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SIMULATING CANCER DEVELOPMENT USING A HYBRID AGENT-/CONTINUUM-BASED MODELLING APPROACH

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Keywords: *Tumour Growth, Hybrid model, Agent-continuum based, Computing Methods* Mathematical and computational models have become a powerful tool to bridge the gap between the theoretical knowledge on cancer and clinical applications. In particular, they enable the combination of various aspects of information into a coherent and unified framework, which facilitates the assessment of hypotheses, and can give rise to experimentally verifiable predictions.

In recent years, agent-based computer models have been extensively applied for a large range of biological topics. They enable the simulation of complex biological processes, including cell-cell interactions and genetic dynamics. However, simulating autonomous agents gives rise to considerable demands in computer resources, especially for large scale models where millions of agents coexist. Continuum models on the other hand are well-suited to perform equation-based simulations and are overall more efficient. However, they are more challenging to model independent cell behaviour.

Combining both modelling approaches would greatly benefit simulation efficiency and verisimilitude. Here, we present an approach that exploits a combination of the agent based platform BioDynaMo and the continuum model FEB3. In particular, we implemented an open source and modular interface to achieve a high performance multi-scale model of tumour growth. BioDynaMo models cell growth and cell division in 3D space, and FEB3S accounts for the macroscopic dynamics involving substance diffusion and interactions with macroscopic blood vessels. More concretely, we apply this approach to computationally model coupled growth in a cubic domain, and heterogeneous tumour growth and proliferation, which demonstrates the combined power of the model.

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