Symmetry Breaking Bacterial Motility

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I will introduce models for two distinct types of bacteria movement, the actin-based motility of Listeria monocytogenes and the gliding motion of Flavobacterium johnsoniae. The physical mechanism for these two different bacteria are very different but bifurcations that break the symmetries are essential in both systems.

A Listeria bacterium moves in the host cell by hijacking the actin polymerization machinary with its special surface protein. Interestingly the motion of Listeria in a quasi two-dimensional environment shows geometrical trajectories ranging from straight lines, circles, S-shape curves, figure eights, etc. With a simple Landau-type model I will show that these trajectories are results of bifurcations in the distribution of actin filaments and force density on the Listeria surface.

On the other hand, a Flavobacterium johnsoniae moves on a substrate by processive adhesive proteins which are distributed in a close-loop track. Even in a homogeneous medium, the bacterium nevertheless breaks the front-rear symmetry and shows directional movement. I will show that at sufficiently high adhesive protein speed, the distribution of closed bonds between the proteins and the substrate has a bifurction that leads to a directional movement for the bacterium. Such mechanism has the advantage that the bacterium can tune the adhesive protein speed to detect small gradient of nutrient or toxin in the environment.