DY 26: Focus Session: Inference Methods and Biological Data (German-French Focus Session) (joint session BP/DY)

Time: Wednesday 15:00–17:45 Location: H 2032

Invited Talk DY 26.1 Wed 15:00 H 2032

Inhibitor-induced transitions in pattern formation and their role to morphogenesis robustness — •Silvia Grigolon — Laboratoire Jean Perrin (UMR 8237), CNRS & Sorbonne Université, Paris, France

Development relies on the finely coordinated expression of morphogens, proteins driving cell differentiation and organ formation. Cell fate specification is achieved thanks to the establishment of morphogen patterns, which act as signals for cells in a concentration dependent manner. By the aid of reaction-diffusion systems, intense studies over the past decades were dedicated to the identification of the underlying microscopic processes leading to robust pattern formation and the classification of the emergent different mechanisms induced by these. In this work, we show that the presence of negative feedbacks in reaction-diffusion systems can lead to a transition in the modes of pattern formation during morphogenesis and induce memory and robustness. We apply this to the study of zebrafish early morphogenesis and show that the aforementioned mechanisms can indeed be found in this system.

DY 26.2 Wed 15:30 H 2032

Bayesian Model Inference for Biological Tracking Data — •Jan Albrecht[1], Lara S. Bort[1], Carsten Beta[1], Manfred Opper[2,3], and Robert Grossmann[1] — [1]Institute of Physics and Astronomy, University of Potsdam, 14476 Potsdam, Germany — [2]TU Berlin, Fakultät IV-MAR 4-2, Marchstraße 23, 10587 Berlin, Germany — [3]Centre for Systems Modelling and Quantitative Biomedicine, University of Birmingham, B15 2TT, United Kingdom

In order to understand and predict the motion patterns of microorganisms, robust methods to infer motility models from time discrete experimental data are required. Due to the internal complexity of the organisms, their movements appear to have random components which motility models need to account for. Bayesian statistical methods provide a way to efficiently extract information from the trajectory data and provide model parameter estimates together with a measure of uncertainty. We showcase that Bayesian methods are especially well suited when the models contain additional layers of stochasticity, for example population heterogeneity or temporal dependence of parameters. Furthermore, we demonstrate how challenges that arise when multidimensional dynamics is only partially observed, e.g. second order dynamics, colored noise or non-observed internal degrees of freedom, can be addressed.

DY 26.3 Wed 15:45 H 2032

Inference and modelling of the stochastic dynamics of cell shape during cellular state transition — •Wolfram Pönisch[1], Iskra Yanakieva[1], Belle Sow[1], Aki Stubb[2], Alex Winkel[1], Guillaume Salbreux[3], and Ewa Paluch[1] — [1]University of Cambridge, UK — [2]MPI for Molecular Biomedicine, Münster, Germany — [3]University of Geneva, Switzerland

The development of an organism involves a series of state transitions in which cells progressively specialize. Many state transitions coincide with changes in cell shape, with emerging evidence suggesting a strong crosstalk between shape and states. An example is epithelial-to-mesenchymal transition (EMT) which plays a crucial role in development and pathogenesis. Yet, there is very limited knowledge about cell morphodynamics during EMT. Here, we present a morphometric pipeline to analyse individual cell shapes in 3D as cells undergo EMT. By modelling the dynamics as a Langevin process, we infer the potential driving EMT and capture temporal dynamics of cell shape fluctuations during the transition. Our findings reveal a peak in cell shape fluctuations coinciding with the time of spreading during EMT. We hypothesize that downstream biomechanical mechanisms are controlling cell shape fluctuations during EMT and combine computational modelling of cell morphodynamics with molecular perturbation experiments. Overall, by combining morphometric approaches with stochastic inference and mathematical modelling, we create a comprehensive understanding of the biophysical basis of shape changes associated with state transitions.

DY 26.4 Wed 16:00 H 2032

From two to three cells: Are three-body interactions important in collective cell migration? — •Agathe Jouneau[1], Tom Brandstätter[2], Emily Brieger[1], Chase Broedersz[2], and Joachim Rädler[1] — [1]Faculty of Physics and Center for NanoScience, LMU Munich, Germany — [2]Department of Physics and Astronomy, VU Amsterdam, Netherlands

During collective cell migration, for example in embryo development or cancer invasion, cells coordinate their movement by actively interacting with each other. How cell-cell interactions shape the dynamics and emergent properties of the cell assembly is not fully understood. In recent work, we showed that the dynamics of two cells interacting on a dumbbell pattern can be captured by a particle model, including cell-cell interaction terms directly inferred from experimental data. However, we do not know if the collective dynamics of more than two cells can be described by pairwise interactions between cells, or if higher-order interactions come into play. To answer this question, we use time-lapse microscopy to record the dynamics of three cells interacting together in a tailored confinement. We collect a large number of cell trajectories and use them to infer the cell-cell interactions by adapting the framework of the two-cell study. Our work reveals that the pairwise interactions between cells appear to be preserved in the presence of a third cell. However, the superposition of the inferred pairwise interactions is not sufficient to fully capture the observed three-cell dynamics. This could indicate the presence of three-body interactions, with possible implications for large-scale collective behavior.

DY 26.5 Wed 16:15 H 2032

Model selection in stochastic dynamical systems — •Andonis Gerardos and Pierre Ronceray — Aix Marseille Univ, CNRS, CINAM, Turing Center for Living Systems, Marseille, France

Analyzing the dynamics of complex biological systems requires stochastic dynamical models; a common choice is stochastic differential equations (SDE). Given a time series, we developed a method that selects, among a class of SDE models, the one that best captures the dynamics and infers its parameters. This method corresponds to an adaptation of the Akaike information criterion (AIC) to SDE. We validated it using synthetic data generated with stochastic Lorenz and competitive Lotka-Volterra equation. Looking ahead, we envision applications of our data-driven method to unravel the hidden mechanisms of dynamical systems.

15 min. break

Invited Talk DY 26.6 Wed 16:45 H 2032

Bayesian inference of chromatin looping dynamics from live-cell measurements — •Christoph Zechner[1], Michele Gabriele[2], Hugo B Brandão[2], Simon Grosse-Holz[2], Asmita Jha[2], Gina M Daily[3], Claudia Cattoglio[3], Tsung-Han Hsieh[3], Leonid Mirny[2], and Anders S Hansen[2] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]Massachusetts Institute of Technology, Cambridge, USA — [3]University of California, Berkeley, Berkeley, USA

Recent live-cell microscopy techniques allow the simultaneous tracking of distal genomic elements, providing unprecedented ways to study chromatin dynamics and gene regulation. However, drawing robust conclusions from such data is statistically challenging due to substantial technical noise, intrinsic fluctuations and limited time-resolution. I will present recent progress we have made in addressing some of these challenges; specifically, we developed a new statistical method to quantify CTCF/cohesin-mediated chromatin looping dynamics from two-point live-cell imaging experiments. The method combines a simple polymer model with a Bayesian filtering approach to infer loop lifetimes and frequencies. Its application to experimental data revealed that chromatin loops are surprisingly rare (~5% looped fraction) and short-lived (~20mins loop lifetime). I will discuss potential implications of these findings and outline future challenges.

DY 26.7 Wed 17:15 H 2032

Rigorous inference of stochastic reaction networks based on moment constraints via semidefinite optimisation — •Zekai Li, Barahona Mauricio, and Philipp Thomas — Imperial College London, London, United Kingdom

Stochastic reaction networks are used in many fields to model the behaviour of complex systems with uncertainty. Inference of the rate parameters has been an essential and challenging task for accurately understanding the network. While numerous inference methods have been proposed and implemented, the uncertainty measures associated with these methods often lack theoretical guarantees. Here, we propose a novel inference approach to obtain rigorous bounds on the parameters via convex optimisation over sets constrained by moment equations and moment matrices. Under the condition that the moment intervals, obtained through bootstrap from the original data, contain the true stationary moments, our bounds on the parameters are guaranteed to contain the true parameters. Our method is also capable in the case that there exists latent species or observation error, and in the former case, we can bound the stationary moments of the latent species.

DY 26.8 Wed 17:30 H 2032

Information rates of neural activity on varying time scales — •Tobias Kühn and Ulisse Ferrari — Institut de la Vision, Sorbonne Université, CNRS, INSERM

Evaluating electrophysiological recordings, time is normally discretized in bins. If one aims at determining the information rate, i.e. the mutual information per time, the time-bin size has to be chosen with care because the result will appreciably depend on it. The framework we suggest gives freedom in this choice because our single-neuron model is not restricted to a binary representation of neural activity - as is the case for Ising-like models of neural networks.

Our method allows to faithfully estimate the entropy of the neural activity and eventually the mutual information between neural activity and stimulus for a given time scale. Like in the Ising model, we restrict ourselves to pairwise interactions, so that we just need the mean activities and the covariances (across neurons or across time) to compute entropies. This estimate requires a number of measures growing only quadratically in the number of neurons, as opposed to the exponential growth associated to the estimate of the full probability distribution, which prohibits using the latter for real data. More concretely, to compute entropies, we use a small-correlation expansion, expressed in a novel diagrammatic framework (Kühn & van Wijland 2023), avoiding the explicit inference or even a concrete choice of a single-neuron model. Our approach enables studying the dependence of information rate on the time scale on which the information is registered, which is crucial to understand how dynamic stimuli are processed.