

Abstract Submitted
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Robustness of MinD oscillation in *E. coli* with diverse cell shapes

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The dynamics of the Min-protein system help *Escherichia coli* regulate the process of cell division by identifying the center of the cell. We model the Min-protein reaction cycle, using a set of reaction-diffusion differential equations, in bacteria that have been forced into unusual flattened shapes as have recently been experimentally observed. We find that a regular two pole oscillation pattern is robust and exhibited in a large variety of cell shapes and sizes. Stability analysis of an infinite slab with our cell thickness yields a characteristic distance at which solutions become unstable, and this distance can be seen to correspond to a cell length below which protein movement dampens out within the cell. We also see evidence of the emergence of more complicated oscillation patterns when the lengthwise direction is well above this characteristic distance and the width is just above.

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