligaments on the basis of CT-data, exemplarily shown for the cruciate ligaments. The method is based on the assumption that especially the posterior condyle bone geometry is strongly correlated with the ligament attachment sites. It has been demonstrated, that the N-ICP-A is applicable to predict the attachments in automatic and robust fashion with high

accuracy. This might help to improve patient-specific biomechanical models and their integration in the clinical routine.

Limitations were the small number of datasets and the approximation of the attachments as single insertion points. Additionally, the ligament attachments were manually segmented by a single surgeon.

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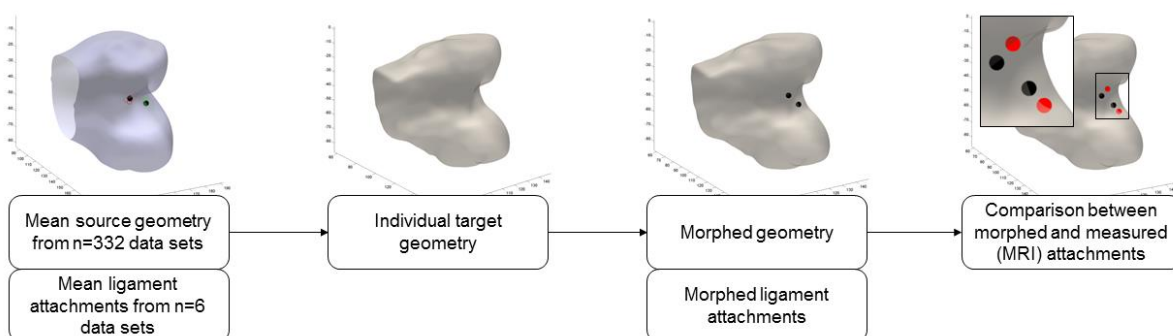


Fig 1: Workflow for validation (in the example of femur)