## **Accepted Manuscript**

A fully coupled space–time multiscale modeling framework for predicting tumor growth

Mohammad Mamunur Rahman, Yusheng Feng, Thomas E. Yankeelov, J. Tinsley Oden

Editors T.J.R. Haghes Austin, TX, USA J.E. Odan Austin, TX, USA
M. Papahistan Aham, Gassa Paunding Editors J.H. Argata' W. Pager'

PII:	S0045-7825(16)31249-X
DOI:	http://dx.doi.org/10.1016/j.cma.2017.03.021
Reference:	CMA 11378
To appear in:	Comput. Methods Appl. Mech. Engrg.
Received date :	1 October 2016
Revised date :	22 February 2017
Accepted date :	14 March 2017

Please cite this article as: M. Rahman, et al., A fully coupled space–time multiscale modeling framework for predicting tumor growth, *Comput. Methods Appl. Mech. Engrg.* (2017), http://dx.doi.org/10.1016/j.cma.2017.03.021

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

## A Fully Coupled Space-Time Multiscale Modeling Framework for Predicting Tumor Growth

Mohammad Mamunur Rahman<sup>1</sup>, Yusheng Feng<sup>1,\*</sup>, Thomas E. Yankeelov<sup>2,3,4,5</sup>, and J. Tinsley Oden<sup>2,3</sup>

## Abstract

Most biological systems encountered in living organisms involve highly complex heterogeneous multi-component structures that exhibit different physical, chemical, and biological behavior at different spatial and temporal scales. The development of predictive mathematical and computational models of multiscale events in such systems is a major challenge in contemporary computational biomechanics, particularly the development of models of growing tumors in humans. The aim of this study is to develop a general framework for tumor growth prediction by considering major biological events at tissue, cellular, and subcellular scales. The key to developing such multiscale models is how to bridge spatial and temporal scales that range from  $10^{-3}$  to  $10^{3}$  mm in space and from  $10^{-6}$  to  $10^{7}$  seconds in time. In this paper, a fully coupled space-time multiscale framework for modeling tumor growth is developed. The framework consists of a tissue scale model, a model of cellular activities, and a subcellular transduction signaling pathway model. The tissue, cellular, and subcellular models in this framework are solved using partial differential equations for tissue growth, agent-based model for cellular events, and ordinary differential equations for

Preprint submitted to Computer Methods in Applied Mechanics and EngineeringFebruary 21, 2017

<sup>\*</sup>Corresponding author

Email address: yusheng.feng@utsa.edu (Yusheng Feng)

<sup>&</sup>lt;sup>1</sup>Center for Simulation, Visualization and Real-Time Prediction, The University of Texas at San Antonio, One UTSA Circle, San Antonio, TX 78249

 $<sup>^{2}</sup>Center for Computational Oncology,$ 

<sup>&</sup>lt;sup>3</sup>Institute for Computational Engineering and Sciences,

<sup>&</sup>lt;sup>4</sup>Departments of Biomedical Engineering and Internal Medicine, The University of Texas at Austin, 201 East 24th St, Austin, TX 78712

<sup>&</sup>lt;sup>5</sup>Livestrong Cancer Institutes, 2201 E. Sixth St. Austin, TX 78702

Download English Version:

## https://daneshyari.com/en/article/4963882

Download Persian Version:

https://daneshyari.com/article/4963882

Daneshyari.com