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**Computational and Mathematical Approaches in Cancer Modelling
and Treatment Prediction**

Abstract

Each individual cancer cell within a cancer cell mass is unique, with its own internal cellular pathways and biochemical interactions. These interactions contribute to the functional changes at the cellular and tissue scale, creating a heterogeneous cancer cell population. Multiscale mathematical models incorporating such complex interactions can help in studying cancer progression and serve as an in silico test base for comparing and optimising various multi-modality anticancer treatment protocols such as chemotherapy and radiation therapy. In this talk, I will consider a hybrid individual cell-based mathematical and computational model, incorporating single-cell based intracellular dynamics, the cell microenvironment and cell-cell interactions to study the growth and progression of cancer cell mass. The model will be then used to study cell-cycle-based tumour heterogeneity and analyse how it contributes to the potential chemotherapeutic drug resistance within a heterogeneous tumour.