

Interrogating patient-specific microvascular network architectures with Agent-based models

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One of the goals of biomedical computational modeling is to be able to predict the effect of treatments on individual patients and thus match each patient to the most efficacious therapy. There is documented patient-to-patient variability in the microvascular network architectures of some tissues (e.g. myocardium). We submit that this variability could have important effects on properties such as arteriogenesis and leukocyte trafficking that impact the severity and response to treatment of diseases ranging from peripheral vascular disease to atherosclerosis. Because of the effects of vascular network architecture, we believe it is important to perform *in vivo* validation of our agent-based model of leukocyte trafficking by comparing multiple simulations of the network architecture of each animal to the data for that animal rather than comparing general properties of an example network to aggregate animal data. Toward this end, we have developed a method of rapidly inputting different network architectures into the model. Images of network architecture in a murine dorsal skinfold window chamber are taken using intravital or confocal fluorescence microscopy. The images are converted to a scale of one pixel per micron and loaded into the model, where a node is placed at each vessel branchpoint or change in direction. The model then fills in the remainder of each vessel. This approach will allow us to more realistically validate our model of leukocyte trafficking, and will give much insight into the role that microvascular network architecture plays in the trafficking process.