

DEVELOPMENT OF A HUMAN WHOLE-BODY MODEL TAKING INTO ACCOUNT THE CONNECTIVE TISSUE

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Introduction

Connective tissue is an essential component of multicellular animal life. Its main component collagen is one of the most important basic building blocks in our body. Connective tissue plays a significant role in spatial organization, stabilization and force transmission. Because almost all structures are interconnected by connective tissue, their stiffness is adapted depending on the requirements. Stiffness is determined by collagen types, proteoglycan content, and structure.

Computer simulations offer a way to analyze these complex structures in more detail. A frequently used method is the finite element method (FEM). Using FEM, the structures under investigation are decomposed into finite elements with specific properties. Geometries and spatial stiffness orientations are crucial for the accurate description of properties/materials. These geometries can be determined by imaging techniques and the stiffnesses can be determined by material samples in experimental setups. The determination of the stiffness orientation is challenging because it requires more resources (Sartori & Stark 2021).

The aim of this study is to build a human model considering the connective tissue to understand the interaction of elements/organs across a larger domain.

Material & Methods

We started from a FE model (trunk-model) that was created in a previous study and is based on the data from the Visible Human Project® (VHP) (Stark et al. 2016). That model contained the geometries for the bony elements, the intervertebral discs and the musculature, including their fiber architecture.

For the present study, we included data sets of a male and female body donor (σ :39 years, 90.26 kg, 1.88 m; φ :59 years, 88 kg, 1.71 m) from the VHP. Digital image processing was used to select and reconstruct collagen-containing structures (Fig. 1). In each case, the data sets consisted of digitized RGB color images of cryosections with a resolution of σ :0.144x0.144x1 mm and φ :0.144x0.144x0.33 mm.

In a second step, a FE-model of the connective tissue with a resolution of 1x1x1 mm hexahedrons was created based on these reconstructions. The material descriptions were taken from the previous model and anisotropies were included. The connective-tissue FE-model was afterwards integrated into the trunk-model. For the simulation, the hip was fixed, and a load was applied to the cervical vertebrae (C1). The FEBio and the Postview software tools from the Musculoskeletal

Research/Biomechanics Laboratories were used for the simulation and evaluation.

Figure and Tables

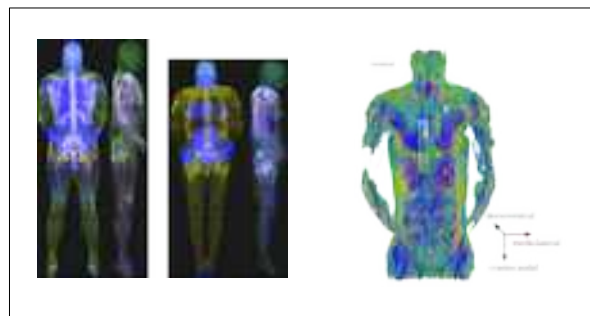


Figure 1: Color-coded visualization (red:far, green:middle, blue:near) of the connective tissue for the male (Left) and female (Middle). As well as, the reconstruction of the fiber architecture (Right).

Results & Discussion

The connective tissue could be reconstructed in detail across organs. Using methods from image processing we determined and analyzed the fiber directions. The data sets obtained in this way were used to expand existent models. Simulation tests are ongoing research. We expect to use our model to analyze e.g., the lateral force transmission between muscles and muscles to tissues. However, a detailed description is necessary for structures with a very high connective tissue content (e.g., knee).

Modelling connective tissue might be an important tool to understand cross-organ interactions.

References

1. Sartori, J., & Stark, H. (2021) Acta Biomaterialia, 120, 146–155.
2. Stark H, et al. (2016) In: Dienstbühl, I.; Stadler, M.; Scholle, H.-C. (eds.): Kongressband 22. Erfurter Tage. S. 227-234. Verlag Bussert & Stadelers.

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