

Abstract Submitted
for the DFD20 Meeting of
The American Physical Society

A computational platform for biomechanics problems in the cell
GOKBERK KABACAOGLU, MICHAEL SHELLEY, Simons Foundation Flatiron
Institute — Polymer filament and motor-protein assemblies are major structural
components of biological cells. Filaments' nonlinear deformation and hydrodynamic
interactions with the other immersed structures lead to complicated flows that have
important mechanical and transport properties. I will review our computational
platform for the large-scale three-dimensional simulations of flexible filaments, motor
proteins and rigid bodies in a Stokesian fluid. We use non-local slender body theory
for the fluid-structure interactions of the filaments and a second-kind boundary
integral formulation for rigid bodies and the confining boundary. We also incorporate
the key biophysical elements such as the filaments' (de)polymerization kinetics and
motor proteins. I will discuss recent applications of this platform: the orientation
and positioning of the mitotic spindle (the organelle that orchestrates the division
of chromosomes); swirling flows induced by the interaction of motor proteins and
thousands of microtubules attached to a cortex, as observed in early development of
the *Drosophila* oocyte; and the dynamics of microtubule arrays in large cells driven
by streaming flows created by moving motor-proteins, as has been proposed as the
basis for centering of spindles in large embryos.

Gokberk Kabacaoglu
Simons Foundation Flatiron Institute

Date submitted: 23 Nov 2020

Electronic form version 1.4