

Equation-assisted computations for a velocity-jump process for bacterial chemotaxis

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[joint work with Mathias Rousset]

We consider a fine-scale model for bacterial chemotaxis subject to a chemoattractant field, in which individual bacteria evolve according to a velocity-jump process. The bacteria move at constant speed and change direction at a discrete set of jump times. The Poisson arrival rate of the jump times is affected by the internal state of the bacterium, which reflects the evolution of the chemoattractant field along the path. Due to this dependency on internal state, the derivation of a closed coarse-scale advection-diffusion equation for the bacterial density can only be done in the hydrodynamic limit of vanishing bacterial velocity. We construct a coarse time-stepper for the bacterial density with finite velocity as a three-step procedure: (1) lifting, i.e. creation of bacterial positions, velocities and internal states, consistent with the density; (2) fine-scale evolution; and (3) restriction, i.e. computation of bacterial density. We define a velocity-jump process that corresponds exactly to the hydrodynamic limit equation, and couple the two stochastic processes to reduce the variance. We provide a theoretical result on the resulting variance reduction, and give numerical illustrations. We will also briefly touch upon the relation between the lifting operator and the simulated coarse-scale model.