Summer 2016 - NSERC USRA
Dynamics of the Min Protein System

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1 Introduction

During cell division in *Escherichia coli* cells, the protein ftsZ forms a Z-ring at the center of the cell [1]. The Z-ring then constricts to cleave the cell into two daughter cells of equal size. The Min protein system consisting of MinC, MinD, and MinE is responsible for ensuring that the Z-ring forms at the cell's midpoint. *In vivo*, the Min proteins alternate between the cell poles. Previous research has shown that in short *E. coli* cells this switching is stochastic and that in longer cells the switching becomes regular oscillations, as shown in Figure 1 [2]. These Min proteins have been observed to form planar surface waves on a flat membrane in vitro [3]. Several models have been proposed to describe the reactions between the Min proteins and the cell membrane [4, 5, 6].

2 Methods

I set out to analyze some of the proposed models to verify that they matched experimental observations. Firstly, I used the Crank-Nicolson method to

Figure 1: Kymograph for MinD in a growing *E. coli* cell from Fischer-Friedrich *et al.* [2] Stochastic exchange turned into regular oscillations at a length of 2.8 μm (green arrow).

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numerically solve a system of partial differential equations (PDEs) that described the biochemical reactions. Secondly, I performed simulations using a particle based stochastic model.

2.1   Numerical solutions to PDEs in Octave

GNU Octave is a high-level interpreted language, primarily intended for numerical computations. It provides capabilities for computing the numerical solution of linear and nonlinear problems, and for performing other numerical experiments.

2.2   Stochastic simulations in Smoldyn

Smoldyn is a computer program for cell-scale biochemical simulations. It simulates each molecule of interest individually to capture the natural stochasticity and to yield nanometer-scale spatial resolution. Simulated molecules diffuse, react, are confined by surfaces, and bind to membranes much as they would in a real biological system.

3   Results

Previous work published by Bonny *et al.* [4] was reproduced to ensure that the Octave code was calibrated correctly. Solving the deterministic dynamic equations for the *in vitro* geometry produced spiral surface waves as expected, see Figure 2.

The deterministic dynamic equations were solved in cell-sized domains. In a cell of length $2 \, \mu m$, the MinD switched to one side and stayed there indefinitely. In a cell of length $3 \, \mu m$, the MinD underwent pole-to-pole oscillations with a period of approximately 50 seconds. In a cell of length $6 \, \mu m$, the MinD exhibited travelling waves from one side of the cell to the other.

Simulations in cell-sized domains were performed using a particle based stochastic model. In cells of length 2 and $3 \, \mu m$, the MinD underwent pole-to-pole oscillations with a period of 20 and 15 seconds respectively. In a cell of length $6 \, \mu m$, the MinD exhibited travelling waves from one side of the cell to the other. See Figure 3 for kymographs of MinD.
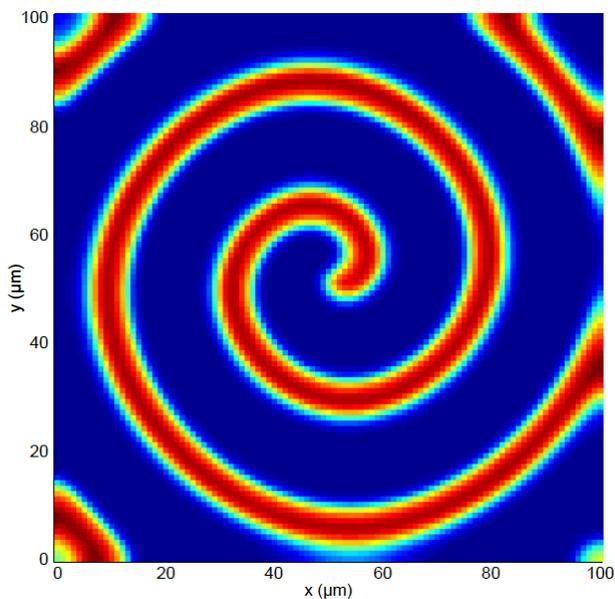
Figure 2: Solutions to the deterministic dynamic equations in the *in vitro* geometry in Bonny *et al.* [4] using the Crank-Nicolson method with a 2D membrane and a 2D bulk. The total MinD concentration is $4.8 \times 10^{-2}\,\mu\mathrm{m}^{-3}$ and the total MinE concentration is $7.0 \times 10^{-2}\,\mu\mathrm{m}^{-3}$. In this and subsequent plots, high MinD is coloured in red while low MinD concentration is blue.

4   Further Research

Further research could focus on analyzing other proposed models for the Min protein system as well as simulating reactions in a 3D cell-shaped environment.
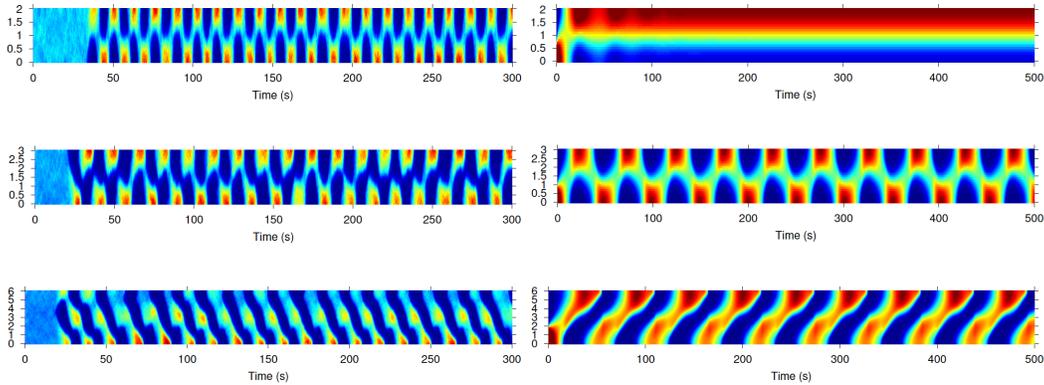
5   Acknowledgements

Figure 3: Kymographs for MinD concentration in cells of length 2, 3, and 6 μm. Smoldyn simulations on the left and numerical solutions to PDEs on the right.

References

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