Abstract Submitted
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Modeling Lymphoma Growth in an Evolving Lymph Node Using a Diffuse Domain Approach[1] YAO-LI CHUANG, University of New Mexico (Pathology), VITTORIO CRISTINI, University of New Mexico (Pathology, Chemical Engineering), YING CHEN, XIANGRONG LI, University of California, Irvine (Mathematics), HERMANN FRIEBOES, University of Louisville (Bioengineering), JOHN LOWENGRUB, University of California, Irvine (Mathematics, Biomedical Engineering, Chemical Engineering and Material Science) — Tumor growth often poses as a multiphase free-boundary problem as tumor cells aggregate into distinct subdomains due to differentiated cell-cell and cell-matrix adhesion. In "Three-dimensional multispecies nonlinear tumor growth - I Model and numerical method" [Wise et al., J. Theor. Biol. 253, pp. 524-543 (2008)], we have developed a multiphase Cahn-Hilliard model to study morphological patterns of tumor growth in a homogeneous open environment, and the results resembled in-vitro experiments. In living tissues, however, tumors are often confined in a closed environment of an organ, where the tissue geometry can also evolve in response to the pressure of tumor growth. Here we adapt our previous Cahn-Hilliard tumor growth model to an evolving geometry using a recently developed diffuse domain approach. We use the model to study the growth of lymphoma in a lymph node that swells during the process. An angiogenesis model for tumor-induced vasculature is also adapted to investigate substrate distribution and drug delivery within the lymph node.

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