TOWARDS INDIVIDUALIZED BIOMECHANICAL MODELS IN MULTIPLE DOMAINS

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Introduction

Musculoskeletal simulations enable the non-invasive computation of biomechanical parameters like muscle forces or joint torques from experimental data, e.g., optical motion capture and force plate data [1]. Error sources like kinematic errors (e.g. soft-tissue artifacts), modelling assumptions or inaccurate model parameters lead to less accurate and reliable calculations. Model individualization methods may be applied to minimize the dynamic error caused by modeling errors, subsequently leading to more accurate calculations [2]. Commonly, musculoskeletal models are scaled using marker point clouds [3]. However, marker-based scaling methods cannot be applied when motion capture methods are used that are not based on optoelectronic marker-tracking (e.g. IMU- or depth camera-based). Therefore, our goal is to create a simple, holistic individualization process independent of the motion capture technique used. Our individualization method comprises multiple domains (muscle strength, mobility and anthropometry) in order to achieve a model that is as representative of the person as possible. This method minimizes the model-person inconsistency and its negative effect on computed biomechanical parameters.

Methods

We are investigating the individualization of musculoskeletal models in multiple domains using a combination of manual measurements and population data [4]. Individualization of the skeletal system (segment lengths) is achieved by measuring specific individual segment lengths using simple tools (e.g. tape or calliper). Individualization of muscle parameters (e.g. optimal fiber length, muscle activation/ deactivation times, force-length - or force-velocity properties) is to be achieved by extending the population data-based strength mapping algorithm (SMA) presented in [4]. The SMA adjusts isometric muscle strength of every muscle of a model based on metadata like biological sex, age, body height and a strength percentile. The model can also be individualized further by adjusting joint rotation axes and centers. This is accomplished by computing the instantaneous center or axis of rotation of a joint using multibody kinematics.

Results

We measured motion capture data and segment lengths for one participant. Both a segment length-based (a) and a marker-based approach (b) were used to scale a generic musculoskeletal model. Exemplarily, functional height measurement (reaching ranges to the front and upwards), the body height and the inseam height were used to compare the resulting models of the two scaling methods. Figure 1 depicts the scaled models and the investigated dimensions. The body and corresponding model dimension values are listed in table 1.

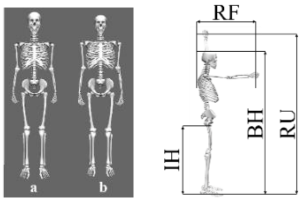

Figure 1: Scaled models (left) and investigated body dimensions (right)

Dimension	Person	Marker -based	Seg. Len-based
Body height (BH)	185	183	184
Inseam height (IH)	87	84	87
Range front (RF)	76	72	73
Range up (RU)	212	213	214

Table 1: Excerpt of compared body and functional dimensions [cm]

Discussion

Our results indicate that segment-length based scaling provides similar results to conventional marker-based scaling results, while both correspond well to manually measured body and functional dimensions. We will further corroborate these indications by means of a laboratory movement study in conjunction with musculoskeletal simulations. Comparison of calculated results to real world data from the measurements should provide insights into the impact of joint axis individualization on the results. At a later stage we aim to investigate which musculoskeletal parameters need to be individualized in addition to the maximum isometric muscle forces.

References

1. Seth et al, Computational Biol, 14(7), 2018.
2. Lund et al, Internat Biomech, 2:1-11, 2015.
3. Delp et al, IEEE Trans Biomed Eng, 54: 1940-1950, 2007.
4. Miehling, Comput Methods Biomech Biomed Engin, 22(15):1209-1218, 2019.

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