Finite element based numerical simulation of tumor brain

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ABSTRACT

INTRODUCTION: Glioblastoma is a primary brain neoplasm that is highly invasive. In order to increase treatment effectiveness it is important to quantitatively explore the interaction between tumor cells and the surrounding microenvironment. To this end, Swanson et al. [1] developed a proliferation-invasion-hypoxia-necrosis-angiogenesis (PIHNA) model. In the present study, the PIHNA model was numerically solved in order to develop a robust and computational efficient framework for patient-specific treatment.

METHODS: The model was discretized in the context of finite elements using the θ-method, and a fixed timestep was chosen for advancing the solution. To dynamically preserve the accuracy of the solution to the requirements of the simulation, an adaptive mesh refinement strategy was adopted. The scheme was tested against a two-dimensional square domain with an initial exponential concentration of normoxic cells located around the center of the square, $c=0.01 \cdot Exp(-100*(x^2+y^2))$, and a constant concentration of vasculature, v=0.01 (dimensionless). All other cell types assumed zero concentration initially. The total flux through the computational domain was set to zero, fixing thus the boundary conditions of the problem [2].

RESULTS: As expected, normoxic cells diffuse and proliferate as depicted by the PIHNA model: depending on the oxygen supply they convert to hypoxic initially and to necrotic finally. In Figure 1, the constant rate of diffusion and proliferation enabled normoxic cells to expand symmetrically from their initial state travelling through the domain. Due to the lack of oxygen (as prescribed by the chosen parameters), the domain was gradually occupied by necrotic cells. Figure 2 presents the dimensionless population of normoxic cells in terms of the total simulation time T.

DISCUSSION: A robust computational framework for the simulation of Glioblastoma can become a valuable tool for the prediction of tumor evolution on a patient-specific basis. To the authors' knowledge, this is the first numerical simulation of its kind in the context of finite elements.

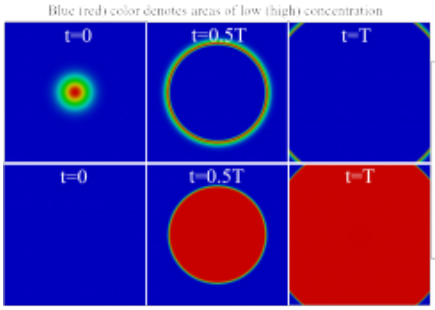

Figure 1: Top row: Normoxic cell concentration.
Bottom row: Necrotic cell concentration

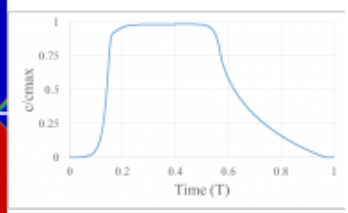

Figure 2: Dimensionless population of normoxic cells

References

[1] Swanson, K et al. *Cancer Res*, **71,** 7366-7375, 2011
[2] Anderson, ARA et al. *Bull Math Biol*, **60**, 857-900, 1998