Multi-scale modeling of deformation of blood clots

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Thromboembolism, one of the leading causes of morbidity and mortality worldwide, is characterized by formation of obstructive intravascular clots (thrombi) and their mechanical breakage (embolization). A novel two-dimensional multi-phase computational model will be described that simulates active interactions between the main components of the clot, including platelets and fibrin. It can be used for studying the impact of various physiologically relevant blood shear flow conditions on deformation and embolization of a partially obstructive clot with variable permeability. Simulations provide new insights into mechanisms underlying clot stability and embolization that cannot be studied experimentally at this time. In particular, multi-phase model simulations, calibrated using experimental intravital imaging of an established arteriolar clot, show that flow-induced changes in size, shape and internal structure of the clot are largely determined by two shear-dependent mechanisms: reversible attachment of platelets to the exterior of the clot and removal of large clot pieces [1]. Model simulations also predict that blood clots with higher permeability are more prone to embolization with enhanced disintegration under increasing shear rate. In contrast, less permeable clots are more resistant to rupture due to shear rate dependent clot stiffening originating from enhanced platelet adhesion and aggregation. Role of platelets-fibrin network mechanical interactions in determining shape of a clot will be also discussed and quantified using analysis of experimental data [2,3]. These results can be used in future to predict risk of thromboembolism based on the data about composition, permeability and deformability of a clot under specific local hemodynamic conditions.

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Bio: Professor Mark Alber earned his Ph.D. in mathematics at the University of Pennsylvania under the direction of J. E. Marsden (UC Berkeley and Caltech). He held several positions at the University of Notre Dame including most recently Vincent J. Duncan Family Chair in Applied Mathematics. He also served as the Director of Graduate Studies in the Department of Applied and Computational Mathematics and Statistics and as the Director of the Interdisciplinary Center for the Study of Biocomplexity at the University of Notre Dame. He is currently Distinguished Professor in the Department of Mathematics and Director of the Center for Quantitative Modeling in Biology, University of California, Riverside. Dr. Alber was elected a Fellow of the American Association for the Advancement of Science (AAAS) in 2011. He is currently a deputy editor of PLoS Computational Biology and member of editorial boards of Bulletin of Mathematical Biology and Biophysical Journal. His research interests include mathematical and computational multi-scale modeling of blood clot formation, epithelial tissue growth, cancer invasion, bacterial antibiotics resistance, wound healing and plants development and growth.