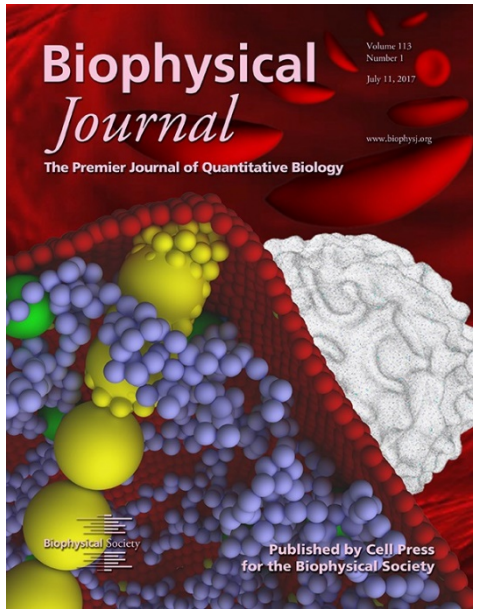
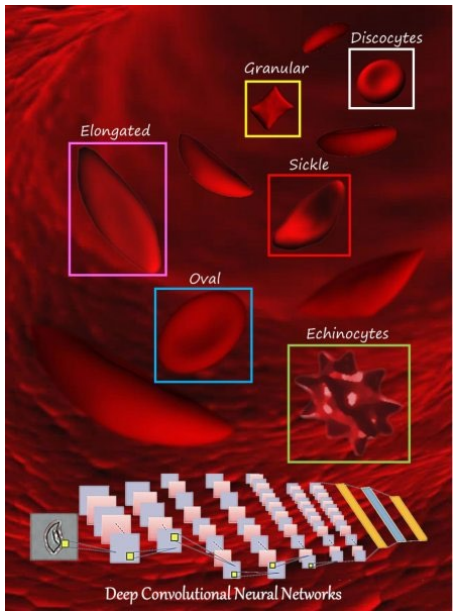
Multiscale Modeling of Sickle Cell Anemia: Methods and Validation

The model: The pathophysiology of sickle cell disease is organ-specific and it involves several processes across multiple time scale from O(10^{-1} s) to O(10^{3} s) and length scales from O(10^{-9} m) for the size of the protein to O(10^{-2}m) for the size of the organ. Therefore, we developed multiscale models to quantify the connections between the pathogenesis and clinical manifestations.

What is new inside?

Synergistic integration of in silico, in vitro, in vivo and ex vivo data: we integrate *in silico* data from multiscale simulations, *in vitro* data from microfluidic experiments, *in vivo* data from sickle cell disease patients and *ex vivo* data from perfusion of human spleen via multifidelity methods. Our group has recently developed *deep and active learning* multifidelity formulations for fusing different information sources (e.g., simulation, experimental and clinical data) in order to derive "unknown" functional relationships for quantities of interest that direct therapeutic interventions as a function of many independent parameters.

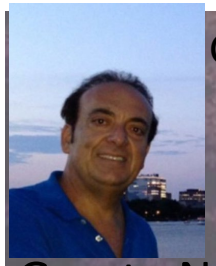




How will this change current practice?

Multiscale modeling is essential in exploring human spleen filtration of sickle red blood cell because these multidimensional processes cannot be directly observed in humans. Existing mouse models are not sufficient to describe the human splenic filtration function due to the different spleen filtering structures. The proposed framework can help physicians determine how fast the function of the spleen declines and thus guide patients and physicians exposed to complex situations required to make decisions (splenectomy or not).

End Users {biomedical engineers, biophysicists, physicians}



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