Abstract Submitted
for the MAR07 Meeting of
The American Physical Society

Particle-based model of Min-protein oscillations in *Escherichia coli*
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— In *Escherichia coli* cells, the Min proteins, which are required for division site selection, oscillate from pole to pole via a Turing instability. During these oscillations, two of the Min proteins, MinD and MinE self-associate and co- associate on the bacterial inner membrane forming dynamic structures including a ring of MinE protein, compact polar zones of MinD, and zebra stripes in filamentous cells. Such rich behavior in a system with so few species has made the Min proteins a model system for applying computational methods to study intracellular dynamics in bacteria. Though mean-field computational models successfully reproduce the coarse-grained oscillatory dynamics in both rod-shaped and round *E. coli* cells and also predict that the Min-proteins actively detect cell shape, the mean-field models cannot address questions raised by the recent finding that MinD forms a small number of large polymers on the membrane. First, it is unclear how the intrinsic dynamics of polymer formation, namely polymer nucleation and growth, affect the pole-to-pole oscillations. Second, it is not understood how the oscillations influence the morphology of the MinD polymers. To study this coupling between MinD polymerization and pole-to-pole oscillation, we employ a particle-based computational model. In this talk, we will describe this model, which produces both large polymers and pole-to-pole oscillations.

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Date submitted: 14 Nov 2006 Electronic form version 1.4