

# Highly Parallel Simulation of the Neuro-Muscular System

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## ABSTRACT

The neuro-muscular system allows humans to perform a wide range of tasks. A skeletal muscle with its adaptable neural recruitment process and large number of muscle fibers is capable of performing fine, coordinated movements for example for gripping a small needle up to powerful or enduring actions such as lifting weights or running a long distance. Due to the difficulty of observing internal quantities in in-vivo experiments, simulation plays an important role. What can be measured on a real subject is the electric potential over time, which is called electromyography (EMG). This can be done either on the surface or intra-muscular by using needle electrodes. A simulation of the muscle activation process can help to understand measured behaviour.

So far, existing simulations of muscle activation and EMG are limited by a lower than realistic number of muscle fibers or they use approximate formulations without explicitly resolving fibers. They often do not make use of parallel execution or only run on a small number of compute nodes.

We simulate propagation of action potentials on a biceps brachii muscle and the generated intra-muscular EMG signal using a detailed, multi-scale model [3] with a realistic number of muscle fibers on a supercomputer. The model comprises three coupled differential equations in 0D, 1D and 3D. The propagation of action potentials along muscle fibers (1D) is described by the Monodomain partial differential equation with a Hodgkin-Huxley-type reaction term (0D) [2]. It is coupled to systems of ordinary differential equations (ODEs), which describe subcellular ionic processes [3]. All moving action potentials together contribute to the EMG which is described by a static 3D Bidomain model [4].

The contribution of this paper is to simulate the accurately resolved neuro-muscular system with a high spatial resolution and a realistic number of 270.000 muscle fibers for the biceps. We tackle the resulting high computational effort by optimized code and high performance computing, using *Hazel Hen*, the supercomputer in Stuttgart, Germany. We present good parallel scalability results of the simulation on 27.000 cores. We evaluate strategies of placing MPI processes on hardware cores.

Furthermore, we present *opendihu*, our open-source, computational software framework to run efficient and highly parallel simulations of the neuro-muscular system. The flexible framework allows to plug in subcellular models through the CellML standard [5], uses modern C++ based template-metaprogramming with parallel I/O and optimized data structures for instruction-level parallelism and gives convenient configuration possibilities by a python interface. Compared to previously used simulation software we achieve a speedup by a factor of 38.

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