ACMS Applied Math Seminar

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154 Hurley Hall
3:30- 4:30 PM

Challenges in Modeling M. xanthus Polarity, Reversal, and Division

Myxococcus xanthus is a model organism largely studied for its characteristic cell polarity mechanisms. However, the link between cell polarity, movement reversal, and division is still unclear [1,2]. This project aims to explain these connections through experimental data and computer simulations, and provide improved accuracy for swarming models of *M. xanthus* and other similar bacteria.

After some background on *M. xanthus* and the used experimental settings, the talk will focus on explaining the observed phenomenon through reasonable biological hypothesis and their realization via computational models, which include both a PDE model and a stochastic simulation of particle moving in a time dependent domain.

The first model consists of a system of coupled partial differential equations (PDEs). These equations describe the distribution of RomR protein in two forms: an unbounded form that can diffuse in the cell body, and a bounded form that attaches to receptors positioned at the poles of the cell body. This model was inspired by the well-studied *E. coli* polarity (MinCDE system) [3,4], but an alternative approach based on circadian rhythm models will also be discussed in this talk [5], to explain how RomR receptors can be activated or deactivated.

In the second model RomR is seen as a system of particles going through Brownian motion of particles in a time dependent domain. This approach is used to justify assumptions for the changes in value of the Diffusion coefficient during cell division in the PDE model, and to observe variability similar to the one seen in the experiments.

The current computational results are able to reproduce the qualitative behavior of this biological system. However, to obtain a quantitative agreement it is necessary to collect more experimental data, obtain an estimate for the biologically relevant parameters in the models, and improve the computational model. The talk will be concluded with a summary of the challenges and possible future directions regarding the tasks currently in progress.

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2. Cameron W. Harvey, Chinedu S. Madukoma, Shant Mahserejian, Mark S. Alber and Joshua D. Shrout [2014], Cell Division Resets Polarity and Motility for the Bacterium Myxococcus xanthus, Journal of Bacteriology 196, 22, 3853-3861.
3. Kerwyn Casey Huang, Yigal Meir, and Ned S. Wingreen [2003], Dynamic structures in Escherichia coli: Spontaneous formation of MinE rings and MinD polar zones, PNAS 100, 22, 12724-12728.
4. Martin Howard, Andrew D. Rutenberg, Simon de Vet [2001], Dynamic Compartmentalization of Bacteria: Accurate Division in E. Coli, Phys Rev Lett, 87, 27, 278102.
5. D. A. Bratsun, D. V. Merkuriev, A. P. Zakharov , L. M. Pismen [2015], Multiscale modeling of tumor growth induced by circadian rhythm disruption in epithelial tissue, J Biol Phys doi:10.1007/s10867-015-9395-y