Quantification and Modeling of the self-organization of *Myxococcus xanthus*.

Chris Cotter[1], Heinz-Bernard Schuttler[2], Oleg Igoshin[3], Lawrence Shimkets[1]

Myxococcus xanthus **provides a model system for self-organizing processes involving motility by means of fruiting body development. Despite numerous models for fruiting body development, very little quantitative data on the process is available. The models that do exist fail to capture all the dynamics of aggregate formation. Here we synchronically track individual fluorescently labeled cells within the biofilm and the forming fruiting bodies to quantify the cell behaviors that lead to aggregation. We use this data to develop *in-silico* models of cell behavior that reproduce the traits necessary for correct aggregation dynamics.**

Keywords **— Self-organization, Cell Tracking, Modeling, Image Analysis, Pattern Formation**

THE bacterium M*yxococcus xanthus* lives in a biofilm of millions of cells many layers thick. Cells glide on semi-solid surfaces along their long axis, reversing direction periodically. Upon starvation conditions, the swarm of cells self-organize into large multicellular aggregates in which spores mature (fruiting bodies). The lack of known diffusible signals and arguments that *M. xanthus* moves too slowly to accurately measure most diffusion gradients [1] has lead to many hypothesized modes of aggregation [2–5]. These models, however, have little quantative work to support them and do not correctly model the dynamics of aggregation growth or disassembly [6]. Dynamics lacking from these models include a period of rapid unstable aggregate growth, the ability to form aggregates over many logs of cell density, and the disassembly of approximately 40% of the once-stable late stage aggregates. *Xie et al.* [7] found the late stage disassembly correlates with small aggregate size but not with neighbor-related parameters such as neighbor size and distance to neighbors. This suggests the disassembly decision is made individually in each aggregate and argues for a pattern formation technique that does not rely on long-range diffusible signals.

To quantify the cell behaviors that lead to aggregation we added fluorescently labeled cells to a wild type biofilm. We then captured synchronous time-lapse images of the forming aggregates using phase contrast microcopy, and individual cells within the biofilm using fluorescent microcopy. Using image analysis we tracked the location, size, boundary, and approximate cell density of each aggregate. We also tracked cell reversal period, speed, and relation of the cells to the aggregates. We used this combined data to develop *in-silico* models of cell movement to test the validity of possible methods of aggregation. Here we compare the results to that predicted by possible models of aggregation, discuss the link between the behavior of individual cells and the emergent behaviors of the biofilm, and evaluate how cell behavior changes in non-aggregating mutants abrogate the emergent behaviors.

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[1]Department of Microbiology, University of Georgia. cotter@uga.edu
[2]Department of Physics and Astronomy, University of Georgia
[3]Department of Bioengineering, Rice University

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