PREDNÁŠKY Z BIOMATEMATIKY

28.06.2023 10:00 (10:45) P08 ÚMAT UPJŠ Jesenná 5, Košice

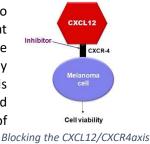
Prof. Roumen Anguelov

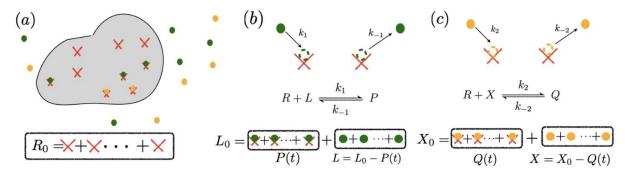
(Department of Mathematics and Applied Mathematics, University of Pretoria, South Africa)

"Dynamical systems modelling approach to quantitative analysis of biological experimental data"

We propose the study of experimental data through the lenses of a mathematical model depicting the underlying biological processes. This process begins with representing in mathematical terms the causal

relationships, which are explored in the experimental work with regard to achieving a specific goal. In this sense, this approach is fundamentally different from the more common approach of conducting experiments and subjecting the obtained data to a statistical analysis. The method is exemplified through assay data obtained from the study of inhibition of the CXCL12/CXCR4 activation axis for the melanoma cells. The existing knowledge on how the activation and inhibition work is embedded into a dynamical system represented as a set of differential equations.





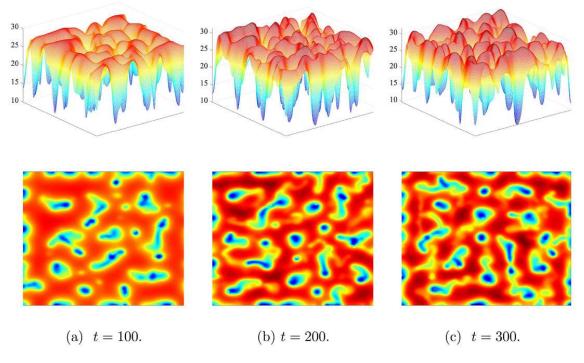
Kinetics: docking places (Red), activating molecules (green) and inhibiting molecules (yellow) (a). Sensors (docking places) on a cancer cell (b) & (c) Chemical reactions along with the relationship between dynamic and static quantities.

Prof. Michael Chapwanya

(Department of Mathematics and Applied Mathematics, University of Pretoria, South Africa)

"Boom-and-bust dynamics in microbial populations under environmental stress"

The physiological structure of microbial communities in natural environments is typically a response to changes in internal and external conditions. External conditions may include the availability of nutrients, and the presence of inhibiting or toxic substances while internal conditions may include cell to cell interactions. In this work, we propose a model for the growth of microbial populations in the presence of environmental stress, present and explore the dynamics of a reaction diffusion model with a quiescent stage that captures the spatio-temporal evolution of a bacterial colony.



Snapshots of microbial density for model system at different time frames