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Modeling growth and dissemination of lymphoma in a co-evolving lymph node: a diffuse-domain approach[1] YAO-LI CHUANG, VITTORIO CRISTINI, University of New Mexico, Dept. Pathology, YING CHEN, XIANGRONG LI, University of California, Irvine, Dept. Math, HERMANN FRIEBOES, University of Louisville, Dept. Bioengineering, JOHN LOWENGRUB, University of California, Irvine, Dept. Math — While partial differential equation models of tumor growth have successfully described various spatiotemporal phenomena observed for in-vitro tumor spheroid experiments, one challenge towards taking these models to further study in-vivo tumors is that instead of relatively static tissue culture with regular boundary conditions, in-vivo tumors are often confined in organ tissues that co-evolve with the tumor growth. Here we adopt a recently developed diffuse-domain method to account for the co-evolving domain boundaries, adapting our previous in-vitro tumor model for the development of lymphoma encapsulated in a lymph node, which may swell or shrink due to proliferation and dissemination of lymphoma cells and treatment by chemotherapy. We use the model to study the induced spatial heterogeneity, which may arise as an emerging phenomenon in experimental observations and model analysis. Spatial heterogeneity is believed to lead to tumor infiltration patterns and reduce the efficacy of chemotherapy, leaving residuals that cause cancer relapse after the treatment. Understanding the spatiotemporal evolution of in-vivo tumors can be an essential step towards more effective strategies of curing cancer.

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