# DY 9: Statistical physics in biological systems

Time: Monday 16:30–18:00 Location: H3

DY 9.1 Mon 16:30 H3

**Anomalous diffusion of migrating biological cells** — Peter Dieterich[1], •Rainer Klages[2], Roland Preuss[3], and Albrecht Schwab[4] — [1]Institut für Physiologie, Medizinische Fakultät Carl Gustav Carus, Dresden, Germany — [2]School of Mathematical Sciences, Queen Mary, University of London, UK — [3]Center for Interdisciplinary Plasma Science, Max-Planck-Institut für Plasmaphysik, Garching, Germany — [4]Institut für Physiologie II, Münster, Germany

Cell migration is a complex dynamical process resulting from an intricate interplay of multiple components of the cellular migration machinery. Our work starts from the experimental observation of single cells moving on substrates. At first view, their paths look like the ones of Brownian particles. However, a detailed data analysis reveals a superdiffusive increase of the long-time mean squared displacement, non-Gaussian probability distributions for the cell positions and power law decays of velocity autocorrelations. This dynamics includes intermittent features resembling the one of foraging animals. On long time scales, all of our experimental data matches to a modeling of anomalous diffusion in terms of a fractional Klein-Kramers equation.

DY 9.2 Mon 16:45 H3

**Meanfield dynamics of evolutionary and coevolutionary processes in infinite populations and finite-size corrections in finite populations** — Arne Traulsen[1], •Jens Christian Claussen[2], and Christoph Hauert[1] — [1]Center for Evolutionary Dynamics, Harvard — [2]Institut f. Theoret. Physik & Astrophys., Univ. Kiel, Germany

Coevolutionary dynamics arises in a wide range from biological to social dynamical systems. For infinite populations, a standard approach to analyze the dynamics are deterministic replicator equations, however lacking a systematic derivation. In finite populations modelling finite-size stochasticity by Gaussian noise is not in general warranted [1]. We show that for the evolutionary Moran process and a Local update process, the explicit limit of infinite populations leads to the adjusted or the standard replicator dynamics, respectively [2]. In addition, the first-order corrections in the population size are given by the finite-size update stochasticity and can be derived as a generalized diffusion term of a Fokker-Planck equation [2]. We explicitely discuss the differences for the Prisoner's Dilemma, and Dawkin's Battle of the Sexes, where we show that the stochastic update fluctuations in the Moran process exhibit a finite-size dependent drift reversal [2]. This framework can be readily transferred to other microscopic processes, as the local Fermi process [3] or the inclusion of mutations [4].

[1] J.C.Claussen & A.Traulsen, Phys.Rev. E 71, 025101(R) (2005) [2] A.Traulsen, J.C.Claussen, C.Hauert, Phys.Rev.Lett, 95, 238701 [3] A.Traulsen, M.A.Nowak, J.M.Pacheco, Phys.Rev.E 74, 011909 (2006) [4] A.Traulsen, J.C.Claussen, C.Hauert, Phys.Rev. E 74, 011901 (2006)

DY 9.3 Mon 17:00 H3

**Pattern Formation and Collective Motion in Bacterial Colonies** — •Pawel Romanczuk[1], Udo Erdmann[2], Harald Engel[3], and Lutz Schimansky-Geier[1] — [1]Humboldt Universität zu Berlin, Newtonstr. 15, 12489 Berlin — [2]Helmholtz-Gemeinschaft, Anna-Louisa-Karsch-Str. 2, 10178 Berlin — [3]Technische Universität Berlin, Hardenbergstr. 36, 10623 Berlin

Complex spatio-temporal patterns of cell clusters were observed in colonies of chemotactic bacteria such as *Escherichia coli* or *Sallmonella typhimurium* [1]. The production of a potent chemoattractor by the bacteria themselves as a reaction to certain nutrients is the essential factor for this pattern formation. Additional collective dynamics, such as collective translocation and rotation of bacterial clusters were reported from experiments on bacterial colonies.

We are able to reproduce the macroscopic behaviour, as well as the collective types of motion using Active Brownian particles including chemotaxis and velocity alignment.

We compare analytical results for macroscopic pattern formation obtained from the overdamped limit approximation with numerical simulations and discuss the collective dynamics of our model. Further on we propose a simple explanation for the occurrence of different collective types of motion in bacterial colonies.

[1] Budrene, E. O. und H. C. Berg: *Dynamics of formation of symmetrical patterns by chemotactic bacteria.* Nature, 376:49-53, 1995.

DY 9.4 Mon 17:15 H3

**Non-equilibrium phenomena in rod-shaped self-propelled particles** — •Fernando Peruani[1,2], Andreas Deutsch[1], and Markus Baer[3] — [1]Technische Universitaet Dresden, Dresden, Germany — [2]Max Planck for the Physics of Complex Systems, Dresden, Germany — [3]Physikalisch-Technische Bundesanstalt, Berlin, Germany

Motivated by orientation and aggregation phenomena in gliding bacteria, we study collective motion in a twodimensional model of active, self-propelled rods interacting through volume exclusion. In simulations with individual particles, we find that particle clustering is facilitated by a sufficiently large packing fraction or length-to-width ratio. The transition to clustering in simulations is well captured by a mean-field model for the cluster size distribution, which predicts that critical value of the aspect ratio is given by C/Eta - 1 where C is a constant and Eta is the packing fraction [1].

In order to study orientational order in more detail, we simplify the above model by considering self-propelled point-like particles interacting through a liquid crystal-based alignment mechanism. We provide numerical evidence that such a system exhibits a continuous phase transition and long-range orientation order. The results are qualitative in line with prediction of a simple mean-field theory.

[1] F. Peruani, A. Deutsch and M. Bär, Phys. Rev. E, 74, 030904 (2006) (R)

DY 9.5 Mon 17:30 H3

**The role of heterogeneity in the dynamics of infectious diseases** — •Alejandro Morales Gallardo, Dirk Brockmann, and Theo Geisel — MPI for Dynamics and Self-organization, Göttingen, Germany

Most sexually transmitted diseases cannot be understood without the strong variability of sexual activity within human populations. Furthermore, emergent infectious diseases such as SARS showed that social heterogeneities play a vital role in the spread and prevalence of some diseases. It is commonly believed that inhomogeneities, for instance the existence of superspreaders can lead to a larger basic reproduction number $R_0$. We examined the role of heterogeneities in a SIS model with variable contact rates. The time between infections as well as the time of being infectious are considered as Poisson processes. The heterogeneity is introduced by variable individual contact rates. Our results show that the degree of fluctuation increases as a function of contact rate variability around the SIS endemic state. Moreover, fluctuations tend to be asymmetric in strongly heterogeneous systems. Although heterogeneities lead to more explosive outbreaks, the number of infected individuals in the endemic state is smaller than predicted for homogeneous populations. Both results indicate that epidemiological data could be misleading when estimating the basic reproduction number $R_0$, a key epidemiological parameter, and in consequence erroneous measures would be adopted in diseases where heterogeneities dominate.

DY 9.6 Mon 17:45 H3

**The role of commuting in spread of infectious diseases** — •Vitaly Belik and Dirk Brockmann — MPI für Dynamik und Selbstorganisation, Göttingen, FRG

Numerous spreading phenomena in population dynamic and ecological systems are successfully accounted for by the Fischer-Kolmogorov-Petrovsky-Piskunov (FKPP) equation. This equation can be derived on the assumption of diffusive dispersal of the reacting species. In epidemiological systems however, host individuals often perform commuting movements between their habitat and its surrounding. For instance, humans travel back and forth between their homes and their place of work day by day, and infectious diseases spread indirectly by a combination of transmission between and commuting of host individuals. Incorporating bidirectional transport of the host we develop a mean field discription for wave propagation that is structurally different from the ordinary FKPP equation, i.e. the diffusion and nonlinear logistic growth term do not decouple. We find that the velocity of the wave front is approximately proportional to the infection rate, unlike the square root dependence of the ordinary FKPP equation. For systems with high reaction rates, this implies a much faster spread of

the infection as compared to common FKPP dynamics. On the other hand, the front shape exhibits a significantly smaller dependence on the infection rate. We conclude that spreading phenomena which are triggered by commuting movements of the host can spread much faster than those carried by diffusing agents, a result of particular importance for human infectious disease dynamics.