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Cytoplasmic flows as signatures for the mechanics of mitotic spindle positioning EHSSAN NAZOCKDAST, ABTIN RAHIMIAN, Courant Institute, NYU, DANIEL NEEDLEMAN, Harvard School of Engineering and Applied Sciences, MICHAEL SHELLEY, Courant Institute, NYU — The proper positioning of the mitotic spindle is crucial for asymmetric cell division and generating cell diversity during development. We use dynamic simulations to study the cytoplasmic flows generated by three possible active forcing mechanisms involved in positioning of the mitotic spindle in the first cell division of C.elegans embryo namely cortical pulling, cortical pushing, and cytoplasmic pulling mechanisms. The numerical platform we have developed for simulating cytoskeletal assemblies is the first to incorporate the interactions between the fibers and other intracellular bodies with the cytoplasmic fluid, while also accounting for their polymerization, and interactions with motor proteins. The hydrodynamic interactions are computed using boundary integral methods in Stokes flow coupled with highly efficient fast summation techniques that reduce the computational cost to scale linearly with the number of fibers and other bodies. We show that although all three force transduction mechanisms predict proper positioning and orientation of the mitotic spindle, each model produces a different signature in its induced cytoplasmic flow and MT conformation. We suggest that cytoplasmic flows and MT conformation can be used to differentiate between these mechanisms.

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