

BP 13: Signaling, Biological Networks

Time: Wednesday 9:30–11:00

Location: BAR 0106

Invited Talk

BP 13.1 Wed 9:30 BAR 0106

Biological signal processes across scales — ●STEFFEN RULANDS — Ludwig-Maximilians Universität München, Arnold Sommerfeld Center for theoretical Physics, Theresienstr. 37, 80333 München — Max-Planck-Institute for theoretical Physics, Nöthnitzer Str. 38, 01187 Dresden

In contrast to many physical systems, biological systems have the remarkable architecture of being organized into a spatial hierarchy of non-equilibrium processes: from molecules embedded into sub-cellular compartments to cells interacting in tissues. In my talk, I will show how biological systems manipulate the transmission of noise and information between and across these scales in order to perform biological functions. By combining theory and experiments I will first describe a general theory describing the propagation of noise and signals in multi-scale non-equilibrium systems. I will then apply these insights to show how cells make use of the propagation of fluctuations on the subcellular scale to perform biological signal processing: by establishing a low-pass filter of concentration fluctuations in the regulation of cell death and by facilitating a gelation phase transition in the innate immune response.

BP 13.2 Wed 10:00 BAR 0106

Protein Dynamics in the Complex Physical Environment of the Synapse — ●SIMON DANNENBERG, SARAH MOHAMMADINEJAD, and STEFAN KLUMPP — Institut für Dynamik komplexer Systeme Georg-August-Universität Göttingen, Göttingen, Germany

The synapse is a complex environment that is densely packed with proteins and has an internal geometry structured by membranes. This affects the mobility of proteins involved in signal transmission and hence, their availability at corresponding reaction sites.

In our work we use dynamic Monte Carlo simulations to investigate the influence of different physical features of the synapse on protein mobility. The simulations are parameterized by mobility measurements via FRAP experiments. Our approach revealed an unexpectedly high sensitivity of the experiments on the geometry of the synapses as well as dependence of protein fluxes on synaptic features such as axon diameter and synapse size.

BP 13.3 Wed 10:15 BAR 0106

How can a single neuron influence behavior? Hints from integrate-and-fire network models — ●DAVIDE BERNARDI¹ and BENJAMIN LINDNER^{2,3} — ¹Italian Institute of Technology, Ferrara, Italy — ²Bernstein Center for Computational Neuroscience, Berlin, Germany — ³Institut für Physik, Humboldt-Universität zu Berlin

Recent experiments challenge the established view that only large neuronal populations can reliably encode information, as is argued on the basis of the large noise and chaotic dynamics of cortical networks. One striking example is that awake rats can be trained to respond to the stimulation of a single cell in the barrel cortex. Here, this problem is framed theoretically by studying how the stimulation of a single neuron can be detected in large networks of integrate-and-fire neurons.

Combining numerical simulations and analytical calculations, we illustrate a simple strategy to detect the single neuron stimulation in the activity of a readout subpopulation or in a second network, which is both more realistic and more efficient. Furthermore, a readout network tuned to approximate a differentiator circuit can detect the single-

neuron stimulation in a more biologically detailed model. In this case, the detection probability increases significantly upon injection of an irregular current, in agreement with experiments.

Our models show how inhibitory synapses could make it possible for the sensitivity to single-neuron perturbation to coexist with a stable asynchronous spontaneous activity, that is, through a mild selective imbalance in the topological (spatial) and temporal sense.

BP 13.4 Wed 10:30 BAR 0106

Towards statistical models of activity recordings from stem cell derived neuronal networks — ●SEBASTIAN WILLENBERG¹, ELIJAH R. SHELTON¹, PAULINA M. WYSMOLEK², FILIPPO D. KIESSLER¹, ACHIM BRINKOP¹, and FRIEDHELM SERWANE^{1,2,3} — ¹Faculty of Physics and CeNS, LMU, Munich, Germany — ²MPI for Medical Research, Heidelberg, Germany — ³Munich Cluster for Systems Neurology, Munich, Germany

Analysis of neuronal activity is the key to understanding the principles of brain circuitry. Theoretical models have been applied on many different scales, ranging from the analysis of single neuron activity to the collective behaviour of large groups of neurons. Models from statistical physics describe the behaviour of networks across spatial and temporal scales with a minimal amount of parameters. Until now, those models have mainly been applied to datasets recorded via 2D electrode arrays. This makes accessing 3D network morphology challenging. I will present our first steps applying statistical models to neuronal recordings of stem cell derived neuronal networks obtained using lightsheet¹ or confocal microscopy. To model the collective firing we map single neuron activity to two states and apply a maximum entropy model to calculate the entropy and energy following the approach of Tkačik et al.². Using this approach, we seek a minimal model describing the firing activity which allows us to understand and predict the collective behaviour of *in vitro* neuronal networks.

1: Wysmolek et al., Sci Rep 12, 20420, 2022

2: Tkačik et al., PNAS 112, 11508, 2015

BP 13.5 Wed 10:45 BAR 0106

Inference of dynamical networks connectivity with Recurrent Neural Networks — ●PABLO ROJAS, MARIE KEMPKE, and MARTIN E GARCIA — Theoretical Physics, University of Kassel, Germany

The inference of directed links in networks of interacting systems is a problem spanning many disciplines. Systems out of equilibrium represent a special case, where samples are not independent but structured as timeseries. In this context, Recurrent Neural Networks (RNN) have attracted recent attention, due to their ability to learn dynamical systems from sequences. We introduce a method to infer connectivity of a network from the timeseries of its nodes, using a RNN based on Reservoir Computing (RC). We show how modifications of the standard RC architecture enable a reliable computation of the existence of links between nodes. While the method does not require information about the underlying mathematical model, its performance is further improved if the selection of hyperparameters is roughly informed by knowledge about the system. The method is illustrated with examples from different complex systems, ranging from networks of chaotic Lorenz attractors to biological neurons. Using simulations of these systems, we demonstrate its power and limitations under a variety of conditions, such as noise levels, delayed interactions, size of the network and hidden variables.