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Reduced-order model to investigate cell-scale hemodynamics through disordered porous networks of the human placenta

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The circulatory system in the human placenta consists of the separate maternal and fetal blood flows which are interlaced across a complex multiscale domain of porous regions and capillaries. As imaging techniques improve, we are able to construct representative porous domains, for organs such as the placenta, with a higher degree of accuracy [1]. High-resolution characterization of the human placenta can enable a greater understanding of the effect of pathologies on the placental transport of oxygen and nutrients. These transport mechanisms are fundamentally interlinked with the geometry and topology of the placental porous domain and the dynamics of red blood cells (RBCs) within this space [2].

One possible avenue to utilize emerging imaging data is via high performance computing, which can be used in conjunction with lattice Boltzmann and immersed boundary methods to simulate the motion of a suspension of highly deformable RBCs through porous domains [3]. However, these simulations are computationally costly, restricting the domain size over which these simulations are tractable. An alternative method comes from the classic work of A . R. Pries and T. W. Secomb, who developed empirical laws for hemodynamics in microvasculature [4]. These laws are widely used in biomedical models, however they are developed based on experimental observations in long cylindrical vessels. As we explore more complex biological tissues, these empirical laws are less accurate and can lead to unphysical predictions of blood flow and oxygen distribution.

New techniques are needed to describe the flow of blood as a suspension of RBCs through porous domains. Pore-network models have long been used to describe flow through disordered irregular domains in areas such as geophysics. These reduced-order models are able to couple complex multiscale mechanics with scalability over a range of different domain sizes [5]. Here we demonstrate how pore-network models can be extended to include a description of particulate blood flow.

Principal component analyses of the RBC flow using lattice Boltzmann simulations suggest a clear dependence on non-dimensional geometric factors which differ from those within the Pries-Secomb formulation. We infer a novel reduced-order model utilising this new data. Disordered 2D porous networks are constructed by randomly placing non-overlapping discs on a plane and using Voronoi tessellation to identify pores and the throats connecting them. We test the reduced-order model by simulating flow through both regular and disordered 2D porous networks and by comparing the results against the quasi-3D lattice Boltzmann simulations.

Pore-network models are a powerful tool enabling us to model suspension flows through complex domains. Informed by recent progress in imaging, this work extends pore-network approach to nonlinear hemodynamics in disordered porous media. The developed methodology can be used to examine the structure-function relationship in the human placenta and other complex microvascular systems.

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Time Block Preference

Time Block A (09:00-12:00 CET)

Participation

Online

Primary authors: DOMAN, Eleanor (University of Manchester); Dr ZHOU, Qi (School of Engineering, Institute for Multiscale Thermofluids, University of Edinburgh, UK); Dr BERNABEU, Miguel O. (Centre for Medical Informatics, Usher Institute, University of Edinburgh, UK); Dr KRÜGER, Timm (School of Engineering, Institute for Multiscale Thermofluids, University of Edinburgh, UK); Prof. JENSEN, Oliver E. (Department of Mathematics, University of Manchester, UK); Dr CHERNYAVSKY, Igor (Department of Mathematics & Maternal and Fetal Health Research Centre (School of Medical Sciences), University of Manchester, UK)

Presenter: DOMAN, Eleanor (University of Manchester)

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