

Abstract Submitted  
for the DFD11 Meeting of  
The American Physical Society

**Modeling tumor growth in a complex evolving confinement using a diffuse domain approach**<sup>1</sup> YAO-LI CHUANG, Pathology, Univ of New Mexico, JOHN LOWENGRUB, YING CHEN, XIANGRONG LI, Mathematics, Univ of California, Irvine, HERMANN FRIEBOES, Bioengineering, Univ of Louisville, VITTORIO CRISTINI, Pathology, Chemical Engineering, Univ of New Mexico — Understanding the spatiotemporal evolution of tumor growth represents an essential step towards engineering effective treatment for cancer patients. At the macroscopic scale, various biophysical models describing tumors as continuum fluids have been constructed, particularly on a Cartesian grid, where efficient numerical schemes are available to analyze the model for general tumor behaviors in a relatively unconfined space. For practical problems, however, tumors are often found in a confined sub-domain, which can even be dilated and distorted by the growing tumor within. To study such tumors, we adopt a novel diffuse domain approach that enables us to adapt a model to an evolving sub-domain and formulate the modified problem on a Cartesian grid to utilize existing numerical schemes. To demonstrate this approach, we adapt a diffuse-interface model presented in Wise et al. [2008, Three-dimensional multispecies nonlinear tumor growth - I Model and numerical method, *J. Theor. Biol.* 253, 524-543] to simulate lymphoma growth in a lymph node structure.

<sup>1</sup>Supported by NIH-PSOC grant 1U54CA143907-01.

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Date submitted: 15 Aug 2011

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