Incorporating Patient-Specific Imaging Data and Treatment Regimes to Predict the Response of Breast Cancer in the Neoadjuvant Setting

Stephanie L. Barnes, Matthew T. McKenna, David A. Hormuth, II, Jared A. Weis, Michael I. Miga, and Thomas E. Yankeelov

Purpose: To develop a multi-scale model of tumor growth that incorporates patient-specific, non-invasive imaging data coupled with treatment-specific efficacy and pharmacokinetic data to predict tumor response to treatment.
Methods: MRI and PET data sets have been acquired from a cohort of patients undergoing neoadjuvant treatment for breast cancer. Data sets were collected at three time points (once pre-treatment and at two times during the course of treatment) and thus provide patient-specific information regarding the cellular and molecular environment of the tumor. For example, the apparent diffusion coefficient derived from diffusion-weighted MRI provides an estimate of tumor cell density. Vascular parameters such as flow and permeability can be estimated by Ktrans from dynamic-contrast enhanced MRI. Additionally, 18F-fluorodeoxyglucose PET measurements provide estimates of glucose concentration and consumption. We have developed a system of coupled partial differential equations to describe tumor growth and treatment response with respect to tumor cell number and glucose concentration; these equations are populated with data that is obtained non-invasively from MRI and PET imaging protocols for each patient. Included with the imaging data is the treatment regimen for each patient (i.e., type, duration, and frequency). With this data, we are investigating the feasibility and utility of incorporating drug-specific in vitro efficacy data and in vivo pharmacokinetic data into our tumor growth model.
Results: Preliminary evaluations of the tumor growth model have shown that the reaction diffusion equation alone is insufficient to describe tumor behavior. Specifically, while overall tumor volume is represented with some accuracy, the heterogeneity of the tumor cell distribution is frequently lost. This work aims to evaluate whether regional cellular responses to individualized treatment regimens can be ascertained and incorporated within the current model. Such a framework will allow for an investigation of whether heterogeneous drug delivery and response can describe the observed tissue heterogeneity. Current work is focused on integrating patient-specific treatment data into the aforementioned tumor growth model.