

Transport phenomena in mathematical biology

The primary objective of the current project is the mathematical analysis of partial differential equations arising from various biological studies. One could distinguish two main branches of research in this field. On the one hand, voluminous literature deals with parabolic equations. On the other hand, an abundance of models is formulated using transport equations, hence of hyperbolic type.

The problems that we aim at in the current project will mostly involve hyperbolic equations, however we shall also deal with some parabolic (or hyperbolic-parabolic) problems. In particular we will consider mathematical models of structured populations, collective dynamics and tissue growth. These models are of essential interest in mathematical biology, with applications in the study of cell growth and division, polymerization, cell saturation or prion proliferation.

The mathematical tools we shall employ and further develop are some of the most modern tools of mathematical analysis. Indeed, the problems of mathematical biology considered in this project benefit considerably from applying the analytic techniques developed within the field of mathematical physics, where an isolated system can be described as a system of conservation laws. Many of the techniques used primarily in the study of those conservation laws of continuum mechanics can be, after appropriate modifications, successfully applied to the related balance laws of mathematical biology. As a notable example, one can think of the classical relative entropy method of Dafermos, which has been adapted to the systems of mathematical biology by Perthame and his collaborators, not twenty years ago. We plan on further developing this *generalized relative entropy* method, and to extend it to *measure solutions* of structured population models and collective behaviour models.

Among other research goals we shall study are the problems of existence, regularity and uniqueness of solutions to reaction-diffusion systems modelling tissue growth, long-time asymptotics for measure solutions of structured populations, and perturbations of structured population models.

We expect the results of the project to be twofold. On the one hand, we expect to contribute to the field of mathematical biology by providing a detailed analysis of the basic problems (existence, uniqueness, regularity, convergence of numerical methods) for the models of tissue growth, which have well-established applications in the modeling of cancer. Further, the question of long-time asymptotics for structured population models is one of the classical problems of mathematical biology. Due to an increased interest in measure solutions for such models, the extension of the long-time asymptotics studies to the measure setting seems of great value. On the other hand, to obtain these results one will have to foster new ideas and mathematical techniques, which might be of wider scientific interest. Furthermore, our studies on perturbations in structured population models is expected to be of value in the field of optimal control as well as numerical analysis.

The current project can therefore make impact on various fields, ranging from applied mathematics through medicine to food and health industries.