Special Issue on
In Silico Oncology: Computational Modeling Approaches Targeting Clinical Application in Cancer

CALL FOR PAPERS

Computational modelling has been proved to be a powerful tool for studying and understanding the complexity arising from the various phases and scales of cancer, as well as the effect of tumor heterogeneity, clonal evolution, and the microenvironment on drug therapy. Computational modelling approaches have provided valuable insights into the underlying mechanisms of cancer evolution, drug delivery, and therapy response fostering the development of new drug and therapeutic strategies. However, most of the approaches in computational oncology miss specificity and predictive power that is important in translational oncology and clinical settings. Most of these efforts have been hampered due to the insufficient data/physiological parameters available in routine examinations. As a consequence, the validation efforts of the available cancer models have been rather limited by insufficient data-sharing, limited confidence from the clinicians, and, critically, intrinsic constraints of the models themselves dealing with hundreds of model parameters that are roughly estimated or taken for granted as theoretical values based on bibliography. Such approaches, however, are far from being rigorous and often cause instability flaws leading to inaccurate generalizations that may be misleading in a way to discourage wider clinical adoption.

Future approaches should be able to produce concrete clinically exploitable results that could potentially support the clinician in the process of selecting the most appropriate treatment scheme for each individual patient. This will be achieved by bringing together state-of-the-art computational models, genetic tools, and cutting-edge imaging modalities to significantly increase the reliability of the proposed models and efficiently monitor tumor growth and treatment outcome. We invite investigators to submit original research articles and reviews to this special issue demonstrating the benefits of the use of computer-based cancer models in the clinical environment.

Potential topics include but are not limited to the following:

- Recent developments in the understanding the complex phenomenon of cancer: the role of microenvironment and the importance of inter- and intratumor heterogeneity on tumor evolution and therapy efficacy
- Cell-based modeling approaches: influence of cell population characteristics (genotype-phenotype relations) for the prediction of cancer outcome
- Multiscale modeling approaches: from cellular to tissue scale
- Systems medicine approaches tailored for both research and clinical directions towards more effective cancer therapies
- Model validation based on preclinical imaging of patient-derived xenografts and clinical imaging of well-phenotyped patient cohorts
- *In vivo/in vitro* laboratory experiments for tumor growth and drug screening constructed to provide the mathematical models important parameter values: screening to test possible therapeutic modalities in monolayers/3D cultured cancer cells and sequencing tools of the individual patient genetic background
- Cutting-edge molecular imaging modalities to enhance the modelling accuracy and predictive value for clinical decision support
- Novel advanced imaging techniques for developing and assessing state-of-the-art computer modelling tools enabling personalized cancer prediction and treatment planning

Authors can submit their manuscripts through the Manuscript Tracking System at http://mts.hindawi.com/submit/journals/cmmm/iso/.

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