Towards optimisation of cancer therapeutics by taking into account patient-specific constraints: mathematical models for individualised medicine

Jean Clairambault
INRIA Paris-Rocquencourt, France
(e-mail: jean.clairambault@inria.fr)

Abstract- In this talk, I will present some physiologically based dynamic mathematical methods that are currently being designed to help optimise multidrug, multitarget anticancer treatment. These methods include:
a) Modelling by ordinary differential equations (ODEs) drug kinetics and metabolism in blood and the liver, and at the intracellular level, account being taken of enzymatic genetic polymorphism, of toxic side effects on healthy cells, and on the possible occurrence of resistances to the treatment.
b) Modelling by age-structured partial differential equations (PDEs) the proliferation of cell populations represented by the evolution of these populations, healthy and tumoral, in the cell division cycle and the controlling effect of anticancer drugs on this evolution.
c) Using optimisation algorithms that aim at finding best drug delivery time schedules by maximising tumour cell kill under patient-linked constraints, that can be general state of health-linked treatment tolerability, genetic polymorphism of drug metabolising and DNA mismatch repair enzymes, and the expression of ABC transporters.