

A Novel Computational Integration of Agent Based and Finite Element Models: Predicting Cell Homing

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Circulating cell trafficking and homing in tissues is central in angiogenesis, inflammation, and the immune response. Although the literature is rich with mechanistic detail describing key aspects of these processes, integration of signaling events and cell behaviors within a unified spatial and temporal framework is needed to achieve fuller understanding. Toward this end, we present a novel computational framework that combines agent based modeling (ABM) with finite element analysis (FEA). Initial *in vivo* microvascular network architectures, along with their known anatomical parameters (vessel length, diameters, and connectivity), are incorporated into the ABM, which then calls the FEA (based on Poiseuille's law) to calculate flow velocity, shear stress, and pressure throughout the network. In turn, these parameters serve as inputs to the ABM, which uses a literature-defined rule set to predict cell-cell and cell-matrix interactions in a spatially heterogeneous environment. In this manner, circulating cell flow direction is governed by calculated pressure drops, and endothelial cell adhesion is determined in part by fluid shear stress. The simulation output predicts adhesion and transmigration. This fully integrated computational model, which is capable of continuous updates from Matlab, will allow the generation and evaluation of hypotheses relating to the dynamic recruitment and participation of circulating progenitor and inflammatory cells in physiological and pathological tissue settings, including hypoxia and ischemia.