

Structured Models for Cell Populations: Direct and Inverse Problems.
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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 a short 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. Finally, we will discuss real data reconstructions with *E. Coli* data. This is joint work with Marie Doumic (INRIA, Paris), Pedro Maia (UW, USA) and Benoit Perthame (UPMC, Paris).