



COLLOQUIUM

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Mechanisms Underlying Spatiotemporal Patterning in Microbial Collectives: A Model's Perspective

Friday February 26th at 3pm on Zoom

<https://csuohio.zoom.us/j/91945126460>

Bio: Prof Karamched received a B.S. in Mathematics and a B.S. in Biochemistry from the University of Oklahoma in 2012. Thereafter, he received his Ph. D. in Mathematics at the University of Utah in 2017 under Professor Paul Bressloff, with emphasis on mathematical cell biology. His research is focused on applications of partial differential equations and stochastic processes to biological processes in order to reveal underlying mechanisms. He then did a postdoctoral fellowship in the Department of Mathematics at the University of Houston and the Department of Bioengineering at Rice University working with Professors Krešimir Josić, Matthew Bennett, and William Ott on developing stochastic models of synthetic microbial consortia and decision-making in social networks. His interests in biomathematics are diverse, ranging from dynamical systems models of glucose-insulin dynamics to stochastic models of microbial dynamics and cancer tumor treatment. I am specifically interested in developing analytically tractable models that provide insights into underlying mechanisms of biosystems.

Abstract: We describe a spatial Moran model that captures mechanical interactions and directional growth in spatially extended populations. The model is analytically tractable and completely solvable under a mean-field approximation and can elucidate the mechanisms that drive the formation of population-level patterns. As an example, we model a population of *E. coli* growing in a rectangular microfluidic trap. We show that spatial patterns can arise because of a tug-of-war between boundary effects and growth rate modulations due to cell-cell interactions: Cells align parallel to the long side of the trap when boundary effects dominate. However, when cell-cell interactions exceed a

critical value, cells align orthogonally to the trap's long side. This modeling approach and analysis can be extended to directionally growing cells in a variety of domains to provide insight into how local and global interactions shape collective behavior. As an example, we discuss how our model reveals how changes to a cell-shape describing parameter may manifest at the population level of the microbial collective. Specifically, we discuss mechanisms revealed by our model on how we may be able to control spatiotemporal patterning by modifying cell shape of a given strain in a multi-strain microbial consortium.