Title: Biophysical Model of glioma growth constrained by in vivo imaging data.

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Background: Non-invasive imaging methods, particularly MRI and PET, have matured to the point where they can provide quantitative and 3D characterizations of, for example, blood blow, vessel permeability, blood volume, cellularity, hypoxia, metabolism, and cell proliferation. These measureable properties can be incorporated into realistic biophysical models of tumor growth that can potentially be used to predict tumor growth and therapy response on an individual basis. The tumor modeling literature has typically been limited to system of equations describing components that are measured by highly invasive methods (surgery, biopsy, or animal sacrifice) or within idealized (in vitro) systems. However, these models can be revised to incorporate non-invasive imaging data allowing for repeatable measurements of tumor properties as well as validation of predicted tumor growth. Towards this end, we have built a biophysical model of cell proliferation and angiogenesis that can be constrained almost entirely by co-registered PET and MR images of molecular, cellular, and physiological data which provide initial values of tumor characteristics to drive the model. Combining imaging data with models of tumor cell proliferation provides a “forecast” of predicted tumor growth that can be compared directly to experimentally observed tumor growth.

Methods & Results: MRI and PET data acquired from rats with C6 gliomas were employed to initialize a model consisting of two coupled partial differential equations describing the time dependent changes in tumor cell number and endothelial cell number. Changes in tumor cell number over time are due to the proliferation (determined from the delivery of nutrients) and random movement of tumor cells. Changes in endothelial cell number over time are due to angiogenesis (in response to a low nutrient to cell ratio) and regression (in response to vessel occlusion due to high cell density). The system is solved numerically using standard finite difference methods in Matlab. Preliminary results indicate the potential of the approach as predicted tumor characteristics generally correspond to those observed in vivo.

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