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Numerical methods for simulating flows in biological networks

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Network structures can be detected in almost every biological system, since they are often responsible for the transport of fluids, nutrients or oxygen. Such a network structure is for example a blood vessel network supplying organs with oxygenated blood or removing metabolic waste from the tissue [1]. A further example is the root network of a plant, ensuring the water supply of the plant.

One way to obtain a realistic model for such processes is based on a decomposition approach. Thereby, the network structure is separated from the surrounding medium and different models are assigned to both domains. Quite often the surrounding medium (e.g. tissue or soil) can be considered as a three-dimensional (3D) porous medium. In order to decrease computational costs while maintaining a certain degree of accuracy, flow and transport processes within the networks are modeled by one-dimensional (1D) PDE-systems. A coupling of the network and the porous medium model is achieved by first averaging the 3D quantities and projecting them onto the 1D network structure. As a next step, the difference of the averaged 3D and 1D quantities is computed and incorporated into the source terms of both the network and the porous medium model, where the source term of the 3D problem exhibits a Dirac measure concentrated on the 1D network [2].

In this talk, numerical solution algorithms for PDE systems arising in the context of this model concept, are presented. In particular, the performance of a finite difference method with a regularized Dirac source term is investigated [3,4]. Therefore, elliptic model problems with Dirac source terms and averaging operators are considered. Theoretical results are confirmed by numerical tests.

Participation

In-Person

References

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- [3] U. Råde and C. Zenger. On the treatment of singularities in the multigrid method. *Multigrid Methods II*. Springer, Berlin, Heidelberg (1986): 261-271.
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