DY 2: Statistical Physics in Biological Systems I (joint with BP)

Time: Monday 9:30–11:30 Location: H47

DY 2.1 Mon 9:30 H47

Cardiorespiratory data segmentation during sleep — •Sabrina Camargo[1], Maik Riedl[1], Celia Anteneodo[2], Thomas Penzel[3], and Niels Wessel[1] — [1]Department of Physics, Humboldt Universität zu Berlin, Berlin, Germany — [2]Department of Physics, PUC-Rio, Rio de Janeiro, Brazil — [3]Sleep Center, Charité University Hospital, Berlin, Germany

The variability in cardiorespiratory data is closely related to the regulation of sleep. When the brain is very active as in the REM sleep stage, heart rate as well as respiration have long-range correlations, while, in contrast, in deep sleep those correlations vanish after a few seconds, indicating that cardiovascular data can be useful to reflect sleep disturbances. But physiological data usually display a highly nonstationary behavior, caused by either environmental conditions or the inherent complexity of the underlying dynamics of the biological rhythms. Considering that the signal is composed of stationary segments, we apply a nonparametric segmentation approach in order to detect such locally stationary segments, where statistical measures of first and second order, for example, mean and variance, are more likely to remain constant. Thus, segmentation provides a picture of the nonstationarity of a time series, in particular, the intrinsic time scales. Moreover, by finding the stationary regimes, we are able to identify changes in time series, as those coming from the cyclic reduction of the airflow. We compare the segmentation outcomes in the presence and the absence of respiratory induced sleep disturbances and we verify an increased variability in blood pressure in patients suffering from this events.

DY 2.2 Mon 9:45 H47

Extended diffusion models for sleep stage switching — Anna Barkentien and •Jens Christian Claussen — INB, University of Lübeck, Germany

Short awakening periods especially occuring during the second half of the night follow a peculiar power law [1] for which biologically plausible models still are not available. A pure Markov analysis [2] assuming random switching however ignores any deterministic components in the dynamics which are manifest in time correlations. The phenomenological model proposed in [1] describes sleep depth by a one-dimensional diffusion process with a reflecting border for sleep and a restoring force for wake. In contrast to an Ornstein-Uhlenbeck process the restoring force is inversely proportional (or a power law with negative exponent) to the excursion distance from the sleep/wake border. We extend this model in [3] to account for the REM state and modify the restoring force law to account for deviations to the power law that are observed in data from some (but not all) labs and obtain a better fit to data [3].

[1] C.-C. Lo, L. A. Nunes Amaral, S. Havlin, P. Ch. Ivanov, T. Penzel, J.-H. Peter, and H. E. Stanley. Dynamics of sleep-wake transitions during sleep. Europhysics Letters, 57, 631, 2002.
[2] J. W. Kim, J. -S. Lee, P. A. Robinson, D. -U. Jeong, Markov Analysis of Sleep Dynamics. Phys. Rev. Lett. 102, 2009.
[3] A. Barkentien and J.C. Claussen (in preparation).

DY 2.3 Mon 10:00 H47

Caveats in Modelling Coarse-Grained Descriptions of a Bistable Frustrated Unit — •Darka Labavić[1], Hannes Nagel[2], Wolfhard Janke[2], and Hildegard Meyer-Otrmanns[1] — [1]School of Engineering and Science, Jacobs University Bremen — [2]Institut für Theoretische Physik, Universtät Leipzig

From a coarse-grained perspective the motif of a self-activating species, activating a second species which acts as its own repressor, is widely found in biological systems. In [1] we studied this model on the proteonic level in a fully stochastic version. In [2] we zoom into the level of genes which are described as directly producing proteins. We focus on the effect that inherent time scales of the underlying scale of this genetic circuit can have on the bifurcation patterns on the coarser scale of proteins. Depending on the ratio of binding and unbinding rates of the transcription factors to the decay times of the proteins, the appropriate averaging procedure for obtaining a coarse-grained description changes and leads to sets of deterministic equations, which considerably differ in their bifurcation structure. In particular, the desired intermediate range of regular limit cycles fades away when the binding rates of genes are not fast as compared to the decay time of the proteins. Our analysis illustrates that the common topology of the widely found motif alone does not imply universal features in the dynamics.

[1] Garai A, Waclaw B, Nagel H, and Meyer-Ortmanns H, J. Stat. Mech. (2012) P01009;
[2] Labavić D, Nagel H, Janke W, and Meyer-Ortmanns H, submitted

DY 2.4 Mon 10:15 H47

DNA denaturation in correlated environments — Viktoria Blavatska[1], •Christian von Ferber[2], and Yurij Holovatch[1] — [1]Institute for Condensed Matter Physics, NAS Ukraine, Lviv — [2]Applied Mathematics Research Centre, Coventry University, UK

We revisit the problem of DNA denaturation in the frames of the Poland-Scheraga model. This model predicts a first or second order transition depending on the value of the loop exponent.

Usually an unperturbed background is assumed within this model. However, in a biologically relevant environment correlated structures are prevalent and the transition may change due to the influence of this environment.

Applying renormalisation group methods we determine the loop exponent in higher orders up to the fourth order in the ϵ-expansion. In the absence of disorder this allows us to determine the numerical value of the exponent using resummation techniques.

Performing corresponding calculations for the situation of correlated environments we find strong disorder effects.

DY 2.5 Mon 10:30 H47

Simulations of aggregation in homopolymer systems — •Johannes Zierenberg and Wolfhard Janke — Institut für Theoretische Physik, Universität Leipzig, Germany

We investigate the aggregation transition of a coarse-grained many-polymer system. To this end we apply parallel multicanonical simulations for different system sizes and densities. Our data suggests that the aggregation process in the simple model is a first-order phase transition. We investigate the dependence of the transition temperature on the density and size of the system and look at generic properties.

DY 2.6 Mon 10:45 H47

Collective behaviour of competing, coupled particles on a 1d chain — •Ines Weber[1], Ludger Santen[1], and Martin Evans[2] — [1]Department of Theoretical Physics, Saarland University, 66041 Saarbrücken, Germany — [2]Department of Physics & Astronomy, University of Edinburgh, Edinburgh EH9 3JZ, UK

Biopolymers are dynamic filaments involved in a wide variety of biological processes such as intracellular transport. Experiments have shown them to exhibit non-equilibrium fluctuations and deformations induced by molecular motors. I will present a simple model of such processes, which comprises competing species of interacting particles on a lattice. They perform a 'tug-of-war' and induce deformation and drift on a 1d chain. Constraints given by hard core coupling to next-neighbour sites influence the system's dynamics and result in collective particle behaviour.

DY 2.7 Mon 11:00 H47

Coexistence and survival in conservative Lotka-Volterra networks — •Johannes Knebel[1], Torben Krüger[2], Markus Weber[1], and Erwin Frey[1] — [1]Arnold-Sommerfeld Center for Theoretical Physics and Center for NanoScience, Theresienstraße 37, 80333 München — [2]Department of Mathematics, Ludwig-Maximilians-Universität München, Theresienstraße 38, 80333 München

Conservative Lotka-Volterra (LV) models play a fundamental role in many fields of science such as population dynamics. New insights into the maintenance of biodiversity can be gained by understanding the long-term behavior of complex LV interaction networks and by revealing their coexistence and survival scenarios.

Here we present a classification scheme for coexistence scenarios in well-mixed, conservative LV networks. Our theoretical approach to study global stability properties builds on a deterministic analysis by using the Pfaffian of the interaction matrix, a simpler form of the determinant for skew-symmetric matrices. We find that the classification of conservative LV dynamics on the basis of their interaction topology is incomplete and that non-cyclic networks can also maintain coexis-

tence of all species. The deterministic analysis also leads to a deeper understanding of the stability of ecological networks in finite populations as is reflected by a generalized scaling law for the extinction time in the vicinity of critical reaction rates. Our general results are illustrated for systems composed of four and five species.

DY 2.8 Mon 11:15 H47

Evolutionary game dynamics between random mutants — •Weini Huang[1], Bernhard Haubold[2], Christoph Hauert[3], and Arne Traulsen[1] — [1]Evolutionary Theory Group, Max Planck Insitute for Evolutionary Biology, August-Thienemann-Straße 2, 24306, Plön,Germany — [2]Bioinformatics Group,Max-Planck-Insitute for Evolutionary Biology, August-Thienemann-Straße 2, 24306, Plön,Germany — [3]Department of Mathematics, The University of British Columbia, 1984 Mathematics Road, Vancouver V6T1Z2, British Columbia, Canada

Polymorphism occurs when more than one genotype or phenotype exist in the same population. Although polymorphisms are often observed in populations, the emergence and maintenance of polymorphsims remain unclear.We investigate this question by introducing a new model, named as mutant games. In evolutionary game theory, the interactions of different types in a population are described by payoff matrices. However, the number of types is usually fixed and payoff matrices are typically predefined. This can be a limit to model a biological population with random mutations. In our mutant games, the interactions of mutants and resident types are represented by a dynamical payoff matrix. The resulting dynamics caused by random mutants under frequency dependent selection, leads to a remarkably higher diversity, compared to the mutants under constant selection. Interestingly, although arbitrary number of mutants are allowed in mutant games, an intermediate level of diversity is maintained.