Abstract Submitted
for the DFD17 Meeting of
The American Physical Society

Direct numerical simulation of cellular-scale blood flow in microvascular networks[1] PETER BALOGH, PROSENJIT BAGCHI, Rutgers University — A direct numerical simulation method is developed to study cellular-scale blood flow in physiologically realistic microvascular networks that are constructed in silico following published in vivo images and data, and are comprised of bifurcating, merging, and winding vessels. The model resolves large deformation of individual red blood cells (RBC) flowing in such complex networks. The vascular walls and deformable interfaces of the RBCs are modeled using the immersed-boundary methods. Time-averaged hemodynamic quantities obtained from the simulations agree quite well with published in vivo data. Our simulations reveal that in several vessels the flow rates and pressure drops could be negatively correlated. The flow resistance and hematocrit are also found to be negatively correlated in some vessels. These observations suggest a deviation from the classical Poiseuilles law in such vessels. The cells are observed to frequently jam at vascular bifurcations resulting in reductions in hematocrit and flow rate in the daughter and mother vessels. We find that RBC jamming results in several orders of magnitude increase in hemodynamic resistance, and thus provides an additional mechanism of increased in vivo blood viscosity as compared to that determined in vitro.

[1]Funded by NSF CBET 1604308

Prosenjit Bagchi
Rutgers University

Date submitted: 27 Jul 2017 Electronic form version 1.4