Numerical Modeling of Tumor Growth using Solid Murine 3D Finite Element Model

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Abstract: This study presents the reconstruction and finite element (FE) modeling of three-dimensional murine solid tumor growth, integrating perfusion processes with real-time volumetric changes. Tumor geometries were reconstructed from DICOM images obtained from Houston Methodist Hospital at multiple time points (7–16 days), incorporating both vasculature and surrounding tissue. The 3D models were generated in CAD Field and Solid (CADFiS) software, defining independent solid tissue and capillary domains, material parameters, and flow boundary conditions, simulating the interstitial fluid transport and pressure distribution over a 20-day period using PAK solver. Results indicate progressive tumor expansion, with volume increases of ~30% by day 10 and over 200% by day 16 relative to the initial configuration. Pressure field analysis revealed spatial variations associated with tumor morphology and vascular structure. The developed approach demonstrates the capability of coupled solid–fluid FE modeling to predict tumor growth dynamics, offering a computational framework for future studies on tumor biomechanics, vascularization, and therapy response prediction.

Keywords: tumor growth, finite element analysis, lung cancer, 3D modeling, vascular perfusion

1. Introduction

Tumor growth process is characterized by a continuous and enormous deviation in the volume control mechanisms, which normally maintain a balance between the rate of cell proliferation and the rate of apoptosis (controlled cell death). Most of the tumors grow as solid masses of tissue; solid tumors have a distinct structure that mimics that of normal tissues and comprises two distinct but interdependent compartments: the parenchyma (neoplastic cells) and the stroma that the neoplastic cells induce and in

which they are dispersed [1]. Tumors, however, can only grow if their complex tissue environment provides them with a milieu that can sustain their growth and spread. During the last decades, there are numerous studies that have increased knowledge of intertumor heterogeneity, intratumor heterogeneity, and cancer evolution which has improved the understanding of anticancer treatment resistance [2-4]. However, there is a lack of studies that focus on finite element modeling of the tumor growth, especially a 3D finite element models, capable to couple perfusion process with real- time volumetric mass change of the initial tumor configuration. Therefore, the focal point of this study is the reconstruction of the tumor 3D model based on DICOM images, development of a 3D computational model and determination of the pressure field within the capillary domain of the tumor tissue as well as the growth rate in a defined time period.

2. Methodology and model generation

Computational procedure and FE model generation are initiated with reconstructing the 3 tumors, (both vasculature and surrounding tissue) from each group of the time steps (t=7 up to t=16 days), in order to calculate the volumes of each reconstructed tumor which will serve as a basis for calculating the average volumes of each time step (15%, 25%, 60% and 80% tumor models), from the DICOM images (images sent by the Houston Methodist hospital, Texas, USA) followed by exporting the obtained geometry in .stl file format (Figure 1). The described model is then imported in pre-processing CADFiS (Fields and Solids) software [5], selecting various options within the environment, including the appropriate CAD module, model geometry definition, material properties, time step configuration, and other parameters. Specific dialog interfaces facilitate the definition of geometrical parameters for independent solid tissue and large capillaries components, fluid flow parameters and boundary conditions, mesh generation, and material properties of the both solid and fluid domain. The FE model data are then exported as a *.dat file, which serves as the input for the PAK solver. Upon simulation completion, numerical results—such as velocity components (both scalar and vectorial), and pressure distributions—are stored in an output file with the *.unv extension, which is automatically imported into the CAD software for numerical results analysis.

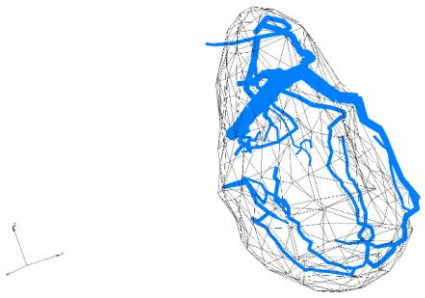

Figure 1. Reference configuration model. Finite element model with tissue part (wireframe) and immersed vasculature mesh (marked blue).

3. Results and Discussion

Our computational 3D model, generated in CAD Field and Solid software, contains 14 160 nodes, as well as 12 356 3D elements. Numerical simulation consists of 20 time steps, each lasting 1 day. For the purpose of modeling the transport within the model, we have used the following transport parameters: permeability of the tissue (cell fraction in our code) and vasculature are unitless, since they represent the fractions (parameters are interpolated from the imported tables). Capillary diameters are in μm, also interpolated from the imported tables. Filtration coefficient value is set to 1.57 × 10−3 μm/(Pa·s). Regarding the boundary conditions, pressures at the boundaries of the tumor are 0 mmHg, while within capillaries pressure is 10 mmHg (constant). Below are displayed pressure distribution fields (Figure 2), in the tissue domain, for 4 different time steps (7 days, 10 days, 13 days and 16 days). Tumor growth is notable, regarding the initial configuration, in the second displayed step (10 days) growth is around 30%, as well as in the last displayed step (16 days) where the volume of tumor is around 213 % larger than the initial tumor configuration (Figure 3).

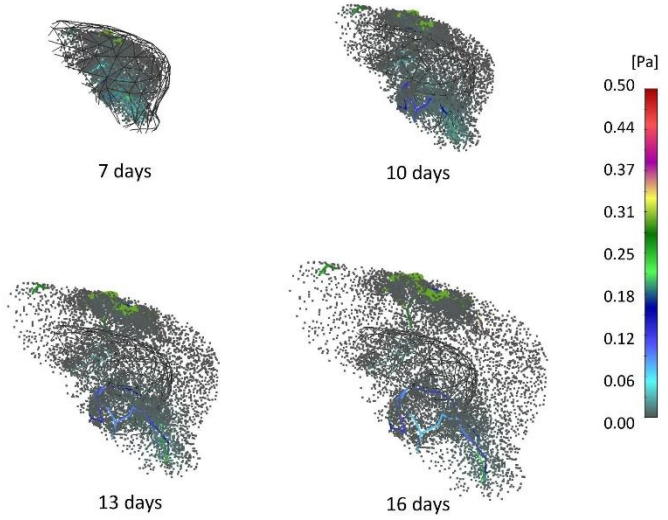

Figure 2. Pressure field within tissue domain for 4 different steps; dotted representation of half tumor growth model (initial mesh showed)

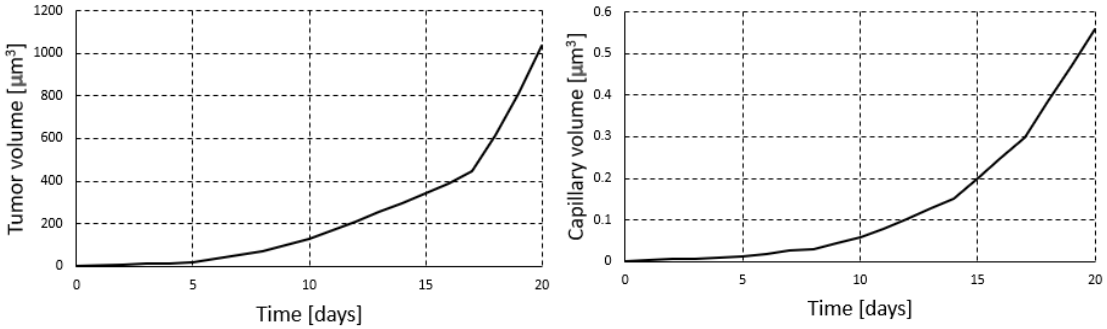

Figure 3. Tumor [left panel] and capillary mass volume [right panel] change during the 20-day period.

4. Conclusions

The presented 3D finite element model successfully integrates tumor geometry reconstruction with coupled solid–fluid simulations to capture the spatial and temporal dynamics of murine tumor growth. The approach provides quantitative insights into tumor volume expansion and pressure distribution, establishing a robust computational framework for studying tumor biomechanics and evaluating potential therapeutic strategies.

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