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A Coupling Method for Modelling Flow and Transport Processes in Vascularized Biological Tissue using a Finite Volume Scheme

Timo Koch[*1], **Bernd Flemisch**[1] **and Rainer Helmig**[1]
[1] University of Stuttgart, Department of of Hydromechanics and Modelling of Hydrosystems,
Pfaffenwaldring 61, D-70569 Stuttgart, timo.koch@iws.uni-stuttgart.de

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ABSTRACT

Mathematical models of flow and transport processes in and between the microcirculation and the surrounding tissue can contribute to understanding complex biological processes and guide treatment of vascular diseases and cancer. The vast number of vessels demands reduced models of the vascular system to model the interaction with the possibly tumorous tissue on a reasonable scale. Possible applications of interest for such reduced models are the description of angiogenesis e.g. triggered by tumor growth, the prediction of local oxygen concentrations in the brain after a stroke, tumor cell proliferation and mestastasis, or treatment of tumors with a therapeutic agent.

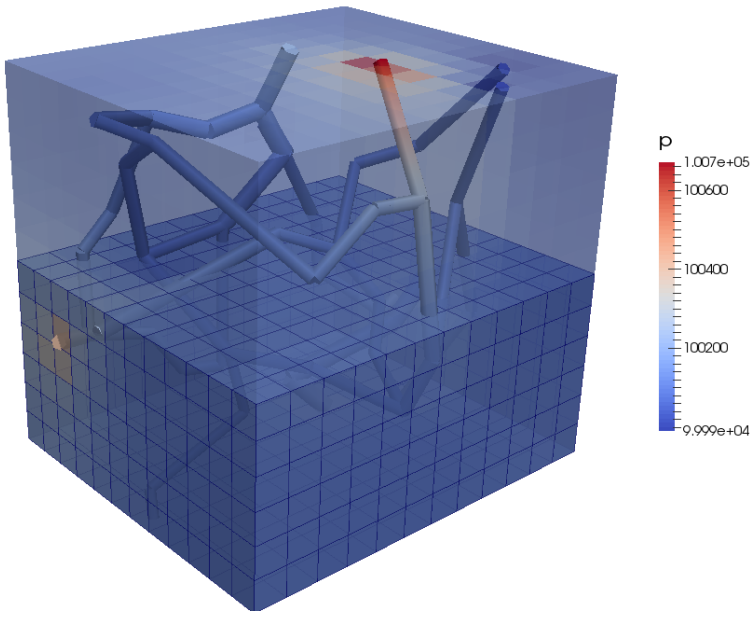

Figure 1: Effective absolute pressure distribution in a capillary network and the surrounding tissue. Three-dimensional capillary network geometry from a rat brain taken from [1].

Fully spatially resolved models usually go not further than modelling a single vessel, e.g. [2]. A multi-dimensional approach where capillaries are modelled as a one-dimensional network

structure embedded in a three-dimensional tissue domain has been recently investigated in [3]. We present a derivation of the coupled system employed in [3] starting from a fully spatially resolved three-dimensional coupled Stokes-Darcy model for a capillary-tissue system. The assumptions made are an important basis to decide in which scenarios the model reduction remains a valid choice. Numerical comparisons between the fully spatially resolved three-dimensional model and the newly derived mixed one- and three-dimensional model show the model error introduced by the reduction for example at vessel bifurcations.

We further follow the results of the dimensional analysis of the reduced system in [3] and propose an iterative domain decomposition method for its solution. The iterative scheme accounts for the different physics in the sub-domains and considers the different time scales of the transport processes. We discuss the advantages and limitations of such an algorithm. In terms of discretization scheme, we use an h-adaptive locally conservative finite volume method for better description of fronts of e.g. a concentration of a therapeutic agent. As a special feature, our one-dimensional vessel network is allowed to grow which might allows us to describe effects like tumor induced angiogenesis in the future.

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