

### **University of Stuttgart**

### Introduction

- Detailed simulation of electromyography (EMG) and muscle contraction is a challenging task
- 10<sup>2</sup> fascicles per muscle x 10<sup>3</sup> fibers per fascicle x 10<sup>4</sup> sarcomers per fiber
- → Inherent multi-scale and multi-physics problem
- $\rightarrow$  Requires high-performance computing

## **Multi-scale Model**



- $\rightarrow$  Muscle modeled via a transverse isotropic Mooney-Rivlin material<sup>3</sup>
- $\rightarrow$  Implemented in open-source software OpenDiHu (<u>"Dig</u>ital <u>Hu</u>man")<sup>1</sup>
- $\rightarrow$  Linear Algebra relies on the PETSc library<sup>5</sup>





# **Bridging Scales with Volume Coupling** — **Scalable Simulations of Muscle Contraction and Electromyography**

Benjamin Maier<sup>†</sup>, David Schneider<sup>†</sup>, Miriam Schulte<sup>†</sup>, and Benjamin Uekermann<sup>†</sup> <sup>†</sup>Institute for Parallel and Distributed Systems (IPVS), University of Stuttgart

# **Computational Approach**

- Mixed *u-v-p* finite element method for solid mechanics • Linear single-field finite elements for 3D EMG model
- Different requirements:
- $\rightarrow$  Finely resolved EMG model vs coarse solid mechanics → Independent partitioning of the 3D models within one
- solver not possible
- $\rightarrow$  Trade-off: limited degree of parallelism (at least one cell per core) vs. refining the solid mechanics? • Idea: use two solvers and introduce volume coupling via
- preCICE<sup>2</sup>



Performance







- → Run on Hawk at HLRS **References**
- $\rightarrow$  270 x 10<sup>3</sup> fibers realistic for biceps brachii
- $\rightarrow$  Runtime dominated by 0D sarcomere model
- $\rightarrow$  Conditioning of the 3D model deteriorates with problem size (more CG iterations)

- Weak scaling of the coupled multi-scale model
- $\rightarrow$  Additional cost of volumetric mapping 2 102 with preCICE negligible
- $\rightarrow$  Mechanics solver runs in serial

### Results

- Computations performed on 64 nodes (HLRS Hawk) • Electrophysiology model consists of 625 fibers and
- 51,915,625 DOFs

- Trans-membran voltage<sup>4</sup> (left), EMG signal the domain with the contraction (right)



Computational Physics, 2021.

Advances in Fluid-Structure Interaction.

5(498):1-14, 2014.

Zampini S., Zhang H., Zhang H. PETSc Web page. http://www.mcs.anl.gov/petsc, 2018.







• Coarse mechanic model consists only of 1,395 DOFs • Simulating a timespan of 190ms took around 8h 27min extracellular potential (middle), and the reference



- [1] Maier, B., Göddeke, D., Huber, F., Klotz, T., Röhrle, O., Schulte, M., OpenDiHu Efficient and Scalable Software for Biophysical Simulations of the Neuromuscular System (under review), Journal of
- [2] Bungartz H.-J., Lindner F., Gatzhammer B., Mehl M., Scheufele K., Shukaev A., Uekermann B., preCICE - a fully parallel library for multi-physics surface coupling. Computers & Fluids, 141:250–258, 2016.
- [3] Heidlauf T., Röhrle O., A multiscale chemo-electro-mechanical skeletal muscle model to analyze muscle contraction and force generation for different muscle fiber arrangements. Frontiers in Physiology,
- [4] Shorten P. R., O'Callaghan P., Davidson J. B., and. Soboleva T. K., A mathematical model of fatigue in skeletal muscle force contraction. Journal of Muscle Research and Cell Motility, 28(6), 2007. [5] Balay S., Abhyankar S., Adams M., Brown J., Brune P., Buschelman K., Dalcin L., Dener A., Eijkhout V., Gropp W., Kaushik D., Knepley M., May D., McInnes L., Mills R., Munson T., Rupp ., Sanan P., Smith B.,

