

COMPUTATIONAL MODELS FOR CANCER RESEARCH AND ONCOLOGY

TRACK NUMBER 300 - BIOMECHANICS AND MECHANOBIOLOGY

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Keywords: computational oncology, cancer forecasting, mechanistic modeling, machine learning, inverse problems, model calibration, uncertainty quantification, model selection, optimal control theory, digital twins

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 cancer development and response to therapies. These multimodal, multiscale datasets can be exploited to constrain data-driven and biophysical models of cancer dynamics in preclinical and clinical settings [1-3]. These models can then be used to test biological and clinical hypotheses, produce individualized predictions to guide clinical decision-making, and, ultimately, to design optimized monitoring and treatment plans.

The overall goal of this minisymposium is to present and discuss recent developments in computational models and methods for predicting cancer progression and treatment response, with special focus on the following 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) personalized optimization of monitoring plans and treatment regimens; (iv) uncertainty quantification and model selection methods; (v) hybrid strategies combining machine learning and mechanistic modelling; and (vi) digital twins in cancer research and clinical oncology.

REFERENCES

- [1] G. Lorenzo, *et al.* (2024). Patient-specific, mechanistic models of tumor growth incorporating artificial intelligence and big data. *Annu. Rev. Biomed. Eng.*, **26**(1), 529-560.
- [2] N. Cogno, *et al.* (2024). "Agent-based modeling in cancer biomedicine: applications and tools for calibration and validation", *Cancer. Biol. Ther.*, **25**, 1.
- [3] M. Alber, *et al.* (2019). Integrating machine learning and multiscale modelling - perspectives, challenges, and opportunities in the biological, biomedical, and behavioral sciences. *npj Digit. Med.*, **2**, 115.