

Contribution ID: 101

Type: Oral Presentation

Fast algorithms for the dense matrices arising from the Method of Regularized Stokeslets

Monday, 9 July 2018 16:00 (30 minutes)

The swimming motion of microorganisms such as sperm and cilia can be modelled by several methods, all of which entail solving equations of fluid-structure interaction. Among them, the Method of Regularized Stokeslets (MRS) and the Rotne-Prager-Yamakawa tensor have the advantage of not requiring a 3D Eulerian grid and using the fundamental solutions to the underlying equations instead. However, the computations required by both methods entail the use of dense matrices, and they tend to be large and very costly to work with for practical models in which the number of micro-swimmers is large.

The 'data-sparse' structure of these matrices enables the development of fast algorithms. To compute the matrix-vector products efficiently, we extend the Kernel-Independent Fast Multipole Method (KIFMM) to the kernels associated with the MRS. To solve linear systems with the same matrices efficiently, we consider both a data-sparsener preconditioner and a block-diagonal preconditioner; to expedite the application of the preconditioners, we employ a number of techniques such as Krylov subspace recycling. We apply the proposed algorithms to study the dynamics of a large group of sperm and the flow field induced by a carpet of cilia.

Primary author: ROSTAMI, Minghao (Syracuse University)

Co-author: Prof. OLSON, Sarah (Worcester Polytechnic Institute)

Presenter: ROSTAMI, Minghao (Syracuse University)

Session Classification: From solitary swimmers to coordinated groups: Modelling motion in fluids at very low Reynolds number

Track Classification: Minisymposium: From solitary swimmers to coordinated groups: modelling motion in fluids at very low Reynolds number