**Towards a mechanistic understanding of haematocrit changes in tumour vasculature**

Miguel O. Bernabeu[1], James A. Grogan[2], Helen M. Byrne[2]

[1] Centre for Medical Informatics, The University of Edinburgh
[2] Mathematical Institute, University of Oxford

There is growing experimental evidence of anomalous patterns of blood flow in solid tumours. This includes deviations from the typical distribution of haematocrit (the blood volume fraction occupied by red blood cells, RBCs) observed in the vasculature of healthy tissue. These abnormalities present a challenge for drug delivery and have been linked to tumour hypoxia and angiogenesis.

Existing computational models of tumour blood flow typically characterise blood as a homogeneous fluid and employ phenomenological rules to determine haematocrit changes at vessel bifurcations. Such models fail to capture the dynamics encountered in tumours. This is, in part, due to the computational challenges associated with simulating haematocrit changes in a mechanistic way, i.e. using a model of interacting deformable particles to describe the transport of red blood cells, RBCs, in the plasma.

Dr Bernabeu and colleagues at The University of Edinburgh and University College London have recently extended the HemeLB blood flow simulation platform to characterise blood as a suspension of RBCs (http://www.archer.ac.uk/community/eCSE/eCSE01-010/eCSE01-010.php).

Through generous support from the UK Fluids Network, Dr Bernabeu visited the group of Prof. Byrne at the University of Oxford to pump prime a new collaboration focused on constructing and validating computational models of blood flow in realistic tumour microvasculature based on experimental data recently obtained by Byrne and colleagues (Figure 1). The proposed workflow is being used to develop a mechanistic model of haematocrit changes in tumour vasculature that will, in the longer term, enable us to elucidate biomechanical processes that regulate tumour hypoxia. A publication based on this preliminary work is in preparation and will form the basis for future joint research.

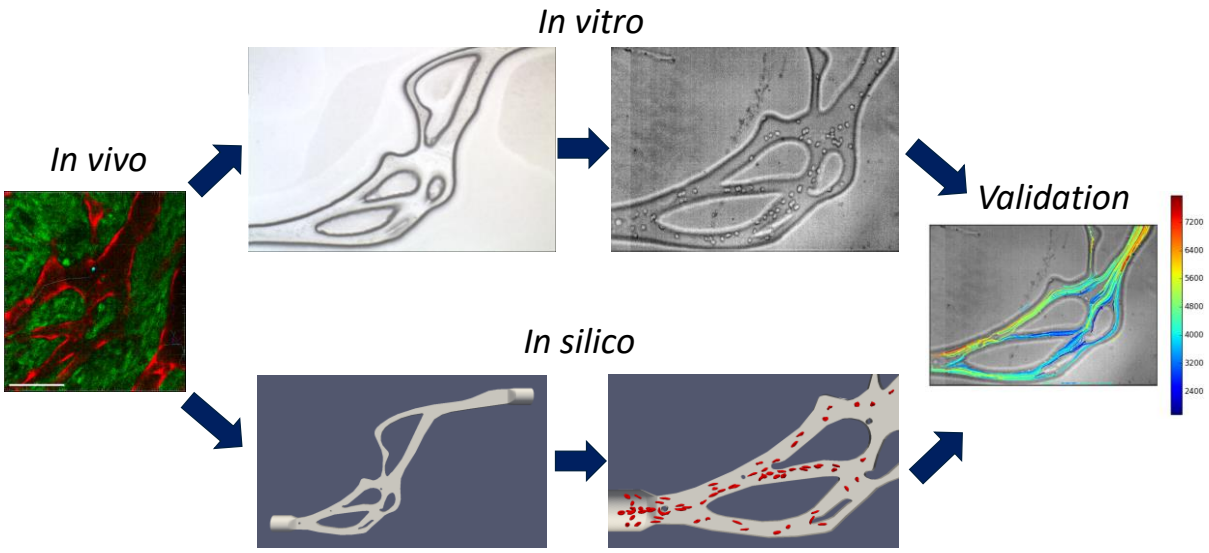

Figure 1: *In vivo* images of tumour microvasculature are obtained in mouse, segmented and used to construct microfluidics and computational models for characterising blood flow. *In vitro* measurements and *in silico* predictions are then compared using a common post-processing workflow.