# SIMULATION OF THE HIP MUSCLES KINEMATICS DURING GAIT USING HIGHLY DISCRETISED ANATOMICAL MODELS

Luca Modenese (1), Arnault Caillet (1), Clement Favier (1), Andrew Phillips (1), Josef Kohout (2)

1. Imperial College London, UK; 2. University of West Bohemia, Czech Republic

#### Introduction

The use of medical images for personalising computational models of the lower limbs is becoming a feasible approach in applications requiring accurate anatomical representations of the musculoskeletal (MSK) system, e.g. prediction of surgery outcome. Semi-automated procedures have been proposed for creating personalised MSK models, however the definition of the muscular anatomy (attachments and lines of action) has mostly relied on manual registration of existing models based on bone morphology, e.g. [1]. In this work we propose a fully automated technique for generating muscle lines of action (also called "fibres" in the following) from muscle geometries obtained from *in vivo* datasets and we apply it to a kinematic simulation of walking.

#### **Material and Methods**

Magnetic resonance imaging (MRI) scans (3D T1weighted VIBE, field of view: 450x450 mm, pixel size: 1.41x1.41 mm, slice thickness and increment: 1 mm) were collected for the lower limbs of a healthy volunteer (male, 37 years old, 180 cm, 87 kg), followed by a standard gait analysis in the MSKLab at Charing Cross Hospital, London, UK. The MRI scans were segmented using ITK-Snap and the bone geometries of the right leg used to create a model in OpenSim 4.0 format [2] using NMSBuilder [3] (hip joint: 3 DoF, knee and ankle joints: 1 DoF). An experimental trial was then processed with the OpenSim inverse kinematics tool to compute the joint angles for a gait cycle. The muscle geometries of the right gluteus maximus, gluteus medius and iliacus were also segmented (Figure 1A) and the quality of their triangular meshes improved in MeshLab using standard filters. Muscle attachment areas from a cadaveric dataset (female, 81 years old, 167 cm, 63 kg) [4] were then mapped on the participant's bone geometries through a non-rigid registration [5] (Figure 1B) and used as the input of a custom OpenSim plugin together with the muscle geometries and the gait kinematics. The plugin decomposed the muscle triangular meshes in 100 fibres, each consisting of 15 straight-line-segments, by mapping onto them a volumetric template of parallel fibres, similarly to [6]. The muscles' lines of action were updated at each kinematic frame using weight functions that modified the position of each fibre point based on that of the attachment bones (Figure 1C). Finally, the total length of the fibres was calculated at each frame.

# Results

The lines of action of the considered muscles were successfully generated through the automated

workflow. The fibre decomposition was almost instantaneous (<20 ms), while the gait simulation took less than 4 s on a standard Z640 Dell Workstation. The fibre lengths across the gait cycle were on average  $15.2\pm1.5$  cm for gluteus medius (range: 10.6-19.1 cm),  $20.7\pm5.2$  cm for gluteus maximus (range: 11.8-34.1 cm) and  $20.8\pm2.6$  cm for iliacus (range: 16.1-27.9 cm).

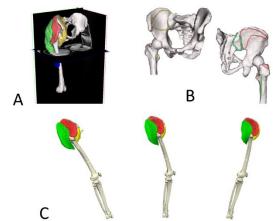


Figure 1: (A) Bone and muscle geometries segmented from the MRI images, (B) Muscle attachment areas mapped on the participant's bones, (C) frames from the walking simulation using highly discretized muscles.

## **Discussion and Conclusions**

The proposed approach was previously validated [7] for simple hip joint movements against literature data [6] using a cadaveric dataset [4] but there was no evidence of its applicability *in vivo*, so making this study necessary. The developed plugin is a promising modeling tool allowing to customise the number of generated muscle fibres while maintaining the low computation times of standard MSK models. Ongoing processing will extend the current results to muscle moment arms and other muscles of the lower limb.

## References

- 1. Modenese et al, J Biomech, 73:108-118, 2018.
- 2. Seth et al, PLoS Comp Biol, e1006223, 2018.
- 3. Valente et al, Comp Meth Progr Biom, 152:85-92, 2017.
- 4. Viceconti et al, J Phys Sc, 58:441-446, 2008.
- 5. Audenaert et al, CMBBE, 22:6444-657, 2019.
- 6. Blemker et al, Ann Biomed Eng, 33:661-673, 2005.
- 7. Modenese et al, Abstract ISB/ASB Conf, 2019.

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