

Multi-scale Modeling in Biology and Medicine

Mark Alber

Department of Applied and Computational Mathematics and Statistics
University of Notre Dame

Wednesday, February 13, 2013

007 Kemeny, 4:00PM

Tea is at 3:30 pm in 300 Kemeny

Abstract

A three-dimensional multi-scale modeling approach will be described for studying fluid-viscoelastic cell interaction during blood clot formation, with cells modeled by subcellular elements (SCE) coupled with fluid flow sub model. Using this method, motion of a viscoelastic platelet in a shear blood flow was simulated and compared with experiments on tracking platelets in a blood chamber. It will be shown that complex platelet-flipping dynamics under linear shear flow can be accurately recovered with the SCE model [1,2]. The structural features and mechanical properties of different types of fibrin networks grown in microfluidic devices will be also described including networks formed from normal plasma with and without cells, and from plasma from a hemophilic patient [3]. The mechanical model based on the microstructures within the network will be used to calculate the bulk properties of the network.

In the second half of the talk, population of bacteria *P. aeruginosa*, main infection in hospitals, will be shown to propagate as high density waves that move symmetrically as rings within swarms towards the extending tendrils. Biologically-justified cell-based multi-scale model simulations suggest a mechanism of wave propagation as well as branched tendril formation at the edge of the population that depend upon competition between the changing viscosity of the bacterial liquid suspension and the liquid film boundary expansion caused by Marangoni forces [4]. Therefore, *P. aeruginosa* can efficiently colonizes surfaces by controlling the physical forces responsible for expansion of thin liquid films and by propagating towards the tendril tips. The model predictions of wave speed and swarm expansion rate as well as cell alignment in tendrils were confirmed experimentally.

References

1. Christopher R. Sweet, Santanu Chatterjee, Zhiliang Xu, Katharine Bisordi, Elliot D. Rosen and Mark Alber [2011], Modeling Platelet-Blood Flow Interaction Using Subcellular Element Langevin Method, *Journal of the Royal Society Interface* 8 (65), 1760-71.
2. Zhiliang Xu, Oleg Kim, Malgorzata Kamocka, Elliot D. Rosen and Mark Alber, *Multiscale Models of Thrombogenesis* [2012], *Wiley Interdiscip Rev Syst Biol Med.* 4(3):237-46.
3. Eungjun Kim, Oleg V. Kim, Kellie R. Machlus, Xiaomin Liu, Timur Kupaev, a Joshua Lioi, Alisa S. Wolberg, Danny Z. Chen, Elliot D. Rosen, Zhiliang Xu, and Mark Alber [2011], Correlation between fibrin network structure and mechanical properties: an experimental and computational analysis, *Soft Matter* 7, 4983.
4. H. Du, Z. Xu, M. Anyan, O. Kim, W. M. Leevy, J.D. Shrout and M. Alber [2012], High density waves of the bacterium *Pseudomonas aeruginosa* in propagating swarms result in efficient colonization of surfaces, *Biophysical Journal* 103(3), 601-609.

This talk should be accessible to graduate students.