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A novel five-phase model for (a-)vascular tumor growth within a flexible computational framework

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We present a dynamic vascular tumor growth model derived from Thermodynamically Constrained Averaging Theory. Our framework is based on [1] where four phases have been considered: the extracellular matrix as a porous solid phase and three fluid phases: tumor cells, host cells and the interstitial fluid. Nutrient consumption, hypoxia, necrosis and drug delivery are included. The main novelty of our contribution [2] is the extension of the angiogenesis model by treating the neovasculature as a proper additional phase with volume fraction or blood vessel density in a continuum approach similar to [3]. Consistent inter-phase exchange terms between the neovasculature and the interstitial fluid have been defined such that transcapillary leakage and lymphatic drainage can be modeled. The physiologically observed high interstitial pressure in tumors, which is a crucial factor in drug delivery, can be reproduced by including these phenomena.

We have also investigated different methods for resolving the nonlinear coupling between the distinct constituents, namely a fully monolithic, a hybrid monolithic-partitioned and a partitioned scheme with Aitken relaxation. We found that the fully monolithic algorithm was superior in terms of robustness and computational efficiency as compared to the two other approaches [2]. Our flexible computational framework with an arbitrary number of phases and species makes further extensions straightforward.

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