Sara Hamis (Swansea)

Predicting *in vivo* treatment responses using an *in vitro*-calibrated mathematical model

Abstract

Mathematical models, and their corresponding in silico experiments, can be used to simulate both in vitro and in vivo tumour scenarios. However, the microenvironment in an in vitro cell culture is significantly different from the microenvironment in a solid tumour and many details that influence tumour dynamics differ between in vitro and in vivo settings. These details include cell proliferation, oxygen distribution and drug delivery. It follows that translating quantitative in vitro findings to in vivo predictions is not straightforward.

In this talk I will present an individual based mathematical cancer model in which one individual corresponds to one cancer cell. This model is governed by a few observable and well-documented principles, or rules. To account for differences between in vitro and in vivo scenarios, these rules can be appropriately adjusted. By only adjusting the rules (whilst keeping the fundamental framework intact), the mathematical model can first be calibrated by in vitro data and thereafter be used to successfully predict treatment responses in mouse xenografts in vivo.