Structured Population Models: Direct and Inverse Problems

Jorge P. Zubelli[1], Anna Marciniak-Czochra[2], Benoît Perthame Perthame[3]

and Marie Doumic-Jauffret[4]

[1]IMPA, Rio de Janeiro, Brasi
[2]Institute of Applied Mathematics, University of Heidelberg
[3]Laboratoire J.-L. Lions, Univ. Pierre et Marie Curie, Institut Universitaire de France and INRIA
[4]INRIA Rocquencourt and Jacques-Louis Lions Laboratory, Univ. ParisVI

[1]zubelli@gmail.com, [2]Anna.Marciniak@iwr.uni-heidelberg.de
[3]benoit.perthame@upmc.fr, [4]marie.doumic-jauffret@inria.fr

Structured population models in biology lead to integro-differential equations that describe the evolution in time of the population density taking into account a given feature such as the age, the size, or the volume. These models possess interesting analytic properties and have been used extensively in a number of areas.

After giving an introduction to this subject, we will discuss the inverse problem. In this part, we consider a size-structured model for cell division and address the question of determining the division (birth) rate from the measured stable size distribution of the population. We formulate such question as an inverse problem for an integro-differential equation posed on the half line. We develop firstly a regular dependency theory for the solution in terms of the coefficients and, secondly, a regularization technique for tackling this inverse problem which takes into account the specific nature of the equation. Our results rely also on generalized relative entropy estimates and related Poincare inequalities. This second part is joint work with Benoit Perthame (UPMC, Paris) and Marie Doumic (ENS and INRIA, Paris).

Finally, if time allows, we will discuss novel applications to stem cell modelling. In this part we study different mathematical aspects of a continuous model of stem cell developments.