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Hydrodynamics of pronuclear migration EHSSAN NAZOCKDAST, Courant Institute, NYU, DANIEL NEEDLEMAN, Harvard School of Engineering and Applied Sciences, MICHAEL SHELLEY, Courant Institute, NYU — Microtubule (MT) filaments play a key role in many processes involved in cell devision including spindle formation, chromosome segregation, and pronuclear positioning. We present a direct numerical technique to simulate MT dynamics in such processes. Our method includes hydrodynamically mediated interactions between MTs and other cytoskeletal objects, using singularity methods for Stokes flow. Longranged many-body hydrodynamic interactions are computed using a highly efficient and scalable fast multipole method, enabling the simulation of thousands of MTs. Our simulation method also takes into account the flexibility of MTs using Euler-Bernoulli beam theory as well as their dynamic instability. Using this technique, we simulate pronuclear migration in single-celled Caenorhabditis elegans embryos. Two different positioning mechanisms, based on the interactions of MTs with the motor proteins and the cell cortex, are explored: cytoplasmic pulling and cortical pushing. We find that although the pronuclear complex migrates towards the center of the cell in both models, the generated cytoplasmic flows are fundamentally different. This suggest that cytoplasmic flow visualization during pronuclear migration can be utilized to differentiate between the two mechanisms.

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