In budding yeast, we model stochastic microtubule dynamics and their regulation in 2D- and 3D geometries created with COMSOL. Our C++ simulation engine improves on state-of-the-art in performance. Its results can be used for virtual microscopy and experimental design.

We tested our C++ Next Subvolume Method (NSM) solver against the state-of-the-art C solver URDME on the well-known MinD model from E. coli:

We achieved a 2-fold performance increase:

\[ \text{C++ Next Subvolume Method (NSM)} \]

\[ \text{URDME} \]

\[ \text{Time to integrate 10000 timesteps on 1000 voxels} \]

\[ \text{4.5 ms} \]

\[ \text{194 ms} \]

\[ \text{4.5 μm} \]

\[ \text{E. coli Mesh} \]

\[ \text{Model Schematic} \]

\[ \text{in vivo, we often image at the resolution limit, where distinguishing hypotheses may not be trivial.} \]

\[ \text{To accurately simulate a fluorescence microscopy experiment in silico, our collaborators and us developed a method to enable physically-based microscopy of our simulation results:} \]

\[ \text{5 μm} \]

\[ \text{GFP-MinD Timelapse} \]

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