BP 7: Posters: Statistical Physics in Biological Systems

Time: Monday 17:15–20:00   Location: P3

BP 7.1   Mon 17:15   P3
Boundary-induced polarity of random intra-cellular filament networks and vesicle agglomerations — ●Philip Greulich[1] and Ludger Santen[2] — [1]University of Edinburgh, Edinburgh, UK — [2]Universität des Saarlandes, Saarbrücken

The distribution of nutrients and metabolic products within cells is crucial for cell function. It is performed by active directed transport of vesicles along polarized intracellular filaments, mediated by motor proteins.

We present a model that captures basic features of active vesicle transport on randomly evolving filaments. The filaments form disordered random networks. Filament-filament interactions are neglected and dynamics are homogeneous and isotropic. Due to these symmetries, there is no net bias of filament orientations for periodic boundary conditions. However, symmetry breaking by confining boundary conditions induces a self-organization towards a polarized structure. This occurs despite unbiased dynamics and the absence of external gradients. It leads to a separation and accumulation of vesicle species, following the geometry of the cell volume. The phenomenon can be theoretically understood by using an analogy to Electrostatics. For realistic geometries the model reproduces vesicle agglomerations as can be experimentally observed.

BP 7.2   Mon 17:15   P3
Quorum sensing by yeast cells — ●André Weber[1], Yury Prokazov[2], Thomas Mair[1], Werner Zuschratter[2], and Marcus Hauser[1] — [1]Abteilung Biophysik, Institut für Experimentelle Physik, Otto-von-Guericke-Universität Magdeburg, Universitätsplatz 2, 39106 Magdeburg, Germany — [2]Leibniz-Institut für Neurobiologie, Speziallabor Elektronen- und Laserscanmikroskopie, Brenneckestr. 6, 39118 Magdeburg, Germany

Glycolysis is a central pathway in the energy metabolism of cells, and it may display temporal and spatiotemporal self-organization, which can be observed in cell colonies of the yeast Saccharomyces carlsbergensis. The dynamics of the cell population dependens on the cell density: At high cell densities all cells of the population show synchronous and coherent oscillations, which can be detected as global oscillations in a population of yeast cells. The collective behaviour ceases at a critical, low cell density. This phenomenon is called 'quorum sensing'.

So far, little is known about the behaviour of the individual cells at concentrations below the quorum. Using highly sensitive single photon counting fluorescence microscopy, we study the dynamics of individual, immobilized yeast cells at low cell densities. Our focus lies in elucidating the mechanism of the transition between individual and collective dynamics. At very low cell densities, the individual cells perform metabolic oscillations, the frequencies of which show a very broad distribution. As the cell density approaches the quorum, we observe that the frequency distribution narrows and synchronized collective behaviour sets in.

BP 7.3   Mon 17:15   P3
Universal clustering properties in bacteria — ●Fernando Peruani[1], Joern Starruss[2], Vladimir Jakovljevic[3], Lotte Sogaard-Andersen[3], Marks Baer[4], and Andreas Deutsch[3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Center for Information Services and High Performance Computing - Technische Universität Dresden, Dresden, Germany — [3]Max Planck Institute for Terrestrial Microbiology, Marburg, Germany — [4]Physikalisch-Technische Bundesanstalt, Berlin, Germany

Collective behaviour of individual cells marks the onset of the transition to multicellularity. This transition is thought to rely on some specific intercellular communication between cells. In this talk, we will show that the transition from single cell to collective behaviour in a Myxococcus xanthus mutant can be understood as a dynamical self-assembly process where no biochemical communication is required. The transition is characterized by a scale-free cluster size distribution that emerges at a critical cell density. The experimental data is consistent with predictions from a mathematical model in which bacteria are described as self-propelled rods with merely steric interactions. Our findings provide a universal mechanism for pattern formation in bacteria that only depends on the physical properties of the system, in particular, on cell shape and cell density. Interestingly, similar results

have been reported for Bacillus subtilis.

BP 7.4   Mon 17:15   P3
Species deletion stability of model food webs that include allometric scaling and adaptive foraging — ●Lotta Heckmann[1], Christian Guill[2], and Barbara Drossel[1] — [1]Institut für Festkörperphysik, TU Darmstadt, Germany — [2]Systemic Conservation Biology, J.F. Blumenbach Institute of Zoology and Anthropology, Georg-August-University Göttingen, Germany

Ecosystems are subjected to various types of perturbations, many of which are due to human influence, including the extinction of species. Knowing the response of ecosystems to large perturbations is of importance for preservation politics, but also for a deeper understanding of the stabilizing mechanisms in ecosystems or food webs. We investigate numerically the response of model food webs that are dynamically stable to the deletion of a species. We quantify the species deletion stability by counting how many species survive after one species has been removed. The data are evaluated in dependence of the trophic function and properties of the eliminated species in order to determine which species are significant for the persistence of the whole food web. Our food web models include nonlinear population dynamics equations with Holling type II functional response, intraspecific competition, and adaptive foraging. The metabolic rates of the species scale allometrically with body mass, and we investigate the influence of different body mass ratios between predator and prey on the stability of the food webs.

BP 7.5   Mon 17:15   P3
Coexistence of mass-selective predators feeding on a growing prey — ●Laurin Lengert, Christian Guill, and Barbara Drossel — TU Darmstadt, Institut für Festkörperphysik

The body mass of an organism affects many ecologically relevant quantities, such as maximal food ingestion and respiration rate, population growth rate, carrying capacity, and prey choice.

Many empirical studies confirm that the body masses of predator and prey are positively correlated and the attack rate has been revealed as being a hump shaped function of the body mass ratio between predator and prey.

In natural food webs, species ontogeny, especially growth in body mass, alters body mass ratios. When considering seasonal species, the correlation between prey and predator body mass leads to a variation of the food web structure.

We present for the first time a model that includes several predator species, together with a prey that grows in size, leading to time dependent attack rates.

We will focus on the question how prey growth affects the coexistence of predators.

BP 7.6   Mon 17:15   P3
Upstream swimming of a model micro-swimmer in a microchannel — ●Andreas Zöttl and Holger Stark — TU Berlin

Many microorganisms in the human body swim in confined environments like sperm cells in the Fallopian tube or E. coli bacteria in the colon. Also pathogens use narrow channels like the urethra to swim to their destinations. Micro-swimmers exhibit hydrodynamic interactions with bounding surfaces that change their swimming speeds and orientations. In particular, pushers and pullers show different behavior. Pushers such as sperm cells or bacteria propel themselves with flagella attached at the back of the cell body and get attracted by a wall. Pullers like the algae Chlamydomonas typically have a propelling apparatus in the front and are reflected by a wall.

As a simple model microorganism we use the so-called squirmer. It has a spherical shape with a prescribed axisymmetric tangential surface velocity, different for pushers and pullers. We model the hydrodynamics of squirmers including thermal noise using multi-particle collision dynamics. This method introduces ballistic and collision steps of effective particles in order to solve the Navier-Stokes equations. We systematically investigate the swimming behavior of both pushers and pullers in a cylindrical microchannel with an imposed Poiseuille flow. When the strength of the flow is sufficiently small, pushers swim upstream at the wall. Pullers can swim upstream between the walls when the channel width is small enough. Increasing the imposed flow

strongly, pushers and pullers now swim downstream and tumble due to flow vorticity similar to passive particles.

BP 7.7 Mon 17:15 P3

A Switch Like Response of Photosynthetic Bacteria to Changing Redox and Light Conditions — •Rakesh Pandey[1], Dietrich Flockerzi[1], Marcus J. B. Hauser[2], and Ronny Straube[1] — [1]Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany — [2]Institute of Experimental Physics, Otto-von-Guericke University, Magdeburg, Germany

Facultative photosynthetic bacteria switch their energy generation mechanism from respiration to photosynthesis depending on oxygen tension and light. Part of this transition is mediated by the conserved transcriptional repressor PpsR which specifically represses components of the photosynthetic apparatus under aerobic conditions. In *Rhodobacter sphaeroides* the repressive action of PpsR is antagonized by the redox and blue light sensitive flavoprotein AppA. At intermediate oxygen levels the interaction between AppA and PpsR leads to the repression of photosynthesis genes under high light illumination which is believed to reduce the risk of photo-oxidative stress. To elucidate the underlying mechanism for this phenotype we developed a simple mathematical model. Investigations of the steady-state behavior show that high light repression can indeed occur at intermediate oxygen levels if PpsR is reduced on a faster time scale than AppA. The model further shows that if AppA copy numbers exceed those of PpsR the low to high light transition can occur via a bistable switch which might help the bacterium to cope with changing light conditions, especially at intermediate oxygen levels.

BP 7.8 Mon 17:15 P3

The influence of stochastic fluctuations on the cyclic dominance of pacific salmon — •Christoph Schmitt, Christian Guill, and Barbara Drossel — Institut für Festkörperphysik, TU Darmstadt

The four-year oscillations of the number of spawning sockeye salmon that return from the ocean to their native lake within the Fraser River basin in Canada are a striking example of population oscillations. A recently introduced three-species model for these fish, their predators and their prey, was able to reproduce the four-year oscillation as a stable attractor of the dynamics. This model describes the population dynamics in the lake between spring and fall by coupled differential equations, while the survival of the adult salmon in the ocean and the resulting initial condition in the lake at the beginning of each season are modeled by a discrete map. Since the sockeye populations are subject to various types of fluctuations due to the many factors affecting their growth and survival, we investigate now the behaviour of this model under several types of noise. In particular, we evaluate the frequency of phase shifts in the four-year oscillation, and the extent of synchronization between different sockeye populations.

BP 7.9 Mon 17:15 P3

Phase transitions in competitive foraging of bats — Pia Backmann and •Alexander K. Hartmann — Universität Oldenburg

Foraging of animals is driven by competition, hence it can be seen as complex system of interacting individuals. Each animal has the aim to increase its profit by developing different foraging strategies.

We use an Individual Based Model to optimize the competitive foraging of bats feeding from nectar - a renewable resource - by improving the bats' ability to perceive, if the individual profit of a flower is high or not.

It shows, that a higher notice of flower quality yields to applying different foraging strategies and thus to individually and globally better harvesting results.

We use the Kullback-Leibler-Divergence to show that the more foraging is optimized, the more do bats divide their habitat into territories, several for each bat, so the intersection in resources is lower and flower-visits more efficient.

We find a phase transition between a solvable and a not-solvable phase for finding a given target amount of nectar. By applying finite-size scaling we find the critical exponent $\nu = 1.9(3)$ describing the growing correlation when approaching the phase transition.

BP 7.10 Mon 17:15 P3

Age dependent branching in phylogenetic trees — •Stephanie Keller-Schmidt[1], Murat Tugrul[2,3], Victor M. Eguiluz[2], Emilio Hernandez-Garcia[2], and Konstantin Klemm[1] — [1]Bioinformatics Group, Leipzig University, Germany — [2]IFISC,

Palma de Mallorca, Spain — [3]IST Austria, Klosterneuburg, Austria

The evolutionary diversification of biological species is a branching process reconstructed as phylogenetic trees. According to analysis of large databases (TreeBase and PANDIT), these trees have a shape (systematic imbalance) not explained by a process of uncorrelated branching events. Here we introduce the *age model* where the branching probability of a node (species) is inversely proportional to the time since the node was last involved in speciation. We find that the scaling of the average number of ancestors (called depth d) with total number of species n scales as $d \sim (\log n)^2$. This result is in agreement with the scaling observed by exhaustive analysis of the databases Treebase and Pandit. Compared with a previously suggested model [1], the age model yields larger likelihood values on the trees in the databases with up to 20 leaves (where exact likelihood computation is feasible).

[1] M.G. Blum and O. François, Syst. Biol. 55, 685-691 (2006).

BP 7.11 Mon 17:15 P3

The Influence of local Symmetries on the Properties of large Complex Systems — •Helge Aufderheide, Lars Rudolf, and Thilo Gross — MPI-PKS, Dresden, Germany

The stability of large complex systems is a topic of intense scientific research. In this work, we investigated topological properties of their graph representations. In particular, we focused on local symmetries, called orbits, whose properties were connected to those of the whole network by applying results from graph theory. A powerful tool to study stability in this context is the generalized models approach, which can be used to study asymptotic stability properties of complex systems without being limited to the specific functional forms of a model. Combining graph theory arguments with generalized modeling we investigated the example of trophic food webs. Thereby we were able to establish a link between the occurrence of local symmetries and stability on the global level.

BP 7.12 Mon 17:15 P3

Winning the marathon. Multiplayer games at the mutation-selection equilibrium — •Chaitanya Gokhale and Arne Traulsen — Research Group for Evolutionary Theory, Max-Planck-Institute for Evolutionary Biology, August-Thienemann-Str. 2, 24306 Plön, Germany

Evolutionary game theory is an abstract and simple, but very powerful way to model evolutionary dynamics. Even complex biological phenomena can sometimes be abstracted to simple two player games. But often, the interaction between several parties determines evolutionary success. In these cases, one can resort to multiplayer games, which are inherently more complicated than two-player games, yet can yield simple results. Another important evolutionary force is mutations, which has only recently yielded to analytical methods [1,2]. We derive the composition of a multiplayer, multiple strategy system in the mutation-selection equilibrium. We obtain the average frequencies of the strategies at this equilibrium. The result is a simple expression which can be obtained by recursions using coalescence theory [3]. This approach can be modified to suit a variety of contexts, e.g. to find the equilibrial frequencies of a finite number of alleles in a polymorphism or the equilibrial frequencies of different strategies in a social dilemma in a cultural context.

References: [1] T. Antal *et al.* Proc. Natl. Acad. Sci. USA, 106, 2009. [2] T. Antal, A. *et al.* J. Theor. Biol., 258, 2009. [3] J. Wakeley. Coalescent theory: an introduction. Roberts and Company Publishers, 2008.

BP 7.13 Mon 17:15 P3

Interaction Dynamics of Colloidal Particles in Scanning Line Optical Tweezers — •Benjamin Tränkle and Alexander Rohrbach — Lab for Bio- and Nano-Photonics, University of Freiburg, Germany

Inter-particle distances are of vital importance for the accomplishment of biological processes, e.g. the fusion of vesicles or drug delivery. Here, the vesicle motions are confined by compartments inherent to the cell structure and also determined by physical interactions, i.e. hydrodynamic and entropic forces. We mimic the biological system by observing the diffusive modes of silica spheres in an elongated potential, which is generated by an oscillating optical trap. The particle positions in 3D are obtained by back focal plane interferometry. Scanning frequencies up to 10 kHz and a spatial precision in the nanometer range are achieved. Our model system allows the particles to get in close

contact to one another due to Brownian position fluctuations. Thus pair interactions and dynamics of microspheres can be investigated, e.g. by analyzing the particle trajectories in terms of correlated and anti-correlated motions. Here, the characteristic timescales, i.e. the interaction times are impaired by the shape and stiffness of the trapping potential. We use an acousto-optic deflector to control the laser intensity and hereby vary the trap properties in a broad range. This enables the study of different aspects of particle dynamics.

BP 7.14 Mon 17:15 P3

Evolution in Group-Structured Populations — •Jonas Cremer, Anna Melbinger, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics, Department of Physics, Ludwig-Maximilians Universität München

Populations of microbial organisms show a very versatile evolutionary behavior. One very important factor co-determining the evolutionary dynamics is the structure of the population in a complex environment. In fact, the evolutionary outcome in highly structured populations can strongly alter from well-mixed ones; different sub-populations can evolve almost separately, only in weak contact to each other. Here, we study the evolution of cooperation in a population regularly forming new sub-colonies. While, due to their metabolic costs, cooperative traits have a selection disadvantage within each group, groups with a higher level of cooperation grow faster. As we show, there are two distinct evolutionary mechanism which allow for both, the evolution and maintenance of cooperation.

BP 7.15 Mon 17:15 P3

Supertree construction using superparamagnetic clustering — •Pascal Fieth[1], Alexander K. Hartmann[1], and Olaf R.P. Bininda-Emonds[2] — [1]Institute of Physics, University of Oldenburg — [2]Department of Biology and Environmental Sciences, University of Oldenburg

Superparamagnetic clustering [1] is a non-parametric clustering method for a set of data points using the Potts model with a suitable distance definition. In a numerical simulation [2] of the data points represented as spins in a thermodynamic system, regions of aligned spins, corresponding to clusters, are detected. Here, this method is used for supertree construction, a phylogenetic approach to merge phylogenetic trees only according to their tree topologies, so that overlapping rather than identical taxon sets are needed [3].

The corresponding distance definition is empirically optimized for the used method. Further the dependency of the quality of the reconstruction of a known tree on the size and number of the used source trees is analyzed.

[1] M. Blatt, S. Wiseman and E. Domany, *Superparamagnetic Clustering of Data*, (Physical Review E, 1998)
[2] A.K. Hartmann, *Practical Guide to Computer Simulations*, (World Scientific, 2009)
[3] O.R.P. Bininda-Emonds *The evolution of supertrees*, (TRENDS in Ecology and Evolution, 2004)

BP 7.16 Mon 17:15 P3

Investigating intrinsic fluctuations in biochemical systems — •Joseph Challenger[1], Juergen Pahle[2], Alan McKane[1], and Pedro Mendes[2] — [1]School of Physics and Astronomy, The University of Manchester, Manchester, UK — [2]School of Computer Science, The University of Manchester, Manchester, UK

Mathematical models of biochemical reaction systems are usually constructed from determinstic rate equations. However, this approach is not appropriate when the number of molecules involved is low. Here the underlying stochasticity present in the system becomes important.

The rate equations treat the molecular concentrations as smoothly varying functions. In this talk, a master equation approach is used, where the system is described by discrete states, namely the molecular populations of the chemical species involved. In the mean field limit the rate equations can be recovered. In addition to this, leading order corrections to the rate equations can be obtained by using the system-size expansion due to van Kampen.

We have incorporated these results into COPASI, a software package designed to simulate and study biochemical reaction systems. This allows the expansion procedure to be automated. Once the reaction system has been described, COPASI can calculate the covariance matrix associated with the fluctuations exhibited by the chemical species present in the system. We give examples of the application of the method to biologically relevant systems.

BP 7.17 Mon 17:15 P3

Carpets of chiral motors — •Maria Strempel[1,2], Sebastian Fürthauer[1,2], Stephan W. Grill[1,2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden

We study the flows and stresses emerging in a two-dimensional arrangement of chirally beating cilia close to a surface using a continuum theory for active polar fluids, including chiral terms. Our theory is generic, as it is based on conservation laws and the symmetries of the system. Considering the force and torque balance in the thin interfacial layer close to the surface, we identify a novel chiral friction term which is proportional to the cilias local rotation rate. This term is related to the difference of the forward and the backward stroke of the tilted cilia. Our generic approach allows us to relate the vorticity of the emerging flow to the local rotation rate of the cilia. Furthermore we confirm that in an arrangement of tilted cilia, the chiral symmetry of the emerging flow is broken. Such symmetry breaking flows are observed in experiments on Kupfers vesicle in the zebrafish and the ventral node of mouse embryos and seem to play an important role in left-right symmetry breaking of the vertebrate body.

BP 7.18 Mon 17:15 P3

Active chiral fluids — •Sebastian Fürthauer[1,2], Stephan W. Grill[1,2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Intitute of Molecular Cell Biology and Genetics

Dynamic cellcular processes such as cell division and cell motility rely on the cytoskeleton, a meshwork of polar elastic filaments. Motor molecules provide active crosslinking between these filaments and exert internal forces in the network as they consume a chemical fuel (ATP). We extend previous continuum descriptions of active gels in the hydrodynamnic limit to take into account active chiral effects. Such chiral effects stem from the chirality of motor-filament interactions and are for example very prominent in the chiral beat of cilia. We derive generic constituve equations for a chiral active fluid. Our theory can describe generic behaviors on large scales in active chiral systems ranging from chiral swimmers to the collective motion generated by cilia that beat on surfaces.

BP 7.19 Mon 17:15 P3

Evolution of increasingly complex molecules — •Philipp Zimmer[1], Christian Lay[2], Eva Wollrab[2], Albrecht Ott[2], and Karsten Kruse[1] — [1]Universität des Saarlandes, Theoretische Biologische Physik, Postfach 151150, 66041 Saarbrücken — [2]Universität des Saarlandes, Biologische Experimentalphysik, Postfach 151150, 66041 Saarbrücken

Biological evolution started at the level of molecules. A long standing aim is to identify conditions under which molecules of increasing complexity can emerge. Such a process must necessarily be out of thermodynamical equilibrium. We consider a simple case, where the complexity of a molecule is given directly by its length. Starting from a fixed number of identical subunits, we consider two processes that can lead to molecules of increasing length: assisted and spontaneous catenation. Assisted catenation is achieved when the head-to-tail conformation of two molecules is stabilised by pairing these molecules with a third molecule. We find that below a critical rate of spontaneous catenations, the system produces "islands" of increasing complexity. We suggest that this situation can be realized experimentally using palindromic DNA sequences and ligases.

BP 7.20 Mon 17:15 P3

Protocells: From a Closed to an Opened System — •Hans Kubitschke and Claus Fütterer — Institut für Experimentalphysik I, Universität Leipzig, Linnéstraße 5, 04009 Leipzig

Nutrition and energy management is crucial for preventing an early protocell to run into the thermodynamic equilibrium with lethal consequences. But cell membranes per se are impermeable to many required molecules and hence a controlled passage possibility for nutritive substances as amino acids or nucleotides has to be realized to escape starvation. How this is accomplished is not only an indispensable element of the development of the first cells but also a surprisingly simple but very sensitive (since amplification due to feed-back is involved) bioreactor suited for high throughput screening of the properties of all components: transcription apparatus, membrane pore, phospholipids, co-expressed other proteins. The system can be used to measure pro-

cessing rates of enzymes, flux and effective diffusion coefficients membrane pores. Noireaux and Libchaber published experimental results in 2004 integrating a transcription apparatus into a vesicle expressing pores getting spontaneously inserted into the vesicle membrane. This work inspired our basic model describing the dynamics of pore proteins and the transcription dynamics, which we present here. The set of ordinary non-linear differential equations balance membrane pore generation due to gene expression, allowing to keep metabolism alive, against its degradation due to blockage or chemical destruction. Integration of other properties allows to extend the model conveniently to various other assays.

BP 7.21   Mon 17:15   P3

Tuning a genetic oscillator — Ernesto M. Nicola[1], Saul Ares[2], and •Luis G. Morelli[3,2] — [1]IFISC (CSIC-UIB), Campus Universitat Illes Balears, E-07122 Palma de Mallorca, Spain — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

Self regulatory elements are a fundamental component of cellular control systems. These elements can regulate their own abundance through closed feedback loops. A pure negative feedback loop can result in oscillations on the levels of gene products, while a positive feedback may lead to multi-stability. Recent work has recognized that network motifs combining both positive and negative feedback loops can be very robust oscillators, offering the possibility to tune the frequency of the oscillations without affecting their amplitude. In this contribution we propose a family of simple models that combine positive and negative feedback loops. We perform a detailed study to determine the conditions which ensure tunability. Our analysis of this generic models reveals general principles underlying the tunability of oscillations.

BP 7.22   Mon 17:15   P3

How is the timing of cell division influenced by variation in temperature? — •Federico Vazquez[1], Abigail Klopper[1,2], Maria Begasse[2], and Stephan Grill[1,2] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Max Planck Institute for Molecular Cell Biology and Genetics

Accurate timing of early embryogenesis is crucial for the development of an organism, and is subject to sensitive dependence on fluctuations in temperature. We investigate the correlation between timing and temperature using *C. elegans* as a model organism, which benefits from rapid early cell divisions and an inability to maintain a constant body temperature independent of ambient conditions. We propose a simple model which attributes an observed Arrhenius temperature dependence to the combined dependence of individual chemical reactions involved in the cell cycle. We question whether the experimental results are best explained by just one limiting chemical reaction, as suggested in previous studies, or by a more complex sequence of reactions that function in synchrony. We compare the temperature dependence of *C. elegans* and *C. briggsae*, two closely related organisms known to differ in their optimal temperature range.

BP 7.23   Mon 17:15   P3

Traveling Waves in Strong-Noise Reaction-Superdiffusion Systems — •Marc Szabo and Oskar Hallatschek — Biophysics & Evolutionary Dynamics Group, MPI for Dynamics and Self-Organization, Göttingen, Germany

Traveling waves resulting from reaction and diffusion of particles describe a wide range of phenomena like epidemic waves, range expansions of populations or the dispersal of a chemical concentration. In systems of discrete particles, number fluctuations are inevitable and significantly affect the velocity and shape of such traveling waves. Here we investigate the effect of anomalous diffusion on noisy traveling wave solutions of the Fisher- Kolmogorov equation. Instead of a regular random walk, particles perform scale free Lévy Flights leading to long-range migration. Latter concept has proven to successfully describe the dynamics of human travel [1] and can also be applied to expanding populations in the context of biological evolution. While this problem has already been studied in the regime where number fluctuations are small [2], we discuss here the case of strong noise. We analyze the dependence of the wave velocity on the Lévy exponent and noise strength. Our results show considerable differences to the weak noise regime. We confirm our analytical results with detailed simulations.

[1] D.Brockmann, L.Hufnagel, T. Geisel, Nature 439, 462-465 (2006).
[2] D.Brockmann and L.Hufnagel, Phys. Rev. Lett. 98 178301 (2007).

BP 7.24   Mon 17:15   P3

Microbial Stain Effect — •Christopher J. Seedig and Oskar Hallatschek — Biophysics & Evolutionary Dynamics Group, MPI for Dynamics and Self Organization, Göttingen, Germany

Droplets of colloidal suspensions leave annular patterns after drying on solid surfaces [1]. This phenomenon is commonly observed in coffee stains, therefore the underlying effect has been termed coffee stain effect. If the suspended colloids have two different sizes, the coffee stains consist of separate rings: smaller beads end up further away from the droplet centre [2]. Here, we study the coffee stain effect using droplets of yeast suspensions on agar plates. These suspensions are mixtures of large and small cells, which can be distinguished by their fluorescent color. We find that, due to the initial positional head start, the small cells enjoy a significant advantage during the colony formation. As a consequence, the small cells occupy a disproportionally large fraction of the final colony. We quantify this "selection advantage" as a function of important control parameters, such as cell size difference or cell density. We argue that the microbial stain effect may play an important role in molecular biology, as it occurs on a daily basis in most modern bio-labs.

[1] Deegan et al., Nature (London), 389, 827-29 (1997)
[2] Byung Mook Weon, Jung Ho Je, Phys Rev E, 82, 015305(R) (2010)

BP 7.25   Mon 17:15   P3

Construction of Phylogenetic Trees Using a Clustering Approach — •Johannes Josef Schneider[1], Thomas Bukur[2], and Antje Krause[2] — [1]Department of Physics, Mathematics, and Computer Science, Johannes Gutenberg University of Mainz, Staudinger Weg 7, 55099 Mainz, Germany — [2]Fachhochschule Bingen – University of Applied Sciences, 55411 Bingen, Germany

Recently, we introduced an extension of the Traveling Salesman Problem which we coined Traveling Salesman Problem with Clustering [1]. In this extension, the constraint that nodes close to each other should be visited contiguously in the tour is added to the original problem, thus minimizing the overall tour length and generating clusters in parallel. In this talk, we demonstrate how this approach is adopted to the problem of constructing phylogenetic trees, defining the distances between various species with the overlap between them.

[1] Johannes J. Schneider, Thomas Bukur, and Antje Krause, Traveling Salesman Problem with Clustering, J. Stat. Phys. 141, 767-784, 2010.