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## Adapting a tumor growth model to an evolving domain using a diffuse-domain approach

Tumor growth at the macroscopic scale is often characterized by emerging spatiotemporal patterns, which are believed to be a contributing factor to subsequent tumor infiltration and metastasis. Furthermore, the nontrivial spatiotemporal structures can have profound effects on the collective response of tumor cells to their microenvironmental molecules, including chemotherapeutic drugs. Therefore, understanding the spatiotemporal evolution of tumor growth represents an essential step towards the prevention of tumor spread and the engineering of efficient drug delivery protocols.

Various partial differential equation (PDE) models have been formulated to study the spatiotemporal dependence of tumor progression at the macroscopic scale. Among the efforts, we derived a diffuse-interface model based on the Cahn-Hilliard equation and constructed an adaptive multigrid solver to efficiently compute its numerical solutions on a cartesian mesh [ *Wise et al., 2008, Three-dimensional multispecies nonlinear tumor growth - I Model and numerical method, J. Theor. Biol. 253, 524-543* ]. Like many other macroscopic tumor growth models, our model assumed a tumor developing in a mechanically non-restricting environment, where the host tissue is infinitely compliant to the tumor progression. However, most tumors are developing within the confinement of a specific organ, where the confining environment, albeit not completely compliant, can evolve in response to the mechanical pressure from the tumor growth. The proposed tumor growth model may only be applicable within this time-dependent domain.

Using a novel diffuse-domain method [ *Li et. al., 2009. Solving PDEs in complex geometries: A diffuse domain approach, Commun. Math. Sci. 7, 81-107* ], we adapt our tumor growth model to an evolving domain through the weak form of the PDEs. The domain can be solved as a free-boundary problem on a Cartesian mesh, while appropriate boundary conditions are imposed on the domain boundary. We apply this approach to model the growth of lymphoma in a lymph node. The capsule of the lymph node constrains the movement of the lymphoma cells and the lymph fluid, which in turn causes the lymph node to swell. An angiogenesis model is also adapted to describe the neovasculature induced by the lymphoma tumor.