

Modelling Skeletal Muscles: A multi-physics challenge

O. Röhrle¹,

¹Cluster of Excellence for Simulation Technology/Institute of Applied Mechanics, University of Stuttgart, roehrle@simtech.uni-stuttgart.de

The simplest tasks in our daily life require a controlled coordination of multiple muscles within a system, i.e., our entire musculoskeletal system. Before we, however, can begin to study, understand, or analyse, the coordination of parts of the musculoskeletal system, we first need a better understanding of the function and structure of a single skeletal muscle. Despite many decades of dedicated experimental research, there still exist only a "basic" understanding of how the underlying complex mechanisms interact to generate well-controlled forces. One of the biggest challenges hereby is to determine the mechanism behind skeletal muscle recruitment, e.g. how can we deduce from experimental electromyographic (EMG) recordings on the skin surface recruitment strategies. The link between EMG and recruitment would probably also provide us with the essential understanding to distinguish between normal and pathological recruitment.

Like for most biological tissue or complex mechanism, simulations can provide us with a deeper understanding of the complex interplay between function and structure. To do so, one needs to consider different scales and different physical systems/modelling approaches. For skeletal muscles, one requires detailed geometrical models, e.g. the arrangement of fibres, fascicles, and aponeurosis, and detailed biophysical models describing the neurons and the smallest force-producing units on the fibre level, i.e., the sarcomeres. Further, the model needs to link cellular processes of force generation to force-transmission within the muscles (and its influence on the musculoskeletal system). At the same time, one needs to consider receptors and sensors providing (mechanical) feedback to the biophysical (recruitment) models as well as the overall electrical signal propagation within muscles to determine the electrical potential on the skin surface.

Within this talk, a detailed electrochemomechanical skeletal muscle model describing most of the above mentioned physics is presented (cf. [1]). The biophysical processes on the cellular level are mathematically described by a large system of nonlinear ODEs. The action potential propagation within the tissue, e.g. along a particular fibre or within the muscle, is modelled using a reaction-diffusion equation. To determine the overall force generation of an entire skeletal muscle, homogenised cellular state variables are used within a continuum-mechanical constitutive law. All the physical models are solved using the open-source software library OpenCMISS [2].

Furthermore, we will discuss the modelling and simulation challenges leading to future work. For example, the large number of material parameters and the high degree in geometrical details, which should be considered for realistic simulations, provide inherent uncertainties. To better quantify the uncertainties, efficient, ideally real-time simulations are necessary. Furthermore, as the spatial distribution of functional groups of fibres, which are recruited simultaneously, cannot currently be determined using image-based methods *in vivo*, inverse or optimisation problems might be useful to improve the analysis of EMG results. Furthermore, the large number of fibres within muscles (often much greater than 100.000) requires efficient HPC solution strategies.

References

- [1] T. Heidlauf, O. Röhrle *Modeling the Chemoelectromechanical Behavior of Skeletal Muscle Using the Parallel Open-Source Software Library OpenCMISS*. Computational and mathematical methods in medicine, 2013.
- [2] C. Bradley, A. Bowery, R. Britten, V. Budelmann, O. Camara, R. Christie, A. Cookson, A. Frangi, T.B. Gamage, T. Heidlauf, S. Krittian, D. Ladd, C. Little, K. Mithraratne, M. Nash, D. Nickerson, P. Nielsen, Ø. Nordbø, S. Omholt, A. Pashaei, D. Paterson, V. Rajagopal, A. Reeve, O. Röhrle, S. Safaei, R. Sebastian, M. Steghöfer, T. Wu, T. Yu, H. Zhang, and P. Hunter *OpenCMISS: A multi-physics & multi-scale computational infrastructure for the VPH/Physiome project*, Progress in Biophysics and Molecular Biology, 107 (2011), p. 32–47, DOI 10.1016/j.pbiomolbio.2011.06.015.