Genetic Algorithm and Custom Clustering for Discovering Unique Load Transfer Mechanisms in a Knee Joint Model

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Summary

This study proposed a method for discovering unique variants of a dynamic knee joint model with nearly the same outputs – i.e. displacements caused by external moments – but distinct load transfer mechanisms, while assuming parameter uncertainty. The method employed Genetic Algorithm to sample the variants and clustering to quantify the results. It was tested on a high-dimensional, multibody model of the knee in flexion-extension. The results showed that with minimal parameter modification the discovered variants of the knee differed by up to 250 N in ligament forces, while exhibiting nearly the same motion of the bones. This could potentially help explain the differences observed between the published models of the knee.

Introduction

The knee is one of the most complex joints in the body. Its models contain multiple uncertain parameters. This uncertainty can be addressed with many methods, such as Monte Carlo sampling. This study rephrases the problem into a search for unique model variants. The idea is to find variants of the knee model, which feature the same output – here: displacements under load – but with distinct load distributions between ligaments and contact pairs. Such an approach was tested for the ankle joint in [1], but only in angular displacements and statics. The current study extended this by including both linear and angular displacements, employing a dynamic knee model and custom two-step clustering.

Methods

The proposed method extended [1] and was based on Real-Coded Genetic Algorithm (RCGA) [2] and a two-step clustering procedure. The approach was tested on a dynamic knee model assumed after [3], which contained four nonlinear cables representing the ligaments and sphere-to-plane contact pairs connecting tibia and femur. The model was loaded with an external moment and solved in flexion-extension. RCGA was used to sample the variants of this model with bounds set to ±2.5 mm and ±10 % for geometric and other parameters, as in [4]. The custom objective function took into account the closeness of the variant to the original model [3] in terms of displacements under load and ensured that RCGA did not return copies of it. This was followed by a two-step clustering process to further quantify the results. The forces of the four ligaments and contact pairs were standardized and assumed to lie within a five-dimensional ball. Its max radius was computed and then lowered with a coefficient to obtain a threshold value. The model variants with force radius above the threshold represented the extreme configurations and were further quantified with DBSCAN [5].

Results and Discussion

The procedure obtained 106278 models, out of which 2907 had nearly the same displacements as the model [3], but distinct ligament and contact pair loads. The highest differences were seen for the Medial Collateral Ligament (MCL) with its maximal force ranging up to 250 N across the models and the original model [3] being as low as 0 N, see Fig. 1. The contact forces were the least affected.
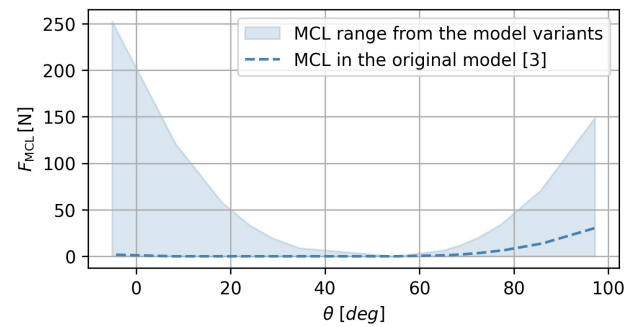

Figure 1: The MCL force in the sampled variants and the original model [3] in flexion extension under external moment load with regards to the knee joint angle θ.

The variants were further quantified with the clustering procedure. It revealed six load transfer mechanisms within the model. These configurations were mainly dictated by the MCL, which could assist other ligaments in different parts of the flexion-extension motion within these configurations.

Conclusions

The obtained results proved the effectiveness of the method in a high-dimensional knee model. Six load transfer mechanisms producing the same motion with ligament forces varying up to 250 N were obtained for the assumed model of the knee. The method could potentially help to explain the differences between the models published in literature.

References

[1] Vořechovský M and Ciszkiewicz A (2024). *J. Comput. Sci.*, **82**: 102425.
[2] Herrera F et al. (1998). *Artif. Intell. Rev.*, **12**: 265–319.
[3] Machado M et al. (2010). *Nonlinear Dyn.*, **60**: 459–478.
[4] Ciszkiewicz A and Dumas R (2024). *Front. Mech. Eng.*, **10**: 1392616.
[5] Schubert E et al. (2017). *ACM Trans. Database Syst.*, **42**: 19.