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Stochastic multi-scale models of cell population with age-structured

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Many biomedical problems fit within population dynamics: The competition between normal and malignant cells in cancer for space and resources; The interaction between the cells of the immune system and infected cells in viral infections; Evolution of drug resistance.

The aim of this work is to illustrate how concepts and techniques from mathematical population dynamics can be used to address and shed some light on a number of issues relevant in different biomedical contexts.

In order to formulate our stochastic model of the intracellular scale, in particular, the coupling between extra-cellular oxygen levels and progression through the cell-cycle, we will reformulate our model as a Markov process in terms of a Master Equation. The resulting model, a continuity equation for a multi-dimensional probability density.

A mathematical model of a population composed by different types of individuals keeps track of the evolution in time and space of the number or density of each one of the species as a function of a number of parameters: birth and death rates, metabolic rates, mutation rates, etc.