

DY 1: Statistical Physics of Biological Systems I (with BP, talks from DY)

Time: Monday 9:30–13:15

Location: MA 001

DY 1.1 Mon 9:30 MA 001

On various types of synchronization in networks of coupled neurons — ●PHILIPP HÖVEL^{1,2}, ALEXANDER FENGLER¹, ALEXANDER HEESING¹, and ECKEHARD SCHÖLL¹ — ¹Technische Universität Berlin, Germany — ²Bernstein Center for Computational Neuroscience Berlin, Germany

Research on complex networks continues to receive more and more attention since the last decades both from a data-driven and dynamics-driven perspective. In the latter case, collective and cooperative dynamics of coupled systems forms a central phenomenon that is of large interest in various fields. These range from social science and economics to biology, physics, and neuroscience and beyond.

In our contribution, we discuss the synchronization of coupled integrate-and-fire neurons with partial reset in various network topologies. These include all-to-all, ring, and scale-free networks. We find a transition from complete synchronization via cluster synchronization to desynchronization in dependence upon the reset parameter. Our results are based on numerical simulations, which we complement by analytical considerations.

DY 1.2 Mon 9:45 MA 001

Complex activation patterns in a simple deterministic model of excitable neural networks — ●GUADALUPE C. GARCIA¹, CLAUD C. HILGETAG², and MARC THORSTEN HÜTT¹ — ¹School of Engineering and Science, Jacobs University, Bremen, Germany — ²University Medical Center Eppendorf, Hamburg University, Hamburg, Germany

Understanding the interplay of topology and dynamics of excitable neural networks is one of the major challenges in computational neuroscience. Here we employ a simple deterministic model of excitation propagation to explore how network-wide activation patterns are shaped by neural network architecture.

The model consists of three discrete states for each node (susceptible S, excited E, refractory R), which are updated synchronously in discrete time steps according to a set of update rules allowing for signal propagation. In particular, an element returns to the susceptible state after r time steps. For small r , the network dynamics settle into an regular oscillatory behavior after a transient period. The set of nodes is thus partitioned into distinct groups of nodes, where two nodes are in the same group when they are simultaneously excited.

Two questions about this process are at the core of our investigation: (1) How does the dynamic partitioning into groups depend on network architecture (investigated by averaging the groupings over many different initial conditions)? (2) How does the length of the transient depend on network architecture? By exploring these deterministic excitation dynamics we aim at better understanding, which topological features facilitate self-sustained activity of neural networks.

DY 1.3 Mon 10:00 MA 001

Dynamics of inhomogeneous neural systems with nonlocal coupling — ●IRYNA OMELCHENKO^{1,2}, PHILIPP HÖVEL^{1,2}, and ECKEHARD SCHÖLL¹ — ¹Technische Universität Berlin, Germany — ²Bernstein Center for Computational Neuroscience Berlin, Germany

We investigate the cooperative dynamics of nonlocally coupled neural populations modeled by FitzHugh-Nagumo systems, which is a generic model for type-II excitability. The individual systems are considered to operate above a Hopf bifurcation, that is, they display oscillatory local dynamics. Furthermore, inhomogeneity of the local elements is introduced in the system via a distribution of threshold parameters. Varying the coupling parameters, i.e., coupling radius and strength, and in dependence on the inhomogeneous system's parameter distribution, we analyze spatio-temporal dynamics in the system. Coherent solutions, their stability and mechanisms of transition from coherence to incoherence are analyzed. Especially, we discuss the occurrence of chimera states that exhibit spatial coexistence of regular synchronized and irregular spatially incoherent regions.

DY 1.4 Mon 10:15 MA 001

Spiral-wave prediction in a lattice of FitzHugh-Nagumo oscillators — ●MIRIAM GRACE and MARC-THORSTEN HÜTT — Jacobs University Bremen, Bremen, Germany

In many biological systems, variability of the components can be expected to outrank statistical fluctuations in the shaping of self-

organized patterns. The distribution of single-element properties should thus allow the prediction of features of such patterns. In a series of previous studies on established computational models of *Dictyostelium discoideum* pattern formation we demonstrated that the initial properties of potentially very few cells have a driving influence on the resulting asymptotic collective state of the colony [1,2]. One plausible biological mechanism for the generation of variability in cell properties and of spiral wave patterns is the concept of a "developmental path", where cells gradually move on a trajectory through parameter space. Here we review the current state of knowledge of spiral-wave prediction in excitable systems and present a new one-dimensional developmental path based on the FitzHugh-Nagumo model, incorporating parameter drift and concomitant variability in the distribution of cells embarking on this path, which gives rise to stable spiral waves. Such a generic model of spiral wave predictability allows new insights into the relationship between biological variability and features of the resulting spatiotemporal pattern.

[1] Geberth, D. and Hütt, M.-Th. (2008). Phys. Rev. E 78, 031917.

[2] Geberth, D. and Hütt, M.-Th. (2009). PLoS Computational Biology 5, e1000422.

DY 1.5 Mon 10:30 MA 001

Spatio-temporal dynamics of bumblebees foraging under predation risk — FRIEDRICH LENZ¹, THOMAS C. INGS², LARS CHITTKA², ALEKSEI V. CHECHKIN³, and ●RAINER KLAGES¹ — ¹Queen Mary University of London, School of Mathematical Sciences, UK — ²Queen Mary University of London, School of Biological and Chemical Sciences, UK — ³Inst. f. Theor. Physics, NSC KIPT, Kharkov, Ukraine

We study bumblebees searching for nectar in a laboratory experiment with and without different types of artificial spiders as predators. We find that the flight velocities obey mixed probability distributions reflecting the access to the food sources while the threat posed by the spiders shows up only in the velocity correlations. This means that the bumblebees adjust their flight patterns spatially to the environment and temporally to predation risk. Key information on response to environmental changes is thus contained in temporal correlation functions and not in spatial distributions.

[1] preprint arXiv:1108.1278 (2011)

DY 1.6 Mon 10:45 MA 001

Fluctuation-sensitive coarse-graining for stochastic dynamics — ●BERNHARD ALTANER and JÜRGEN VOLLMER — Max Planck Institut für Dynamik und Selbstorganisation, Göttingen

We consider Markov processes on a finite state space. Such stochastic processes can be viewed as a random walk on a network. Physically, the states represent a mesoscopic description as they summarize regions of phase space of an underlying microscopic dynamics. For non-equilibrium steady states, probability conservation gives rise to cyclic dynamics. Cycles connect the stochastic, mesoscopic description to the thermodynamic, macroscopic description. Here, we present a method for complexity reduction of the mesoscopic dynamics is where the new stochastic dynamics preserves the most important connections to the other scales. As an example, we consider the stochastic dynamics of the molecular motor protein kinesin.

DY 1.7 Mon 11:00 MA 001

The role of diffusion in the SIRS epidemic model — FERNANDO PERUANI¹ and ●CHIU FAN LEE² — ¹Lab. J.A.Dieudonné, Université de Nice - Sophia Antipolis — ²Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

In the well-mixed limit of the classical SIRS epidemic model, an initial epidemic outbreak will persist if the basic reproductive number is larger than 1. This quantity indicates the number of secondary cases caused by an infected individual and is believed to depend exclusively on the parameters relevant to the spreading of the disease. If the individuals in the system also diffuse, it is unclear how this epidemic threshold will be affected. In this work, we perform extensive lattice-based simulations to demonstrate that the epidemic threshold and the average number of infected individuals are in fact strongly affected by the diffusion coefficient, D , exhibited by the agents. We then support our numerical results with field-theoretic analysis.

15 min, break

DY 1.8 Mon 11:30 MA 001

Generalized Entropies for Clustering, e.g., in Molecular Evolution — ●KAY HAMACHER — TU Darmstadt, 64287 Darmstadt, Germany

Entropy is a key concept in information theory. Analysis of empirical data is often improved by relying on (relative) entropies. In this talk I want to describe current progress in clustering approaches by optimization techniques [1-2] applied to entropy distances via generalized entropy concepts [3], in phylogenies [4,5], finite-size effects in empirical data [6], and in molecular design [7].

[1] K. Hamacher. J.Comp.Phys., 227(2):1500-1509, 2007

[2] K. Hamacher. Europhys.Lett. 74(6):944, 2006

[3] R. Bose, G. Thiel, K. Hamacher. Variation in Local Entropy to Cluster Genomic Sequences, submitted, 2011.

[4] K. Hamacher. Proc. of BIOINFORMATICS 2010, p. 114-122, A. Fred, J. Filipe, H. Gamboa (eds.), ISBN 978-989-674-019-1

[5] K. Hamacher, Information Theoretical Dissection of the Holo-biont - Host-Virus Interaction as an Example, Nova Acta Leopoldina, accepted, 2011

[6] P. Weil, F. Hoffgaard, K. Hamacher. Comp. Biol. Chem. 33:440-444, 2009

[7] K. Hamacher. J.Comp.Chem., 28(16):2576-2580, 2007

DY 1.9 Mon 11:45 MA 001

Stochastic description of birth and death processes governed by a mixture of exponential and non-exponential waiting times — ●STEPHAN EULE — Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen

The dynamics of complex biological systems is significantly influenced by fluctuations originating from intrinsic as well as extrinsic sources. In general, the discrete nature of individual events, such as the birth and death of an individual in a population or the production and degradation of molecules in a chemical reaction, is the main source of intrinsic noise. The occurrence of such events is usually modeled by Poissonian statistics, implying that the probability per unit time for an event to happen is assumed to be constant. Many complex systems however exhibit deviations from elementary Poissonian statistics. Such deviations can arise for example in coarse-grained stochastic models of gene expression, where the waiting time distribution can be more general than the simple exponential distribution.

In this contribution we consider birth and death processes which are governed by both, exponential as well as non-exponential waiting times. We derive the corresponding master equation and present methods to approach this equation analytically. As an example we consider a reaction where the production of molecules is governed by a non-exponential waiting time distribution and the degradation follows regular Poissonian statistics.

DY 1.10 Mon 12:00 MA 001

Discriminating the effects of spatial extent and population size in cyclic competition among species — ●DAVID LAMOUROUX^{1,2}, STEPHAN EULE¹, THEO GEISEL^{1,2}, and JAN NAGLER^{1,2} — ¹Max Planck Institute for Dynamics & Self-Organization, Göttingen, Germany — ²Institute for Nonlinear Dynamics, Department of Physics, University of Göttingen, Göttingen, Germany

Quantifying and understanding the stability and biodiversity of ecosystems is a major task in biological physics as well as in theoretical ecology. From the perspective of game theory, this is highly relevant for questions pertaining to the emergence of cooperation or the coexistence of cyclically competing species. For the latter, it has recently been shown that the mobility of individuals can support the stability of biodiversity by the formation of spirals. In this contribution, we present a population model for species under cyclic competition that extends earlier lattice models to allow the single cells to accommodate more than one individual by introducing a per cell carrying capacity. We confirm that the emergence of spirals induce a transition from an unstable to a stable regime. This transition however does not appear to be sharp and we find a broad intermediate regime that exhibits an ambiguous behavior. The separation of the two regimes by the usual scaling analysis is thus hampered. The newly introduced carrying capacity offers an alternative way of characterizing the transition. We thus overcome the original limitations by separately analyzing the effect of spatial extent and population size.

DY 1.11 Mon 12:15 MA 001

Modelling of DNA-Hybridization — ●OLAF LEIDINGER and LUDGER SANTEN — Universität des Saarlandes

Bringing together two types of single-stranded DNA molecules (targets: perfect matching and those with one mismatch) in a aqueous solution and one type of surface-attached single-stranded DNA molecules (probes) one can observe hybridization of double stranded DNA molecules. The percentage of perfect matching (PM) strands at the surface is found to be independent of the concentration of those with one mismatch (MM). This dominance is not in agreement with a Langmuir adsorption kinetics in contrast to the adsorption of a single species. We introduce a theoretical approach to the competitive adsorption of DNA strands illustrating the prerequisites for the dominant adsorption of PM DNA strands.

DY 1.12 Mon 12:30 MA 001

A Statistical Analysis of Production in Cells: Flux Distributions, Enzyme Time Scales and Metabolic Network Properties — ●MORITZ E. BEBER and MARC-THORSTEN HÜTT — School of Engineering and Science, Jacobs University Bremen, Germany

Numerous studies have addressed statistical properties of metabolic systems, both from the perspective of network structure and of dynamical systems. On a genome-wide scale, the considered dynamics were usually metabolic fluxes, i.e., material flow through biochemical reactions, either measured *in vivo* or computed using flux-balance analysis as a proxy for real behaviour.

In this study, we revisit and modify some of the existing results linking topology and dynamics: (1) We integrate timing information about the principal agents of catalysation of biochemical reactions, the enzymes, in a new way. (2) We carefully analyse the interplay of different network properties and re-compute metabolic network motifs, taking into account the fact that metabolic networks are bipartite, modular, layered, and contain different categories of bidirectional links. (3) Using a minimal model of evolved flow networks as a guideline, we explore, which network properties are correlated with metabolic robustness.

Our object of study is the metabolism of *Escherichia coli*. We use a manually curated metabolic network for topological information, a realistic model of its metabolism for flux balance analysis sampling diverse environmental conditions, and information on the mechanics of enzymes from a specialised database.

DY 1.13 Mon 12:45 MA 001

Active microswimmers with spatially varying self-propulsion — ●ALJOSCHA HAHN¹, GIOVANNI VOLPE^{2,3}, CLEMENS BECHINGER^{2,3}, and HOLGER STARK¹ — ¹Technische Universität Berlin, Germany — ²Max-Planck-Institut für intelligente Systeme, Stuttgart, Germany — ³Universität Stuttgart, Germany

The statistical physics of active microswimmers, which are capable of propelling themselves through a viscous environment, is intensively investigated at the present time. Recently, Janus particles were studied in a subcritical mixture [1] and it was found that the speed of self-propulsion can be controlled by the strength of illumination. In particular, a spatially varying light intensity induces a spatially varying self-propulsion. Based on the Smoluchowski equation, we study how active particles with a position dependent swimming speed behave and speculate about a novel type of ratchet.

[1] G. Volpe et al, Soft Matter 7, 8810 (2011)

DY 1.14 Mon 13:00 MA 001

Continuous Dynamic Photostimulation - delivering defined, in-vivo-like fluctuating stimuli with Channelrhodopsins — ●ANDREAS NEEF^{1,3}, AHMED EL HADY^{1,2,3}, WALTER STÜHMER^{2,3}, and FRED WOLF^{1,3} — ¹MPI für Dynamik und Selbstorganisation, Göttingen — ²MPI für Experimentelle Medizin, Göttingen — ³BFNT

Central neurons typically operate in a noise driven regime: thousands excitatory and inhibitory synapses give rise to a constantly fluctuating conductance. Its statistic is similar to low-pass filtered white noise conductance that can be parameterized by its average, standard deviation and correlation time. An understanding of action potential (AP) generation and encoding in the noise driven regime requires the detection of AP times during stimulation with defined time dependent conductance. Using a light activated ion channel (ChIEF) under continuously fluctuating illumination, we achieve a defined, reproducible conductance modulation that mimicks the effect of the naturally occurring synaptic inputs. Cultured neurons subjected to this continuous

dynamic photostimulation (CoDyPs) generate seemingly random, but reproducible patterns of APs in experiments lasting several hours. The induced conductance waveform can be precisely predicted by convolution of the light signal with the light-conductance transfer function of ChIEF. Together with non-invasive AP detection by extracellular

electrodes, CoDyPs lays the foundation for very long-lasting studies of action potential generation in a fluctuation driven regime. This will allow the measurement of dynamical response properties and the respective cut-off frequencies from individual neurons.