

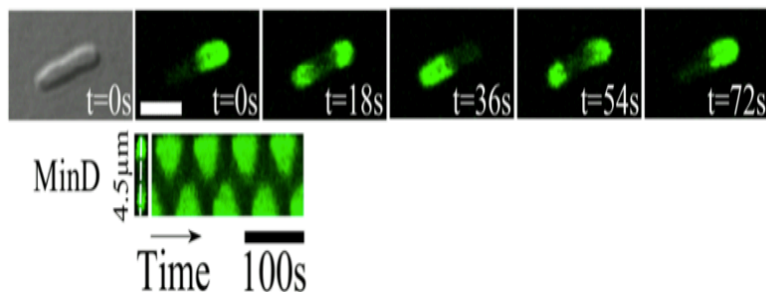
Simulations of Min Proteins

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This summer I had the pleasure of working with Professor Eric Cytrynbaum in a project involving simulations of Min protein behaviour in *E. Coli* bacteria. Min proteins are involved in the *E. Coli* cell division cycle. In the cycle, the cells replicate their genetic material and other cellular components, and must have the contents properly separated spatially to ensure the survival of both daughter cells. To do this, there needs to be proper localization of proteins that are involved in the equal division of the cell. In *E. Coli*, this is accomplished mainly by a group of proteins called Min proteins (C, D, E) and a FitZ ring. The Min proteins are unevenly distributed throughout the cell and oscillate from pole to pole in the cell. Min C and D proteins accumulate at a pole, where Min E forms a ring at the boundary of the Min D. As the Min E ring travels towards the pole, the Min C and D proteins start accumulating at the opposite pole. Min C and D are believed to prevent formation of the FitZ ring at the poles, localizing the FitZ ring to the middle of the cell where Min C and D are not present in high concentration [1].

There are different types of Min protein behaviour observed in *E. Coli* cells, including pole-to-pole oscillations and oscillations with multiple band formations in long cells, and patches of Min proteins seen in spherical cells.



Pole to pole oscillation of Min D in living *E. Coli* (Bonny et al, 2013) [2]

I developed many programs this summer, focusing on:

1. batch production and running of SMOLDYN files,
2. determining cluster behaviour in long and spherical cells, and
3. translating a new model into SMOLDYN format.

To visualize and analyze the Min protein behaviour, I used SMOLDYN, a program used to simulate chemical processes. SMOLDYN allows specification of all the system details, for example, molecule types and positions, and different membrane features. After running simulations, I could then use the output to analyze the system behaviour. I focused on the location of each Min D molecule over time.

For example, in long cells, a K-means plot was used to determine the exact number of clusters of Min D over a given period. While quite accurate, it takes time to produce these detailed results. An alternate is producing a plot of the position of every Min D in the cell at each time step. While not generating the specific number of clusters like the K-means treatment, it quickly produces output that is easy to qualitatively analyze. For spherical cells, intensities for each point were calculated using a Gaussian distribution, then plotted in both Cartesian and phi-theta coordinates.

All my analysis work was done using the Huang Meir Wingreen model. The last part of my summer involved translating a new inclusive Min system model developed by Professor Cytrynbaum's PhD student, William Carlquist, into a format that could be run in SMOLDYN. I did not have success with this, however.

The project this summer really allowed me to develop my problem solving skills as I had to rely on all my computing experience to tackle the issues from different approaches. I had experience programming in C++, R, and MATLAB, and used the XPP and SMOLDYN software programs. Coming from a background in life sciences, mathematics, and computer science, this project combined my interests and exposed me to tackling large problems that span multiple fields.

References

1. Huang, K.C., Meir, Y. & Wingreen N. (2003), Dynamic structures in Escherichia coli: Spontaneous formation of MinE rings and MinD polar zones. PNAS, 100, 12727
2. Bonny, M., Fischer-Friedrich, E., Loose, M., Schwille, P. & Kruse, K. (2013) Membrane Binding of Min E Allows for a Comprehensive Description of Min-Protein Pattern Formation. PLOS Computational Biology. 9, e1003347