

BP 17: Posters - Coupled Problems in Biological Systems: Model Identification, Analysis and Predictions

Time: Monday 17:30–19:30

Location: Poster C

BP 17.1 Mon 17:30 Poster C

Biological cybernetics in human motor control: from single-joint to multi-joint movements — ●ALEXANDRA BAYER^{1,2}, DANIEL HÄUFLER^{1,2}, MICHAEL GÜNTHER¹, and SYN SCHMITT^{1,2} — ¹Institut für Sport- und Bewegungswissenschaft, Universität Stuttgart, Germany — ²Stuttgart Research Centre for Simulation Technology, Universität Stuttgart, Germany

An open question in motor control is how different and complex movements are planned, controlled and organised in the human body. To investigate this question, biophysical modelling provides a framework to understand human motor control. For this method, physiologically motivated and experimentally validated models are required to predict the dynamic interplay of the neural controller with the musculoskeletal biophysics. Numerous model representations with different levels of detail already exist in literature. Therefore, the main goal of our cybernetic approach was to identify the basic biomechanical and biochemical properties of the neuro-musculoskeletal system for single-joint movements. Using a simple model to perform fast goal-directed arm movements, it was found that in addition to the parameterisation of the force-length curve, the movement velocity strongly depends on the model representing the activation dynamics. Based on these findings, it was possible to construct an overall human model applicable for investigations of complex multi-joint movements. Finally, such a multi-body model was used, for example, to investigate internal loads

in human spine during simple movements like sitting down in a seat or during whole-body vibrations.

BP 17.2 Mon 17:30 Poster C

Normalization of Western blot data affects the statistics of estimators — CATERINA THOMASETH and ●NICOLE RADDE — Institute for Systems Theory and Automatic Control, University of Stuttgart, Stuttgart, Germany

Western blotting is a technique for the quantification of proteins, which has made a transition from a purely qualitative to a semi-quantitative method in the last decade. Western blot data are nowadays also frequently used to enrich parameter estimation for models of intracellular processes. This task, however, poses several challenges.

In this work we elaborate on the normalization of data from Western blot experiments and its impact on parameter estimation. Preprocessing of Western blot data includes a two step normalization procedure, in which the raw signals are normalized to a loading control and to a reference condition. If the signals themselves are normally distributed, the normalized data are described by ratios of normal distributions, which have some peculiarities that can complicate further analysis. We recapitulate some properties of these ratio distributions and conditions for various approximations that facilitate further analysis. We illustrate results on a case study in which Western blot data are used to infer the fold change in a knockdown experiment.