

Modeling Blood Vessel Growth: An Integrated Agent Based and Finite Element Analysis Approach

Bryan C. Thorne (Presenting Author)	Alexander M. Bailey	Shayn M. Peirce, PhD
University of Virginia	University of Virginia	University of Virginia
Department of Biomedical Engineering	Department of Biomedical Engineering	Department of Biomedical Engineering
P.O. Box 800759, UVA Health System	P.O. Box 800759, UVA Health System	P.O. Box 800759, UVA Health System
Charlottesville, VA 22908	Charlottesville, VA 22908	Charlottesville, VA 22908
(434) 243-9892	(434) 243-9892	(434) 243-5795
bct3d@virginia.edu	amb3gq@virginia.edu	smp6p@virginia.edu

Abstract:

One of the newer approaches to the study of complex biological systems has been to model tissues as a collection of agents representing individual cells. Here, we apply this approach to a biological process that is important in diabetes, heart disease, and cancer: microvascular growth and remodeling. These physiological processes involve a myriad of cell behaviors, including cell adhesion, migration along gradients of diffusible factors, cell division and death. Cells integrate complex signals that drive these behaviors and lead to formation of emergent tissue patterns, in this case new small blood vessel (microvessel) networks. A previous model developed by this lab predicts the patterning of blood vessel networks induced by different growth factors and was validated experimentally *in vivo*. One of the limitations of this model was the lack of physiological blood and cell flow patterns, which have been shown to influence many of the processes described above. There are many examples of mathematical models that accurately describe fluid flow through a vascular network, but do not use this information to influence individual cell behavior or overall microvascular network growth and remodeling. Using Netlogo, we combined an agent based framework for a vascular network with a traditional finite element model describing fluid flow through a network of pipes. The finite element model calculates blood pressures, flow velocities, and shear stresses at different points of the microvascular network with each change in the architecture. In turn, these outputs are incorporated into a ruleset to determine cell disposition (updated at each time step) within the agent based model. This novel approach to modeling of biological systems will allow the generation and investigation of hypotheses related to inflammatory and progenitor cell adhesion and migration from the microvasculature in different disease states.

Preferred format: Oral presentation, but will do a poster if the topic is unsuitable for a talk.