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COMPUTATIONAL MODELS AND METHODS FOR PREDICTING CANCER PROGRESSION AND TREATMENT RESPONSE

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GUILLERMO LORENZO[1,3], RYAN WOODALL[2], DAVID A. HORMUTH II[3], MICHAEL R. A. ABDELMALIK[4], RUSSELL C. ROCKNE[2], ALESSANDRO REALI[1], THOMAS E. YANKEELOV[3], THOMAS J. R. HUGHES[3]

[1]Department of Civil Engineering and Architecture, University of Pavia
Via Ferrata 3, 27100 Pavia, Italy
Email: guillermo.lorenzo@unipv.it, alessandro.reali@unipv.it

[2]Department of Computational and Quantitative Medicine, City of Hope
1500 East Duarte Road, Duarte, CA 91010, USA
E-mail: rrockne@coh.org, rwoodall@coh.org

[3]Oden Institute for Computational Engineering and Sciences, The University of Texas at Austin
201 E. 24th Street, Austin, TX 78712-1229, USA
Email: david.hormuth@utexas.edu, thomas.yankeelov@utexas.edu, hughes@oden.utexas.edu

[4]Department of Mechanical Engineering, Eindhoven University of Technology
Groene Loper 15, 5612 AE Eindhoven, The Netherlands.
Email: m.abdel.malik@tue.nl

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ABSTRACT

Cancers are highly heterogeneous diseases that involve diverse biological mechanisms, interacting and evolving at various spatial and temporal scales. Multiple experimental, histopathological, clinical, and imaging methods provide a means to characterize the heterogeneous and multiscale nature of these diseases by providing a wealth of temporally and spatially resolved data on their development and response to therapies (e.g., cancer architecture, mechanics, and vascularity; cancer cell mobility and proliferation; drug transport and effects). These multimodal, multiscale datasets can be exploited to constrain biophysical models of cancer growth and treatment response both in preclinical and clinical settings. These models can then be leveraged to test hypotheses, produce individualized cancer forecasts to guide clinical decision-making, and, ultimately, to design optimized therapies. The overall goal of this minisymposium is to provide a forum to present and discuss recent developments in data-informed computational models and methods for predicting cancer growth and treatment response, with special focus on the following research areas: (i) biology-based mechanistic models of cancer growth and treatment *in vitro* and *in vivo*; (ii) computational methods for model initialization, parameterization, and patient-specific simulation; (iii) model-oriented, personalized optimization of treatment regimens; (iv) uncertainty quantification and model selection methods; (v) hybrid strategies combining machine learning and mechanistic modelling; and (vi) digital twins in clinical oncology.

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