

Abstract Submitted  
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**An integrated model of microtubule-based pronuclear motion in the single-celled *C. elegans* embryo** TAMAR SHINAR, MICHAEL SHELLEY, Courant Institute, NYU — We present an integrated computational model of microtubule-based pronuclear motion in the single-celled *C. elegans* embryo. In this model, centrosomes initiate stochastic microtubule growth and these microtubules interact with motor proteins distributed in the cytoplasm. Consequent pulling forces drag the pronucleus through the cytoplasm, here modeled as an incompressible, Newtonian fluid whose motions are constrained by contact with the cell periphery. The cell periphery also limits microtubule growth. Our computational method is based on an immersed boundary formulation which allows for the simultaneous treatment of fluid flow and the dynamics of structures immersed within. Our simulations show pronuclear migration, and moreover, a geometry-dependent pronuclear centration and rotation very similar to that observed *in vivo*. We study the dynamic interaction of motor proteins embedded in the fluid with microtubule filaments, allowing for relative motion of fluid along MT tracks as has been observed experimentally. We demonstrate numerically that this is sufficient to propel the pronucleus while causing a counterflow of the cytoplasm.

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