



Virginia Commonwealth University
VCU Scholars Compass

Biology and Medicine Through Mathematics
Conference

Parallel-in-time simulation of biofluids

Weifan Liu
Syracuse University, wliu07@syr.edu

Minghao Rostami
Syracuse University, mwrostam@syr.edu

Follow this and additional works at: <https://scholarscompass.vcu.edu/bamm>



Part of the [Life Sciences Commons](#), and the [Numerical Analysis and Computation Commons](#)

<https://scholarscompass.vcu.edu/bamm/2020/talk/28>

This Event is brought to you for free and open access by the Dept. of Mathematics and Applied Mathematics at VCU Scholars Compass. It has been accepted for inclusion in Biology and Medicine Through Mathematics Conference by an authorized administrator of VCU Scholars Compass. For more information, please contact libcompass@vcu.edu.

Parallel-in-time simulation of biofluids

Solving for the long-time collective dynamics of micro-structures such as bacteria, sperm and cilia is computationally expensive. In this study, we aim to accelerate the simulation of dynamic micro-structures immersed in a three-dimensional, viscous fluid using Parareal, a parallel-in-time method that decomposes time domain into subintervals and alternate between a fine and a coarse solver iteratively to converge to the solution. Specifically, we model micro-structures using Kirchhoff rods that can bend, twist and translate in the fluid governed by Stokes equation. A Parareal algorithm based on the Method of Regularized Stokeslet (MRS) is applied to solve the equations of fluid-structure interaction. The coarse solver employed uses both a reduced spatial and temporal resolution. Results on the reduction of runtime in simulating the long-time collective swimming of a group of interacting rods are presented to demonstrate the efficiency of the algorithm. We show that when the same number of cores are used, it can be considerably more efficient than the more conventional spatial parallelization.