Pore-network models for haematocrit transport in disordered porous domains reflecting the human placenta

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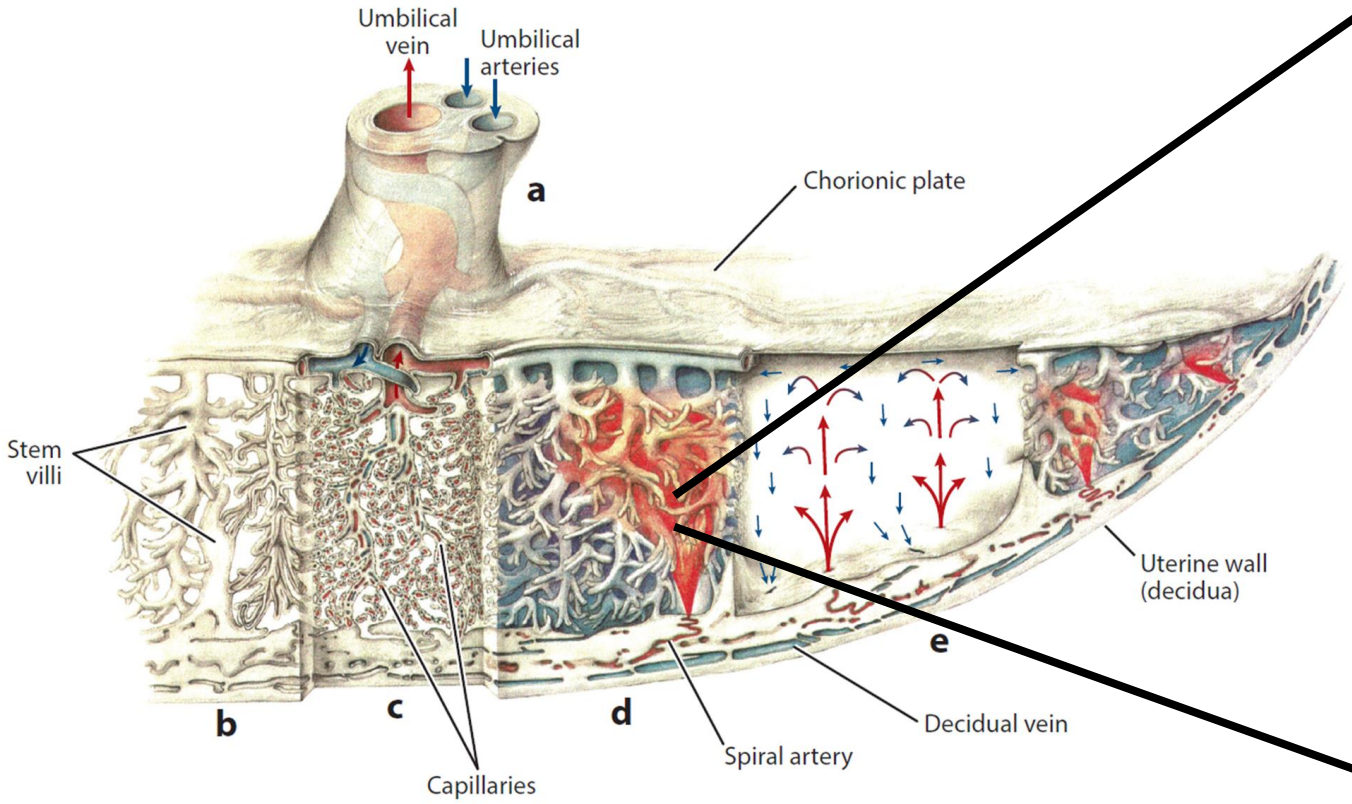
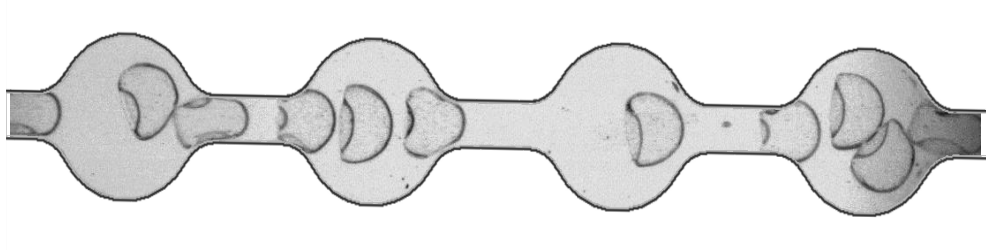
The Human Placenta



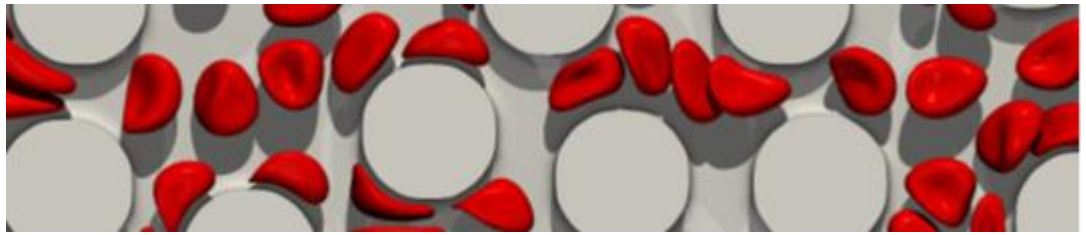
Schematic whole organ structure of human placenta (Jensen & Chernyavsky, Annu Rev Fluid Mech, 2019).

3D synchrotron micro-CT rendering of placental tissue (Tun et al., 2021).

Aim: Construct reduced-order models for blood flow informed by lattice Boltzmann simulations and microfluidic experiments.



Deflated capsuled flowing through channel with varying diameter. Provided by Qi Chen.



Simulation snapshot of deformable red blood cells in disordered porous medium generated using the lattice Boltzmann method.

Describing Blood Flow

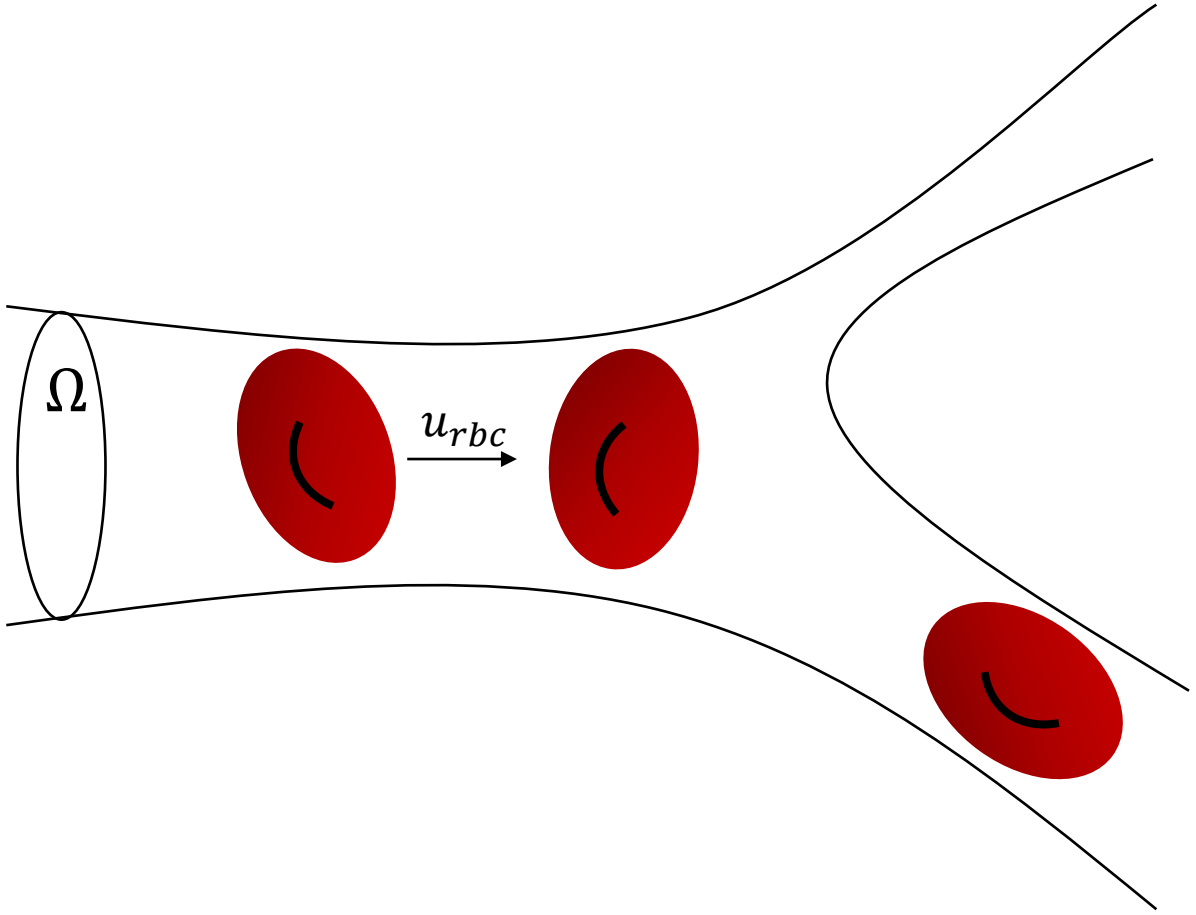
Quantify behaviour of blood using discharge haematocrit:

$$H = \frac{\iint_{\Omega} u_{RBC}(\boldsymbol{x}, t) dA}{\iint_{\Omega} u(\boldsymbol{x}, t) dA}$$

Where u_{rbc} and u are the RBC and whole blood velocities.

Due to particulate nature of blood, rheological accurate models must incorporate:

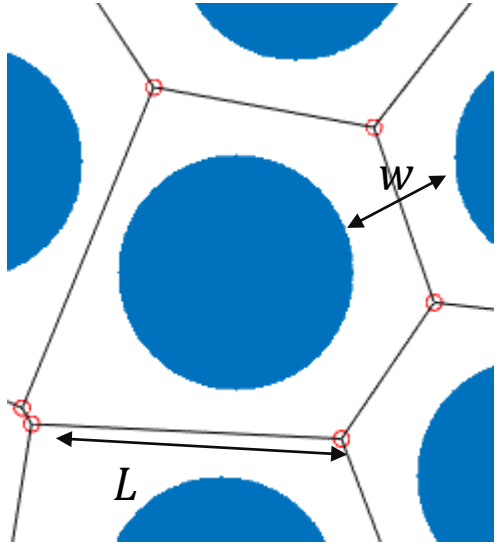
1. Variable viscosity
2. Fåhraeus effect
3. Unequal RBC partitioning



Constructing a reduced-order model

Define the incidence matrix A such that

$$A_{ij} = \begin{cases} 1, \text{if edge } i \text{ points into vertex } j, \\ -1, \text{if edge } i \text{ points out of vertex } j, \\ 0, \text{otherwise.} \end{cases}$$



Define V to be the diagonal matrix containing the volume associated with each vertex, with pressure $\boldsymbol{P}$ and haematocrit $\boldsymbol{H}$ defined on vertices and flux $\boldsymbol{Q}$ on the edges.

$$\begin{cases} \mathrm{A}\boldsymbol{P} = -\mathrm{R}\boldsymbol{Q} & \text{Pressure-flux equation} \\ \mathrm{A}^T\boldsymbol{Q} = \boldsymbol{0} & \text{Conservation of flux} \\ \mathrm{V}\dfrac{d\,\boldsymbol{H}}{dt} = \mathrm{B}\boldsymbol{H} & \text{Conservation of haematocrit} \end{cases}$$

Where we define resistance relative to plasma Stokes resistance

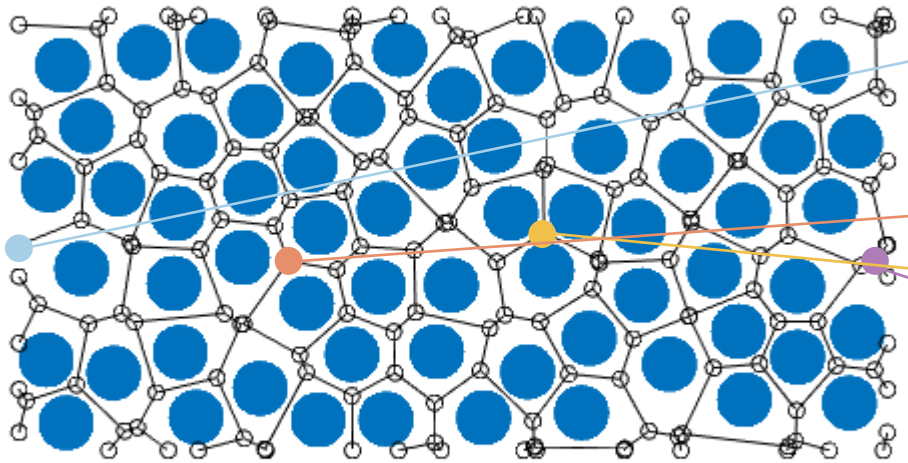
$$\mathrm{R} = \mathrm{R}_p\chi\left(\boldsymbol{H}, \frac{\boldsymbol{w}}{D}, \frac{\boldsymbol{L}}{D}, \ldots\right),$$

and define the transport operator

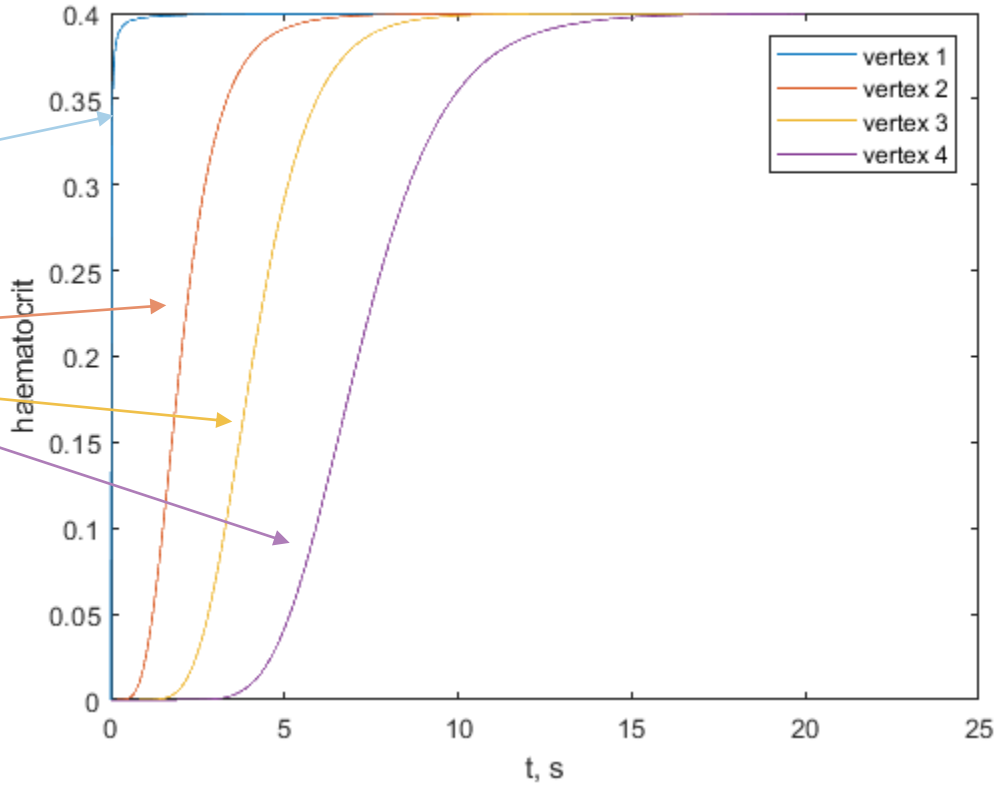
$$\mathrm{B} = \mathrm{B}(\mathrm{A}, \boldsymbol{H}, \boldsymbol{Q}).$$

Evaluating haematocrit across the network

Inlet

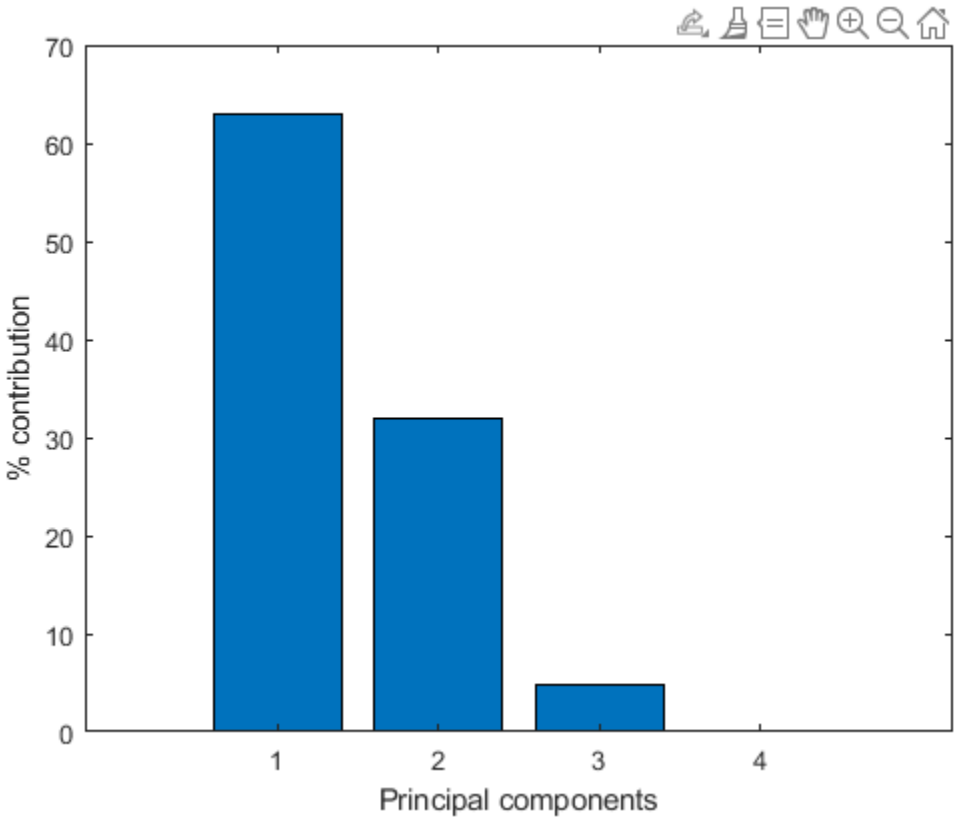


$$R = (1 + H)R_p$$

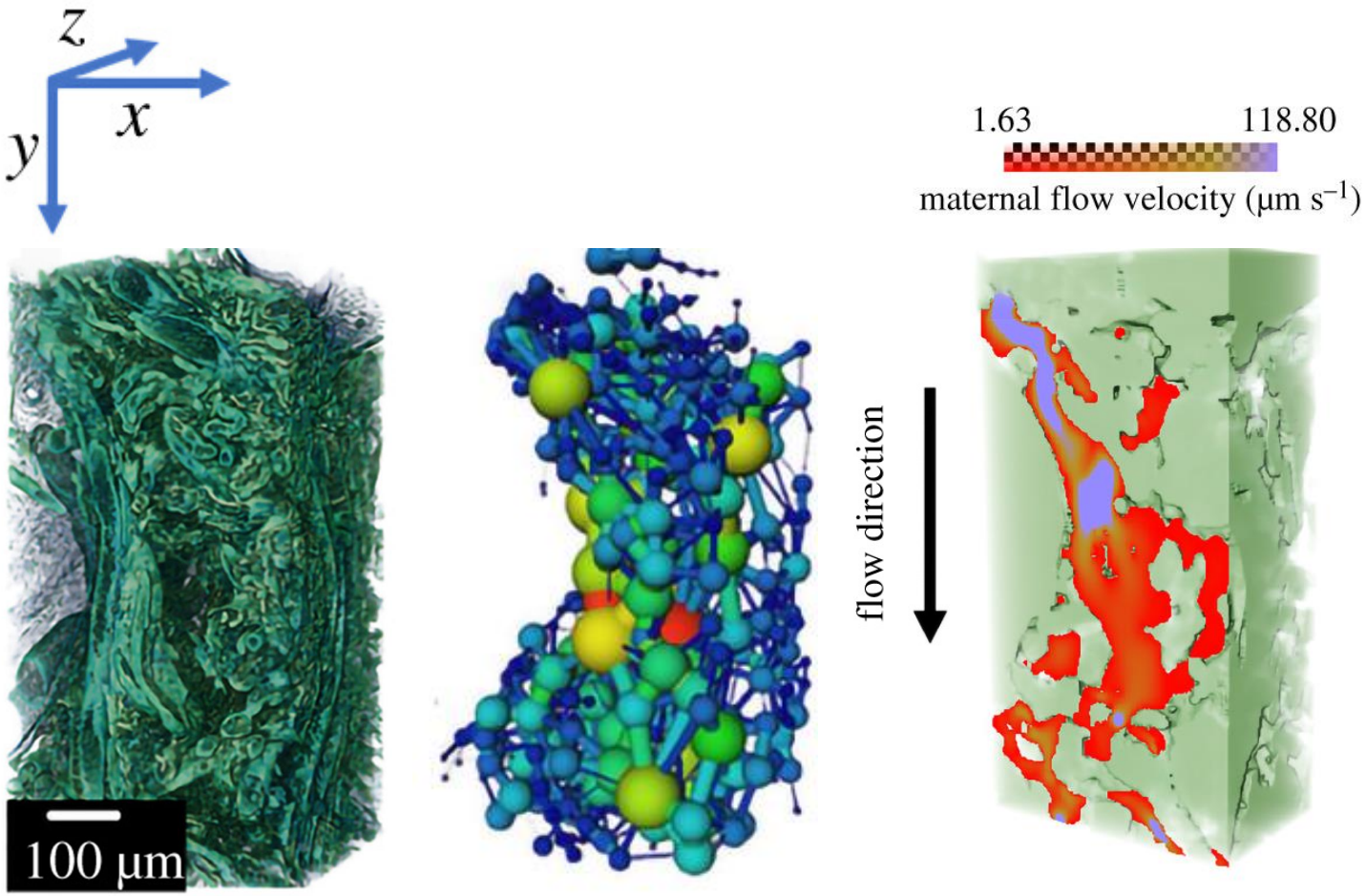


PCA of lattice Boltzmann simulations

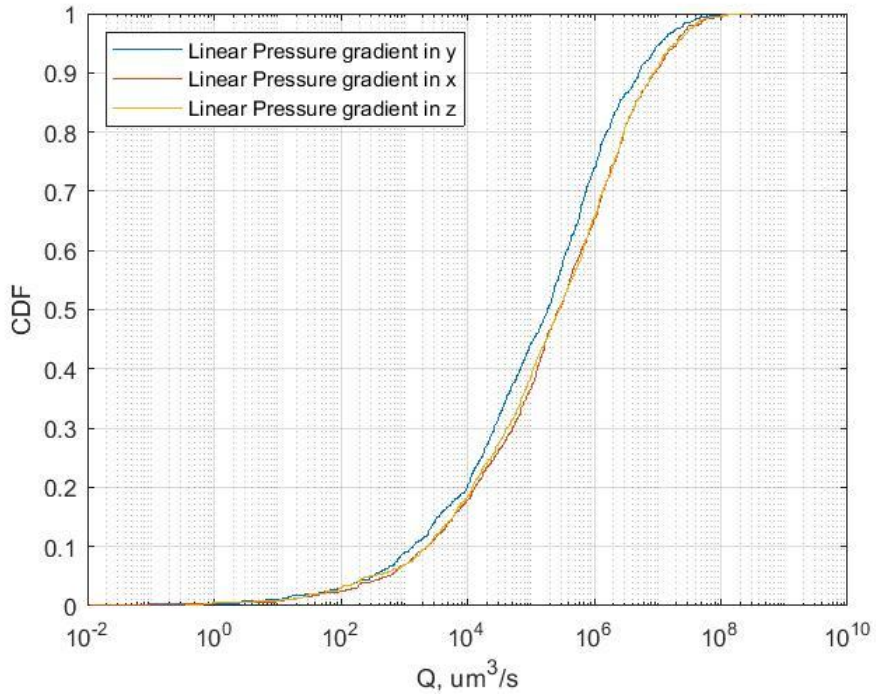
- Principal component analysis (PCA) quantifies parameter contribution to variability within data sets.
- Lattice Boltzmann simulations provide data on relative resistance χ, haematocrit H, and non-dimensionalised throat width $\frac{w}{D}$ and length $\frac{L}{D}$.
- PCs represent an orthogonal linear transformation of data variables.
- PC2 dominated by non-dimensionalised length $\frac{L}{D}$, suggesting $\frac{L}{D}$ must be one of the key determinants of χ.



Effect of tissue heterogeneity on flow



(left) 3D synchrotron micro-CT rendering of placental tissue, (centre) associated ball and stick model showing throats and pores, (right) CFD analysis of flow (Tun et al., 2021).



Kruskal-Wallis Null Hypothesis Test:

H_0: *Groups have same distribution.*

$H = 14.0 > 7.2 = H_C$ *(1% significance level)*

At least one group stochastically dominates.

Summary & Future directions

- New models to characterise blood micro-rheology in porous media are required.
- PCA of lattice Boltzmann data suggests a relationship between relative resistance and geometric variables in the network.
- The discrete network model detects the anisotropy in 3D networks identified by more computationally expensive CFD simulations.
- Work is planned to parameterise relative resistance using regression models using microfluidic experiments and lattice Boltzmann simulation data.

Thanks go to Prof Anne Juel, Qi Chen and Naval Singh.