Approaches to modelling heterogeneity in solid tumour growth

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Biological tissues, including solid tumours, are highly complex, containing multiple cell types, tissue matrix and blood vessels. They are characterised by multiple types of heterogeneity, that operate on space and time scales ranging from the subcellular to the tissue scale and from seconds to months or years. In this series of lectures, we will consider three mathematical approaches that have been used to model different aspects of heterogeneity associated with solid tumour growth. First, we will consider multiphase models, based on mixture theory, that provide a coarse-grained, macroscale description of a tumour's size and composition consistent with imaging modalities such as MRI. Secondly, we will consider structured models that have been used to account for phenotypic heterogeneity within specific cell populations (eg the progression of cancer cells from stem-like to fully differentiated, and the transition of pro-inflammatory, phagocytic, M1-like macrophages to anti-inflammatory M2-like macrophages) that can be captured by single-cell RNA sequencing data. Finally, we will consider multiscale, computational models that permit investigation of the interplay between subcellular, cellular and tissue scale process and are consistent with more detailed spatial transcriptomics datasets. In so doing, I aim to explain the complementary insight that multiscale, multiphase and structured models can provide and also to discuss the challenges associated with validating such models against experimental data.