

## DY 9: Poster I: Statistical Physics in Biological Systems (joint with BP)

Time: Monday 17:30–19:30

Location: Poster B2

DY 9.1 Mon 17:30 Poster B2

**Perturbed self-organized critical networks as a sleep model** — LI CHEN<sup>1</sup> and CHRISTIAN MEISEL<sup>1,2</sup> — <sup>1</sup>Max-Planck-Institut für Physik komplexer Systeme, Noethnitzer Str. 38, 01187 Dresden, Germany — <sup>2</sup>Department of Neurology, University Clinic Carl Gustav Carus, Fetscherstr. 74, 01307 Dresden, Germany

Why do we need sleep is a long mystery for centuries. Here, we propose a perturbed self-organized critical binary networks as a possible model to mimic the whole processes for the brain during awake time and sleep. By systematically characterizing the network activity, our results shows that the input received in awake time always derivatives our brains from critical state, with decreasing computational power, shorter effective response range, worse p-values etc. That is the reason why we need sleep to recover these brain functions by self-organizing back to critical networks by turning off all input from surroundings. An observation of the probability distribution of phase-lock interval from EEG data during growing sleep deprivation is given.

DY 9.2 Mon 17:30 Poster B2

**Information filtering by synchronous spikes in a neural population** — NAHAL SHARAFI — Bunsenstrasse 10, 37073 Goettingen

Information about time-dependent sensory stimuli is encoded by the spike trains of neurons. Here we consider a population of uncoupled but noisy neurons (each subject to some intrinsic noise) that are driven by a common broadband signal. We ask specifically how much information is encoded in the synchronous activity of the population and how this information transfer is distributed with respect to frequency bands. In order to obtain some insight into the mechanism of information filtering aspects found previously in the literature, we develop a mathematical framework to calculate the coherence of the synchronous output with the common stimulus for populations of simple neuron models. Within this frame, the synchronous activity is treated as the product of filtered versions of the spike trains of a subset of neurons. We compare our results for the simple cases of (1) a Poisson neuron with a rate modulation and (2) an LIF neuron with intrinsic white current noise and a current stimulus. For the Poisson neuron, formulas are particularly simple but show only a low-pass behavior of the coherence of synchronous activity. For the LIF model, in contrast, the coherence function of the synchronous activity shows a clear peak at high frequencies, comparable to recent experimental findings. We uncover the mechanism for this shift in the maximum of the coherence and discuss some biological implications of our findings.

DY 9.3 Mon 17:30 Poster B2

**Modelling of rhythmic patterns in hippocampus** — ANASTASIA LAVROVA<sup>1</sup>, MICHAEL ZAKS<sup>2</sup>, and LUTZ SCHIMANSKY-GEIER<sup>2</sup> — <sup>1</sup>Immanuel Kant Baltic Federal University, Kaliningrad, Russia — <sup>2</sup>Humboldt University at Berlin, Berlin, Germany

The hippocampal circuit can exhibit network oscillations in different frequency ranges ( $\gamma$  - 30-80 Hz;  $\theta$  - 4-12 Hz; as well as  $\theta/\gamma$  or a bursting regime) both in vivo and in vitro and switch between them.

Our goal is to investigate how coupling strength and delayed propagation influence synchronization and switching between different oscillatory states in minimal neuronal networks. To this end, we constructed a simple model of neurons comprising two fast-spiking and two slow-spiking cells, respectively. The network is described by coupled FitzHugh-Nagumo equations that well reproduce the dynamical behavior of different cells types: their periods, amplitudes, and phase shifts.

The model allows us to analyze the influence of synaptic strengths on the network synchronization and dynamical switching between  $\theta$ ,  $\gamma$ , and bursting regimes. In particular, we perform a thorough bifurcation analysis and identify parameters of synaptic connections that can efficiently induce switches in the network activity.

DY 9.4 Mon 17:30 Poster B2

**Interaction between Looped-Star Polymers** — DIETER HEERMANN and BENOIT KNECHT — Institut für Theoretische Physik, Universität Heidelberg, Philosophenweg 19, 69120 Heidelberg

We study the properties of looped star polymers, in which each arm is a ring that can be over- or underwound and compare them to the

classic linear-arm star polymer. Looped star polymers are more compact and overwinding increases their density. The effective repulsion between looped stars is similar to that of linear star polymers with twice as many arms half the length, following a logarithmic-Gaussian potential. The force pushing the arms outwards is more than twice as strong for looped star polymers than it is for linear star polymers for a number of arms  $f > 2$ .

DY 9.5 Mon 17:30 Poster B2

**Collective behavior and structure formation of hydrodynamically interacting active particles** — MARC HENNES, KATRIN WOLFF, and HOLGER STARK — Institut für Theoretische Physik TU Berlin

Lattice Boltzmann simulations of active run-and-tumble particles (RTPs) subject to an external trapping force have shown the emergence of a self-assembled pump in the presence of hydrodynamic interactions[1]. Here, we extend these results to active Brownian particles (ABPs), simulated by means of Brownian Dynamics simulation including hydrodynamic interactions. ABPs, in contrast to RTPs, do not tumble but reorient smoothly due to thermal noise, external torques, and vorticity fields in the fluid. Here, we clarify that the pump is a dynamic cluster of ABPs which only forms above a threshold value for the swimming speed. We assign an effective dipole moment to the pump and show that in this non-equilibrium situation the orientations of the particles are Boltzmann-distributed around the pump direction. We also consider bottom-heavy particles in an external gravitational field. Without hydrodynamic interactions and at sufficiently large swimming speeds, these particles accumulate at the top of the simulation box. However, when they interact hydrodynamically, we find this steady state to be unstable and observe the emergence of spatially separated, dynamical toroidal structures, reminiscent of classical bioconvection.

[1] M.E.Cates et al., Phys.Rev.Lett. 104, 258101 (2010)

DY 9.6 Mon 17:30 Poster B2

**Evolutionary food web model on a set of patches coupled by migration** — EVA MARIE WEIEL, KORINNA T. ALLHOFF, and BARBARA DROSSEL — Institut für Festkörperphysik, TU Darmstadt

Ecological food webs in a heterogeneous environment can be modelled by a complex network with two different types of connections. The local connections of these "networks on networks" represent the interaction through predation and competition of ecological populations in each habitat. The second type of connections represents migration between the habitats. Understanding how the spatial dimension affects the structure and stability of these complex networks is of large interest in ecological theory. We investigate the emergence, dynamics and interaction of food webs in a small set of patches. The dynamics in each patch is based on the often-cited evolutionary model introduced by Loeuille and Loreau in 2005. In addition to local evolution we include different types of migration between the patches and analyse their influence on the structure of the emerging food webs.

DY 9.7 Mon 17:30 Poster B2

**Effects of a stage structure in a population dynamics model to explain cyclic dominance of pacific sockeye salmon** — FABIAN FERTIG<sup>1</sup>, CHRISTOPH SCHMITT<sup>1</sup>, CHRISTIAN GUILL<sup>2</sup>, and BARBARA DROSSEL<sup>1</sup> — <sup>1</sup>Institut für Festkörperphysik, TU Darmstadt — <sup>2</sup>Institut für Zoologie und Anthropologie, Georg-August-Universität Göttingen

The number of sockeye salmon that return from the ocean to their lakes of birth in the Fraser River basin in Canada shows a remarkably strong and regular four-year oscillation. This so-called cyclic dominance phenomenon is reproduced as a stable attractor by a recently introduced predator-prey model for salmon fry and their main predator in the rearing lakes, rainbow trout. However, rainbow trout is known to prey also strongly on kokanee salmon, which spend all their life in the lakes. Including kokanee in the model typically leads to a breakdown of cyclic dominance and often also to the extinction of one of the salmon species. This means either that the observed coexistence of the two species together with the occurrence of cyclic dominance in the sockeye population is a transient phenomenon, or that the model is not detailed enough. In order to explore the conditions under which cyclic dominance could persist in the presence of both salmon species,

we investigate various models that take the stage structure of trout and the different preference of adult and juvenile trout for kokanee and sockeye salmon into account. We show that the parameter range for cyclic dominance can be increased in stage structured models.

DY 9.8 Mon 17:30 Poster B2

**Simple models for generation cycles** — •TORSTEN PFAFF<sup>1</sup>, BARBARA DROSSEL<sup>1</sup>, and CHRISTIAN GUILL<sup>2</sup> — <sup>1</sup>Institut für Festkörperphysik, Technische Universität Darmstadt — <sup>2</sup>Institut für Zoologie und Anthropologie, Georg-August-Universität Göttingen

Many biological species show population oscillations due to density dependent competition. The periods of the oscillations are related to the life cycle of the species, and they have been used to classify the oscillating systems.

We present three simple models consisting of a one dimensional time delay equation with only two parameters. These models show all essential properties of generation cycles. Due to their simplicity, they are helpful for obtaining a mechanistic understanding of the population oscillations, and they give new insights into the origin of the periods and into the size of the intervals that are covered by these periods. Based on the insights gained from our simple models, we also obtain a better understanding of the more complex models presented in the classical paper by Gurney & Nisbet 1985, and we can extend their results.

As an outlook, we argue that the simple models are useful for investigating generation effects in many species food webs.

DY 9.9 Mon 17:30 Poster B2

**Nematic microstructure in biopolymer solutions** — •MARC LÄMMEL and KLAUS KROY — Institut für Theoretische Physik, Leipzig, Germany

Domains of aligned filaments play an important role in solutions of semiflexible biopolymers. For instance, they occur as a consequence of shear induced ordering upon sample preparation or as a precursor of bundle formation. Here, we address the influence of such nematic order on the packing structure of semiflexible polymer networks, based on the wormlike chain model. The complicated many-body problem is approached utilizing the concept of the tube [1], which accounts for caging of a test filament by surrounding filaments. It is represented through a cylindrical confinement potential that is self-consistently determined. In particular, we analyze the effect of local nematic order on the micro-structure in terms of the tube radius distribution [2], which can experimentally be measured with high accuracy for F-actin solutions [3], allowing for a precise quantitative comparison of theory and experiment.

[1] Morse, D. C., Phys. Rev. E 63, 031502 (2001)

[2] Glaser, J. et al., Phys. Rev. E 84, 051801 (2011)

[3] Glaser, J. et al., Phys. Rev. Lett. 105, 037801 (2010)

DY 9.10 Mon 17:30 Poster B2

**Stochastic tug-of-war model with symmetric motor properties does not provide processive cargo movement.** —

•SARAH KLEIN<sup>1</sup>, CECILE APPERT-ROLLAND<sup>2</sup>, and LUDGER SANTEN<sup>1</sup> — <sup>1</sup>Theoretische Physik, Universität des Saarlandes, 66123 Saarbrücken — <sup>2</sup>Laboratory of Theoretical Physics, Paris-Sud University, Orsay

Many different types of cellular cargos are transported bidirectionally along microtubules by teams of molecular motors. The motion of this object has been experimentally characterized *in vivo* as processive with rather persistent directionality. By means of an effective theoretical approach, introduced by Lipowsky *et al.* [1], it has been argued that the dynamics of these object are the result of a tug-of-war between different kinds of motors. This picture has been questioned in a recent article by Kunwar *et al.* [2], who considered the coupling between motor and cargo in more detail. In this contribution we discuss possible scenarios within this framework that eventually lead to the observed dynamic patterns of bidirectional cargo transport.

[1] M. J. I. Müller, S. Klumpp, R. Lipowsky, PNAS 105, 4609 - 4614 (2008)

[2] A. Kunwar, S. K. Tripathy, J. Xu, PNAS 108(47), 18960-18965 (2011)

DY 9.11 Mon 17:30 Poster B2

**Modeling diversity of immune genes in host-parasite co-evolution** — •YIXIAN SONG and ARNE TRAUlsen — Max Planck Institute for Evolutionary Biology Plön

We investigate an individual based stochastic model of host-parasite co-evolution. The model is made to simulate the origin and maintenance of the major histocompatibility complex (MHC) polymorphism, i.e., coexistence of diverse genetic variants in a population. In the genes of the MHC, the key component of adaptive immunity, very high levels of allelic diversity are observed. MHC molecules are essential in antigen presentation process by T-cells. The high polymorphism of MHC genes has drawn attention of evolutionary biologists and population geneticists. Our model is focused on one locus with two alleles. Thereby the dynamics of coexisting parasites and alleles are explored. The goal of this model is to develop a theoretical understanding of the dynamic equilibrium in which the MHC diversity in a population approximately remains from generation to generation, but changes in composition.

DY 9.12 Mon 17:30 Poster B2

**Interaction Dynamics of Colloidal Particles in an Optical Light Tube** — •BENJAMIN TRÄNKLE and ALEXANDER ROHRBACH — Lab for Bio- and Nano-Photonics, University of Freiburg, Germany

Specific reactions of Brownian particles are often affected by long and short ranging forces, such as hydrodynamic, entropic and steric forces. An example is the fusion of vesicles within a living cell. Colloidal particles can serve as a model system for the investigation of such interaction events. We trap two particles in a single potential, which is generated by an oscillating optical line trap. In this geometry, the reaction rate is increased due to the confined space, while rotational and translational degrees are preserved. An acousto-optic deflector (AOD) is used to steer the optical trap and therefore achieve kHz scanning rates. The spheres' positions are tracked simultaneously in 3 dimensions with back focal plane interferometry [1]. With this method we can measure the interaction dynamics of spheres diffusing in a single optical potential with a spatial precision in the nanometer range at kHz rates. Static and dynamic interaction information is gained by analyzing the particle trajectories. The AOD is also used to control the line potential, by steering the laser power during the scanning process. Thereby, we are able to change the reaction volume and investigate its effect on the reaction rate and interaction duration [2].

[1] Speidel et al., Interferometric 3D tracking of several particles in a scanning laser focus. Optics Express, 17(2):7-9, 2009.

[2] Tränkle et al., Interaction dynamics of two colloids in a single optical potential. Physical Review E, 86(2):1-5

DY 9.13 Mon 17:30 Poster B2

**A simple polymer in a spherical cage** — •MARTIN MARENZ, JOHANNES ZIERENBERG, and WOLFHARD JANKE — Institut für Theoretische Physik, Universität Leipzig, Postfach 100920, D-04009 Leipzig, Germany

We study the change of the pseudo phase transition of a simple homopolymer inside a spherical confinement. Of particular interest is the shift of the collapse and freezing transitions with shrinking radius of the sphere. The polymer is a simple bead-stick model, where the distance between neighboring monomers is fixed, between three monomers in a row acts a bending potential and all non neighboring monomers interact via a Lennard-Jones potential. We use modern Monte Carlo methods to investigate the phase space of this model. Most of the results are obtained by parallel tempering simulations followed by a multi-histogram reweighting method combining a direct and a recursive procedure. To crosscheck our results, especially near the pseudo phase transition, we used a parallelized kind of the multicanonical simulation.

To characterize the pseudo phase transition we analyse fluctuations of energetic and conformational observables. As zero order case the spherical cage is modeled only as a geometrical constraint without any interaction with the polymer. In further simulations we switched on a interaction between the polymer and the surface of the sphere and looked for effects induced by this interaction.

DY 9.14 Mon 17:30 Poster B2

**Hybrid simulation model for spatiotemporal intracellular calcium signals** — •MARTIN RÜCKL<sup>1</sup>, NAGAIHA CHAMAKURI<sup>2</sup>, and STEN RÜDIGER<sup>1</sup> — <sup>1</sup>Humboldt-Universität, Berlin — <sup>2</sup>RICAM, Linz, Austria

Calcium induced calcium release (CICR) from IP3R channels on the ER membrane and the interplay with calcium buffers can result in complex spatiotemporal calcium distributions in the cytosol which play an important role in intra- and extracellular signaling.

To model those patterns, we solve the coupled reaction diffusion and

master equations for both the DeYoung-Keizer [1] and the four state [2] stochastic IP3R gating models, using an interplay between a 3D finite element method and the Gillespie algorithm. We investigate the impact of the local calcium decay after a channel closing and the diffusive coupling of clustered channels on the collective stochastic behaviour of the channels. To obtain different calcium decays we performed simulations for different buffer configurations while the diffusive coupling is altered by means of a larger inter channel distance within a channel cluster. Our results can also be used to assess the reliability of different computationally cheaper approximations frequently used in other works.

[1] D.W. DeYoung and J. Keizer, Proc. Natl. Acad. Sci. U.S.A 89, 9895 (1992).

[2] G. Ullah, I. Parker, D.D. Mak, J.E. Pearson, Cell Calcium, 52(2):152-160, 2012

DY 9.15 Mon 17:30 Poster B2

**Measuring structural changes in chromatin induced by ionizing radiation: an analysis of localization microscopy images** —

•YANG ZHANG<sup>1</sup>, GABRIELL MÁTÉ<sup>1</sup>, SABINA HILLEBRANDT<sup>2</sup>, PATRICK MÜLLER<sup>2</sup>, MICHAEL G. HAUSMANN<sup>2</sup>, and DIETER W. HEERMANN<sup>1</sup> — <sup>1</sup>Institute for Theoretical Physics, Heidelberg University, Germany — <sup>2</sup>Kirchhoff-Institute for Physics, Heidelberg University, Germany

The elaborate cell response to the arising of DNA double-strand breaks caused by ionizing radiation (IR) involves local remodeling and structural changes of the surrounding chromatin. In particular, experiments indicate different repair characteristics in heterochromatin (HC) and euchromatin (EC). However, there is still no detailed understanding of these changes of the genome organization. In this work we analyzed localization microscopy images by means of statistical physics and graph theory to provide a quantitative description of structural changes induced by IR. HeLa cells were exposed to different doses of IR. Positions of fluorescence stained nucleosomes were determined using localization microscopy. Simultaneously, markers of modified histones indicating HC or EC were localized. We then calculated the pair correlation functions as well as edge length distributions and mean coordination numbers for graphs obtained by triangulations of the marker positions. Our results show that HC regions undergo a relaxation immediately after exposure to ionizing radiation while EC regions show the opposite behavior. We further demonstrate that at later times after irradiation these alterations become less pronounced.

DY 9.16 Mon 17:30 Poster B2

**Pulling experiments on biological molecules: model analysis and simulation** — •KATHARINA WENZEL and ANDREAS HEUER — Westfälische Wilhelms Universität Münster

The implementation of AFM-pulling routines by Steered Molecular Dynamics (SMD) has created a powerful tool to provide information of the unfolding and refolding process of biological molecules. Here, a molecule is stretched under pulling with the help of an umbrella potential where the choice of pull speed and cantilever stiffness can play a critical role in the unfolding pathway. To investigate the influence of these parameters several pull experiments under the same circumstances are simulated with the Trp-cage Miniprotein TC5b in vacuo. It can be shown that simulations can lead to very unstable behaviour, especially for higher force speed and stiff cantilever.

To get a more general understanding a basic setup for pulling experiments with one particle under Brownian motion is implemented. Likewise the chosen pathway over the energy barrier as well as the degree of fluctuations strongly depend on the chosen speed and stiffness.

DY 9.17 Mon 17:30 Poster B2

**Mutation and Migration in Structured Populations** —

•MATTHIAS LECHNER, JONAS CREMER, ANNA MELBINGER, and ERWIN FREY — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München

Despite the risk of exploitation, altruistic individuals are a common phenomenon in nature. The solution to this so called Dilemma of Cooperation is the purpose of many models in the field of evolutionary dynamics. A recent approach to explain this dilemma is to combine population dynamics with evolutionary game theory in a stochastic description, which shows a transient initial increase of cooperation [1]. This model was then extended by a group-structured population that is subject to repetitive regrouping events, giving rise to a long-term maintenance of cooperation under certain initial conditions [2]. Here, we study the consequences of introducing mutation and mi-

gration to this model. With the use of numerical simulations we show that both have similar effects on the system's dynamics. The evolution of purely cooperative groups turns out to be pivotal in the explanation of these changes. For mutation, we support this claim by an analytical approximation, which reproduces our numerical results. In summary, we find that although mutation and migration eventually inhibit cooperation in this model, cooperative behavior is still maintained for a wide range of parameters.

[1] A. Melbinger et al., PRL 105, 178101 (2010)

[2] J. Cremer et al., Scientific Reports, 2, 281 (2012)

DY 9.18 Mon 17:30 Poster B2

**Swimming patterns of bacteria in confined microchannels with obstacles** — •MICHAEL RAATZ, MATTHIAS THEVES, and CARSTEN BETA — Institute of Physics and Astronomy, University of Potsdam, Germany

Depending on environmental conditions, single bacteria can irreversibly attach to a solid-liquid or liquid-air interface and form the cores for surface associated growth into aggregates, where cells are embedded in a polymer matrix and become resistive to antibiotic treatment (biofilms). We use microfluidic channels and high-speed time lapse microscopy to investigate the movement of cells which are swimming in close proximity to the wall interface and interact with various arrangements of circular obstacles. Motility statistics show that in the presence of obstacles, the average run length of a bacterium and the probability distribution of turn angles changes when compared to an obstacle-free channel. At small collision angles with the obstacle, the cell trajectory is slightly deflected while large angle collisions can induce reversals in the direction of propagation of a cell. Furthermore, we observe cases where cells move around the obstacle in a circular path, maintaining a stable 'orbit' at a distance of one or two cell diameters from the obstacle surface.

DY 9.19 Mon 17:30 Poster B2

**Evolution of increasingly complex filamentous molecules** —

•PHILIPP ZIMMER<sup>1</sup>, EMANUEL WORST<sup>2</sup>, EVA WOLLRAB<sup>2</sup>, ALBRECHT OTT<sup>2</sup>, and KARSTEN KRUSE<sup>1</sup> — <sup>1</sup>Universität des Saarlandes, Theoretische Biologische Physik, Postfach 151150, 66041 Saarbrücken — <sup>2</sup>Universität des Saarlandes, Biologische Experimentalphysik, Postfach 151150, 66041 Saarbrücken

On the young earth, molecules with increasing complexity evolved under prebiotic conditions. How the interplay of different, competing molecular species and the spontaneous generation of new ones eventually led to the formation of cells remains poorly understood. Here we investigate a mechanism of "biased variation" and show that it provides a way to generate more complex structures. In this mechanism certain variations of existing molecular species are more likely to occur than others. Combined with an exponential amplification, this process can generate increasing complexity. We investigate this mechanism using a stochastic model for the evolution of linear molecules and we present a DNA-based experimental realization.

DY 9.20 Mon 17:30 Poster B2

**In-phase and anti-phase synchronization in noisy Hodgkin-Huxley neurons** — •XUE AO, PETER HÄNGGI, and GERHARD SCHMID — Institut für Physik, Universitätsstr. 1, 86159 Augsburg, Germany

We numerically investigate the influence of intrinsic channel noise on the dynamical response of delay-coupling in neuronal systems. The stochastic dynamics of the spiking is modeled within a stochastic modification of the standard Hodgkin-Huxley model wherein the delay-coupling accounts for the finite propagation time of an action potential along the neuronal axon. We quantify this delay-coupling of the Pyragas-type in terms of the difference between corresponding presynaptic and postsynaptic membrane potentials. For an elementary neuronal network consisting of two coupled neurons we detect characteristic stochastic synchronization patterns which exhibit multiple phase-flip bifurcations: The phase-flip bifurcations occur in form of alternate transitions from an in-phase spiking activity towards an anti-phase spiking activity. Interestingly, these phase-flips remain robust in strong channel noise and in turn cause a striking stabilization of the spiking frequency.

DY 9.21 Mon 17:30 Poster B2

**Inverse statistical analysis in heart rate variability** — •HALEH EBADI — Bioinformatics Group, Department of Computer Science, University of Leipzig, Germany

This poster presents an investigation on heart cycle time series, using the inverse statistical analysis, a concept borrowed from turbulence. By inverse statistics, also sometimes called exit time statistics, we turn the variables around such that the fluctuating variable becomes the fixed variable, while the fixed variable becomes fluctuating. Using this approach, we studied the distribution of the exit time needed to achieve a predefined level of heart rate alteration. Such analysis uncovers the most likely waiting time needed to reach a certain change in the rate of heart beat. This analysis showed a significant difference between the raw data and shuffled data, when the heart rate accelerates or decelerates to a rare event. We also report that inverse statistical analysis can distinguish between the electrocardiograms taken from healthy volunteers and patients with heart failure.

DY 9.22 Mon 17:30 Poster B2

**Bifurcation analysis of a thalamocortical mean field model** — ●MICHAEL SCHELLENBERGER COSTA, THOMAS MARTINETZ, and JENS CHRISTIAN CLAUSSEN — INB, University of Lübeck, Germany

Multiple studies have shown the importance of slow wave sleep for the development of memories. Furthermore slow oscillatory activity can be modulated by non-invasive stimulation, which leads to an enhancement of memory consolidation [1]. In order to optimize the experimental procedures and thereby further improve the memory consolidation, a detailed knowledge of the cortical response to the applied stimuli is essential. Mean field models of the cortex have been extensively studied [2], however the interplay between the thalamus and the cortex is known to be crucial for both slow wave sleep and the processing of sensory stimuli. Therefore we investigate the dynamic properties of an extended phenomenological mean field model of the thalamocortical system, that is able to resemble the EEG signal during slow wave sleep.

[1] L. Marshall et al, Nature 444, 610 (2006).

[2] M. Ursino, F. Cona and M. Zavaglia, Neuroimage 52, 1080 (2010).

DY 9.23 Mon 17:30 Poster B2

**Limitations on entrainment frequency in cortical slow wave stimulation** — ●ARNE WEIGENAND<sup>1</sup>, LISA MARSHALL<sup>2</sup>, THOMAS MARTINETZ<sup>1</sup>, and JENS CHRISTIAN CLAUSSEN<sup>1</sup> — <sup>1</sup>INB, University of Lübeck — <sup>2</sup>Neuroendocrinology, University of Lübeck, Germany

Stimulation of cortical slow waves during sleep has recently raised considerable attention due to enhancement of memory consolidation [1]. We consider the question how slow waves, comprised by bursty up and quiescent down states, can be entrained or strengthened by exter-

nal stimulation. In a purely cortical model no limitation within the relevant frequency range occurs [2]. Stimulation by TMS or optogenetic methods [3,4] hint at an upper entrainment frequency of 4 Hz. In contrast, our optical stimulation experiments [5] revealed that entrainment is only possible up to 1 Hz. We account thalamic gating for this difference. Hence we consider the inclusion of thalamic feedback loops into generic cortical network models, for adaptation of parameters in a phenomenological mean-field model. We optimize pulse length and frequency to obtain an optimized stimulation protocol.

[1] L. Marshall et al, Nature 444, 610 (2006). [2] Weigenand, Martinetz, Claussen, Cogn. Neurodyn. 6, 367 (2012); Schütt, Claussen, Cogn. Neurodyn. 6, 343 (2012). [3] Massimini et al., PNAS 104, 8407 (2007). [4] Kuki et al, Frequency-dependent entrainment of neocortical slow oscillation to repeated optogenetic stimulation in the anesthetized rat, Neurosci. Res. (2012, in press). [5] Weigenand et al (in preparation).

DY 9.24 Mon 17:30 Poster B2

**Approach for automated sleep stage classification from spectral data** — ●STEPHAN VOLKLAND and JENS CHRISTIAN CLAUSSEN — INB, University of Lübeck, Germany

Manual scoring of sleep stages according to the Rechtschaffen-Kales rule catalogue (or the only simplified AAMS rules) is done on 30s epochs and requires extensive manual labor. Further the inter-rater and intra-rater reliabilities are not fully satisfactory for subsequent quantitative analysis. Hence it would be desired to develop and use automatic methods: attempts in this direction have been tried numerously but not paved their way to clinical practice as the EEG signatures of the sleep stages differ between subjects even in a qualitative way. Furthermore it would be desired to detect and resolve sub-stages as well as achieve a higher time resolution; both is unfeasible for manual scoring which would then be slower than real time. Here we refer and compare to an approach by [1] where three quantitative indexes are derived from EEG and EMG and broken down to 8 possible states. Our approach also is based on EMG and EEG, whereby we also use EOG, and use full information from five physiological EEG bands as input for unsupervised clustering (k-means) of data where clusters then are assigned to sleep stages [2]. We observe that the known difficulties to reliably distinguish S1, REM and wake stages persist. For the range between stages S2 and S4, we however can obtain a reliable interpolation between the sleep stages even for 16s or shorter time intervals.

[1] B. Müller, W.D. Gäbelein, H. Schulz, Sleep 29, 967 (2006).

[2] Stephan Volkland, BA thesis, INB, Lübeck (2012).