Fritz-Haber-Institut der Max-Planck-Gesellschaft, Humboldt-Universität zu Berlin, Max-Delbrück-Centrum für Molekulare Medizin, Otto-von-Guericke-Universität Magdeburg, Physikalisch-Technische Bundesanstalt, Technische Universität Berlin, Universität Potsdam

Berlin Center for Studies of Complex Chemical Systems

Seminar

Complex Nonlinear Processes in Chemistry and Biology

Honorary Chairman: G. Ertl
Organizers: M. Bär, C. Beta, H. Engel, M. Falcke, M. J. B. Hauser, J. Kurths, A. S. Mikhailov, P. Plath, L. Schimansky-Geier, and H. Stark

Tuesday, May 31, 2016, at 10:00
Address: Universität Potsdam, Institut für Physik und Astronomie, Karl-Liebknecht-Str. 24/25, 14476 Potsdam-Golm, Haus 28, Room: 1.001

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Motility of Escherichia coli and Trypanosoma cruzi in confined systems: Experiments and mathematical modeling

Bacterial migration through confined spaces is critical for several phenomena like biofilm formation, bacterial transport in soils, and bacterial therapy against cancer. In the present work, Escherichia coli (strain K12-MG1655 WT) motility was characterized by recording and analyzing individual bacterium trajectories in a simulated quasi-two-dimensional porous medium. The porous medium was simulated by enclosing, between slide and cover slip, a bacterial-culture sample mixed with uniform 2.98 microns spherical latex particles. The colloidal particles are trapped between the two glass plates in a disordered configuration, and the cells are able to swim through the porous media. The porosity of the medium was controlled by changing the latex particle concentration. By statistically analyzing trajectory parameters like: instantaneous velocity and turn angle, as well as mean squared displacement, we were able to quantify the effects that different latex particle concentrations have upon bacterial motility. To better understand our results, bacterial trajectories were simulated by means of a phenomenological random-walk model (developed ad hoc), and the simulated results were compared with the experimental ones.

In addition, we characterized the motility of parasite Trypanosoma cruzi in its epimastigote form in a quasi-two-dimensional geometry, which was built with two glass surfaces separated with 10 microns diameter latex particles. We recorded the trajectories of two strains of this parasite (a wild-type strain and a stable transfected strain, which contains an ectopic copy of LYT1 gene and whose motility is known to be affected). We further extracted parasite trajectories from the recorded videos, and statistically analysed the following trajectory-step features: step length, angular change of direction, longitudinal and transverse displacement with respect to the previous step, and mean squared displacement. Based on the resulting observations, we developed a mathematical model to simulate parasite trajectories. The fact that the model predictions closely match most of the experimentally observed parasite-trajectory characteristics, allows us to conclude that the model is an accurate description of T. cruzi motility.