CENTER FOR THERMO-FLUID MECHANICS

FALL 2018 SEMINAR SERIES

Continuum Modeling of Bacterial Growth in Confined Environments: Stochastic Interactions and Nematic Ordering Under Shear Flow

SPEAKER: James J. Winkle
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WHEN: October 2 2018 2:30 PM - 3:30 PM
WHERE: MREB ROOM 200

Multi-disciplinary Research and Engineering Building BLD#484

ABSTRACT

Bacteria in natural environments are prevalent in close-packed biofilm structures, where intercellular chemical and physical signaling interactions can lead to emergent forms. In experimental synthetic biology, close-packing of cells also exists in microfluidic devices that study bacterial consortia in a continuous, exponential growth phase. Due to their anisotropic, rod-like geometry and axial growth, bacteria in microfluidic experiments exhibit nematic ordering dynamics similar to those of liquid crystals under shear flow. The relative rate of nematic ordering can be vastly different, however, depending on the geometry of the device and cell location with respect to trap boundaries. We extend a continuum model of bacterial growth and nematic ordering to capture the 2D spatiotemporal dynamics of a monolayer of bacterial cells grown in a microfluidic trap. Typical bacterial growth environments of low Reynolds number result in a Poisson's equation PDE formulation for cell growth pressure, which is coupled to a reaction/advection equation for the tensor order parameter under shear flow. We numerically simulate bacterial growth and ordering dynamics and demonstrate how stochastic interactions between cells can lead to persistent destabilization of cell ordering in regions predicted by the model.

BIO:

James Winkle is a postdoctoral research associate with Dr. Matthew Bennett's Biodesign lab in the Dept. of BioSciences at Rice University. He obtained his B.S.E.E. degree from UT Austin and completed his PhD in Applied Mathematics at the University of Houston in 2018 under the advisement of Dr. Krešimir Josić, Dr. William Ott, and Dr. Ronald Hoppe. His research focuses on modeling bacterial growth and signalling in confined environments and on the stochastic modeling of genetic circuits in synthetic biology.

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