BP 2: Computational Biophysics and Neuroscience

Time: Monday 9:30–12:15 Location: H13

BP 2.1 Mon 9:30 H13

Non-ideality in lipid mixtures, a molecular dynamics study — •Lisa Berezovska[1], Fabrice Thalmann[1], and Raisa Kociurzynski[2] — [1]Institut Charles Sadron, CNRS and University of Strasbourg, 23 rue du Loess, F-67034 Strasbourg, France — [2]Faculty of Biology, Albert-Ludwigs-University Freiburg, Schänzlestraße 1, 79104 Freiburg, Germany

Biological membranes are complex environments characterized by multicomponent lipid mixtures[1]. We investigate in this work binary lipid bilayers using the SPICA coarse-grained molecular dynamics model.

Adapting the Kirkwood-Buff theory of liquid mixtures [2] to finite wavelegth density fluctuations statistics, we compare various practical approaches for determining the interaction parameters in a theory of regular solution description of these numerical lipid mixtures.

[1] Ole G. Mouritsen, L. A. Bagatolli. Life as a matter of fat, Springer-Verlag GmbH, 2015

[2] A. Ben-Naim, Water and Aqueous Solutions: Introduction to a Molecular Theory, Plenum Press, 1974

[3] Lisa Berezovska, Raisa Kociurzynski, Fabrice Thalmann, in preparation

BP 2.2 Mon 9:45 H13

Membrane-mediated interactions between non-spherical elastic particles — •Jiarul Midya, Thorsten Auth, and Gerhard Gompper — Theoretical Physics of Living Matter (IBI-5/IAS-2), Forschungszentrum Jülich, D-52425 Jülich,Germany

Transport of particles across lipid-bilayer membranes is important for biological cells to exchange information and material with the environment. Large particles often get wrapped by membranes [1]. However, many particles in vivo and in vitro are deformable, e.g., vesicles, filamentous viruses, macromolecular condensates, polymer-grafted nanoparticles, and microgels. Vesicles may serve as a generic model system for deformable particles [2]. Using the Helfrich Hamiltonian, triangulated membranes, and energy minimization, we predict the interplay of vesicle shapes and wrapping states. Increasing particle softness enhances the stability of shallow-wrapped and deep-wrapped states over non-wrapped and complete-wrapped states. The free membrane mediates an interaction between partial-wrapped vesicles. For the deep-wrapped vesicles, we predict a purely repulsive interaction. For shallow-wrapped states, interaction potential depends on the mutual orientation of the vesicles. Our predictions may guide the design and fabrication of deformable particles for efficient use in medical applications, such as targeted drug delivery.

[1] S. Dasgupta et al., J. Phys.: Condens. Matter **29**, 373003 (2017); [2] X. Yi et al., Phys. Rev. Lett. **107**, 098101 (2011).

BP 2.3 Mon 10:00 H13

RNA structure prediction via Machine Learning — •Alexander Schug[1,2], Oskar Taubert[4], Christian Faber[1], Mehari Zerihun[1], Fabrizio Pucci[1], Fabrice von der Lehr[3], Philipp Knechtges[3], Marie Weiel[4,5], Charlotte Debus[4,5], Daniel Coquelin[4,5], Stefan Kesselheim[1,5], Achim Basermann[3], Achim Streit[4], and Markus Götz[4,5] — [1]Jülich Supercomputing Centre, FZ Jülich, Jülich — [2]Faculty of Biology, University of Duisburg/Essen — [3]Institute for Software Technology, German Aerospace Centre (DLR) — [4]Steinbuch Centre for Computing, Karlsruhe Institute of Technology — [5]Helmholtz AI

Knowledge of biomolecular structure is necessary to gain any detailed understanding of their function For proteins, tools rooted in statistical physics such as Direct Coupling Analysis (DCA) or Machine Learning driven approaches (ML) such as Alpha Fold 2 exploit massive sequence databases to trace evolutionary patterns for structure predictions. We demonstrate how additional information, such as low-resolution experimental information (e.g. SAXS or FRET) can integrated. For RNA there are significantly less data available than for proteins, which makes ML more challenging. Still, we demonstrate how contact prediction for RNA can be vastly improved both via simple convolutional neural networks but also by unsupervised deep-learning approaches by combining multiple self-supervised learning tasks. In an empirical evaluation for RNA, we find a strong increase of prediction quality.

Invited Talk BP 2.4 Mon 10:15 H13

Integrative modeling of dynamic biomolecular structures — •Holger Gohlke — Institute for Pharmaceutical and Medicinal Chemistry, Heinrich Heine University Düsseldorf, 40225 Düsseldorf, Germany — John von Neumann Institute for Computing (NIC), Jülich Supercomputing Centre (JSC), Institute of Biological Information Processing (IBI-7: Structural Biochemistry), and Institute of Bio- and Geosciences (IBG-4: Bioinformatics), Forschungszentrum Jülich GmbH, 52425 Jülich, Germany

Structures of biomacromolecules and their complexes are essential to understand the underlying molecular mechanisms of the biological processes. If biomolecular systems are complex, information from multiple experimental and computational methods is combined by integrative modeling (IM) for generating integrative structure models. We will describe how molecular modeling and simulations contributed to a high-resolution NMR characterization of all apparent states of the prototypic 10*23 DNAzyme and to rationally selecting a single-atom replacement, with which the performance of the DNAzyme could be considerably enhanced. Furthermore, we will address how to overcome the sparsity of FRET experiments to provide state-specific structural information of complex dynamic biomolecular assemblies and probe the robustness of Maximum Entropy Method reconstructions for a flexible system with ordered parts using FRET data as experimental information.

15 min. break

BP 2.5 Mon 11:00 H13

Mechanical stimulation in stem cell-derived 3D neuronal networks — •Elijah Shelton[1], Katja Salbaum[1,2], Filippo Kiessler[1], Paulina Wysmolek[3], Selina Sonntag[1], and Friedhelm Serwane[1,2,4] — [1]Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-Universität, Munich, Germany — [2]Graduate School of Systemic Neuroscience (GSN), Munich, Germany — [3]Max Planck Institute for Medical Research, Heidelberg, Germany — [4]Munich Cluster for Systems Neurology (SyNergy), Germany

Neurons sense and respond to mechanical factors in their local microenvironment. For example, firing activity is modulated in response to amplitude and location of a mechanical stimulation as single cell in vitro experiments have shown. However, it is unclear (i) how these observations translate to the scale of neuronal tissues and (ii) how mechanical stimulation informs the formation and function of neurons in 3D networks. To tackle this problem, we combine stem cell-derived neuronal organoids, magnetic droplets as mechanical actuators, and calcium imaging as tool for neuronal characterization. Using 30-50 micron diameter magnetic droplets, we produce controlled and precise mechanical stimulations inside these 3D tissues. We visualize electrophysiological activity within these networks using genetically encoded calcium sensors and confocal fluorescence microscopy. Here, I present recent mechanical and electrophysiological measurements within these neuronal organoids. Such kinds of recordings might provide insights into how mechanical forces can influence both form and function of neuronal networks.

BP 2.6 Mon 11:15 H13

Characterizing spreading dynamics of subsampled systems with nonstationary external input — Jorge de Heuvel[1], Jens Wilting[2], Moritz Becker[3], Viola Priesemann[2], and •Johannes Zierenberg[2] — [1]University of Bonn, Bonn, Germany — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen Germany — [3]University Medical Center Göttingen, Göttingen Germany

Many systems with propagation dynamics, such as spike propagation in neural networks and spreading of infectious diseases, can be approximated by autoregressive models. The estimation of model parameters can be complicated by the experimental limitation that one observes only a fraction of the system (subsampling) and potentially time-dependent parameters, leading to incorrect estimates. We show analytically how to overcome the subsampling bias when estimating the propagation rate for systems with certain nonstationary external input. This approach is readily applicable to trial-based experimental setups and seasonal fluctuations as demonstrated on spike recordings from monkey prefrontal cortex and spreading of norovirus and measles.

BP 2.7 Mon 11:30 H13

Mesoscopic description of metastability and hippocampal replay in neural networks with short-term plasticity — Bastian Pietras[1], Valentin Schmutz[2], and •Tilo Schwalger[3] — [1]Universitat Pompeu Fabra, Barcelona, Spain — [2]Brain Mind Institute, School of CÉcole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland — [3]Technische Universität Berlin

Sequences of metastable states in neuronal population activities have been linked to various sensory and cognitive functions. Two prominent mechanisms of metastable dynamics are noise-induced transitions among attractors and deterministic transitions induced by slow fatigue processes. The dependence of these mechansisms on neural circuit parameters at the microscopic scale are largely unclear. Starting with a network of linear-nonlinear Poisson spiking neurons with synaptic short-term plasticity, we use a bottom-up approach and derive a stochastic neural-mass model at the mesocopic scale that links to the microscopic circuit parameters. We apply the mesoscopic model to investigate hippocampal "replay" events, i.e. spontaneous sequences of metastable activations of place cells. We study a spiking-neural-network for depression-induced metastability of place-cell activity. The corresponding mesoscopic model precisely reproduces the statistics of metastastable events in the microscopic network model. This enables us to efficiently explore the full range of neuron numbers including the thermodynamic limit. We find a novel dynamical regime in finite-size networks where metastable replay events are fluctuation-driven and exhibit biologically plausible irregularity.

BP 2.8 Mon 11:45 H13

Decision-making and dynamics in a small neural network — •Monika Scholz — Max Planck Institute for Neurobiology of Behavior - caesar

The nematode C. elegans feeds on small microbes which it ingests using a pumping action of the pharynx. Its pharyngeal nervous system, which controls feeding, comprises only 20 neurons. We aim to understand how the animal adapts its feeding rate to environmental conditions and metabolic needs, using a combination of theoretical modelling, voltage imaging and behavioral observations. When imaging the animals feeding behavior we identify two modes of regulating food intake: First, we find burst-pause dynamics which we link to a decision-making process where the animal attempts to measure the external food concentration. We also find a second mode of action, in which the pumping frequency is smoothly adapted to reflect the quality of the available food. Using a conductance model of the pharyngeal muscle and its key regulatory circuit, we ask which of these modes of regulation are in the muscular excitability and which are driven by phasic inputs by the nervous system. We will discuss the utility of this small nervous system in understanding computational principles connecting neural activity to behavior.

BP 2.9 Mon 12:00 H13

Available processing time regulates optimal balance between sensitivity and precision — Sahel Azizpour[1], •Johannes Zierenberg[2], Viola Priesemann[2], and Anna Levina[3] — [1]Donders Institute for Brain, Cognition and Behavior, Nijmegen, Netherlands — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen Germany — [3]Eberhard Karls University of Tübingen, Tübingen, Germany

Solving everyday tasks naturally leads to a trade-off between the time spent on processing some input and the accuracy of the outcome. In particular, fast decisions have to rely on uncertain information about inputs. However, standard estimates of information processing capabilities, such as the dynamic range, are defined based on infinite-time averages that do not incorporate noise effects from finite processing times. Here, we develop estimates of processing capability that explicitly account for noisy outputs. We use these measures to show that limiting the processing time in recurrent neural networks can drastically affect the sensitivity and precision of outcomes. This way, optimal dynamical states shift away from the conventionally expected critical point toward subcritical states for finite processing times. Our results thus highlight the necessity to explicitly account for processing times in future estimates of information processing capabilities.