Mathematical models for cell motion. Parabolic and kinetic systems

Benoît Perthame

Laboratoire J.-L. Lions, Univ. Pierre et Marie Curie

Institut Universitaire de France and INRIA

benoit.perthame@upmc.fr

Several partial differential equations (transport-diffusion, kinetic) systems have been proposed to model cell motion and self organization. A typical question is to explain the fundamental biophysical processes behind the various patterns of bacterial colonies that one can observe.

A first modelling ingredient is to take into account only brownian motion of cells and growth of the colony by a nutrient which is consumed. The systems proposed by Kessler-Levine or by Mimura *et al* are seemingly simple coupled reaction-diffusion equations. However they are typical examples of unstable systems leading to digitation.

A second modelling ingredient is to include chemotaxis (motion of bacterias or amebia interacting through a chemical signal) and leads to the so-called Keller-Segel Fokker-Planck type equation. This system describes the evolution of a density of cells coupled with the evolution equation for a chemical substance through a nonlinear transport term depending on the gradient of the chemoattracting substance. Such systems are successful in recovering various qualitative behaviors as high concentrations.

We will present these models, their main mathematical properties (quantitative and qualitative), numerical simulations. We will also explain the motivations for introducing other models. For instance we will present several hyperbolic models that have been proposed recently. For bacteria E. Coli, we will give a microscopic picture based on a kinetic modelling of the inetraction (nonlinear scattering equation).