BP 6: Systems Biology I

Time: Monday 11:00–13:30 Location: BPc

BP 6.1 Mon 11:00 BPc

Ligation Chain Reactions in Non-Equilibrium Convection Compartments with Microscale pH Cycles — •Annalena Salditt, Dieter Braun, Patrick Kudella, and Leonie Karr — Ludwig-Maximilians-Universität

Early replication mechanisms for the origin of life rely on periodic strand separation to start new rounds of replication necessary to stabilize and accumulate information of long nucleic acids. Especially for catalytically active RNAs, high temperatures required for strand separation promote their hydrolysis, leading to a loss of information. Therefore, a geophysical non-equilibrium environment on early Earth would have required means to separate hybridized strands after replication and to localize long, potentially functional molecules against diffusion while protecting them from hydrolysis. We perform ligation extension experiments in moderate temperature gradients across micrometer thick, water-filled chambers with a water-CO2 interface to induce a miniaturized water cycle while maintaining thermophoretic trapping conditions. In addition to more realistic early atmospheric conditions of the Earth, the CO2-water interface causes periodic pH changes, that induce the hybridization of double strands. We expect this to be a promising autonomous setting for ligation chain reactions starting from a random or semi-random oligomer pool.

BP 6.2 Mon 11:20 BPc

The effects of cross-species gene transfer on genome dynamics — •Mona Förster[1], Isabel Rathmann[1], Jeffrey Power[2], Melih Yüksel[1], and Berenike Maier[1] — [1]Universität zu Köln, Deutschland — [2]Universität Tübingen, Deutschland

Phylogenetic studies have provided strong evidence that gene transfer happens frequently and acts across species. However, the rate at which gene transfer occurs and its short-term effect on genome dynamics are poorly understood. To address the effect of intra- and inter-species gene transfer on genome dynamics we developed an evolution experiment and analysis method to detect horizontal gene transfer. To investigate mechanistic contributions to gene transfer probability, we ensured minimal selection by not allowing for population dynamics. We were able to detect a remarkably high gene transfer rate of 0.4 $\%h^{-1}$ across subspecies of *Bacillus subtilis*. This rate was four times lower when gene transfer was probed between *B. subtilis* and *Bacillus vallismortis* and 125 times lower between *B. subtilis* and *Bacillus atrophaeus*. Interestingly, the average sequence divergence of integrated segments is comparable between all three donors with a mean of about 7 %. We observed that the fraction of replaced genome increases linearly throughout 40 h of DNA uptake, which suggests that transfer of genes, is not yet saturated and could be probed further in evolutionary runs. Following up on this, it will be interesting to use the fitness distribution of the minimal selection replicates to design an evolution experiment with strong selection.

BP 6.3 Mon 11:40 BPc

Genetically engineered control of phenotypic structure in microbial colonies — •Philip Bittihn[1,4], Andriy Didovyk[1,5], Lev S. Tsimring[1], and Jeff Hasty[1,2,3] — [1]BioCircuits Institute — [2]Department of Bioengineering — [3]Molecular Biology Section, Division of Biological Sciences, University of California, San Diego, La Jolla, CA, USA — [4]Department of Living Matter Physics, Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [5]Vertex Pharmaceuticals, San Diego, California, USA

Many essential biological behaviors originate from an entanglement of biological (cellular) and physical processes. This is a challenge not only for traditional biology and physics methodology, but also for synthetic biology, where such interactions severely limit the ability to engineer desired behavior with artificial gene regulatory networks. We show how to achieve control of phenotypic structure in bacterial microcolonies by simultaneously exploiting internal gene expression and metabolism, as well as physical coordination through nutrient diffusion and growth, which leads to self-generated nutrient gradients and a heterogeneous population consisting of both dividing and dormant cells. In microfluidic experiments and a mathematical model, we show that gene circuits which sense and control growth can create a spatio-temporal feedback loop via nutrient transport and generate sustained growth oscillations, while a phenotype-specific lysis circuit can selectively eliminate dormant cells. Our results demonstrate how to understand and control multicellular substrates as complex active physical systems.
Reference: *Nature Microbiology* **5**, 697–705 (2020)

BP 6.4 Mon 12:00 BPc

Dynamics, Statistics and Coding in Random Rate and Binary Networks — •Tobias Kühn[1,2,3], Christian Keup[2,3], David Dahmen[2], and Moritz Helias[2,3] — [1]MSC de l'Université de Paris, ENS, CNRS, Paris, France — [2]INM-6, Forschungszentrum Jülich, Germany — [3]Department of Physics, RWTH Aachen, Germany

Cortical neurons communicate with spikes, discrete events in time. Functional network models often employ rate units that are continuously coupled by analog signals. Is there a benefit of discrete signaling? By a unified mean-field theory for large random networks of rate and binary units, we show that both models can be matched to have identical statistics up to second order. Their stimulus processing properties, however, are different: contrary to rate networks, the chaos transition in binary networks strongly depends on network size, and we discover a chaotic submanifold in binary networks that does not exist in rate models. Its dimensionality increases with time after stimulus onset and reaches a fixed point that depends on the synaptic coupling strength. Low-dimensional stimuli are transiently expanded into higher-dimensional representations that live within the manifold. We find that classification performance first increases and then degrades due to variability in the manifold. During this transient, resilience to noise by far exceeds that of rate models with matched statistics, which are always regular. In their respective chaotic regime, however, rate networks show similar a mechanism of transient signal amplification, same for spiking networks [Keup et al. arXiv:2002.11006]. Ack.: Helmholtz assn. (VH-NG-1028); RWTH (ERS seed fund neuroIC002).

BP 6.5 Mon 12:20 BPc

Long-range and rapid signalling gradient formation by cell-to-cell relay — •Johanna Dickmann[1], Jochen Rink[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute for Biophysical Chemistry, Göttingen, Germany

Development, regeneration and tissue renewal are spectacular tissue patterning events. Tissue patterning, the adaptation of the correct cell fate at the correct position, requires information. This information can be provided by spatially graded distributions of signalling molecules, called signalling gradients. While the formation of signalling gradients is thought to result from diffusion and degradation in the context of embryonic development, it remains controversial how such signalling gradients can be generated on long length scales e.g. during regeneration. We introduce a relay mechanism for gradient formation in which the signal is propagated from cell to cell via a positive feedback loop. That is, each cell produces signalling molecules in response to receiving a signal. We show that polarised secretion of signalling molecules produced in response to the received signal results in an effective drift of signalling molecule concentration through the system, markedly accelerating the formation of signalling gradients. This way, the relay mechanism explains gradient formation on millimetre length scales within hours to days for physiological parameter choices.

BP 6.6 Mon 12:40 BPc

Model for inference of cell dynamics from C14 data — •Julian Rode[1], Fabian Rost[2], Paula Heinke[1], Enikö Lazar[3], Lutz Brusch[1], and Olaf Bergmann[1] — [1]Technische Universität Dresden, Dresden, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]Karolinska Institutet, Stockholm, Sweden

Carbon dating is an established method to determine the age of ancient artefacts. Traditionally, radioactive decay changes the C14 ratio of the sample which can be used to determine the age. Recently, a second route has become available as the drastic change of atmospheric C14 due to atomic bomb tests in the 60's allows to invert this classic C14 dating method. Now, the C14 decay is negligible, but the atmospheric C14 changes quickly, allowing an accurate age measurement even of human samples. This method allows to estimate the cell turnover in vivo using the C14 carbon ratio of the DNA from many cells. But a simple matching of C14 values is not sufficient because the measured

C14 values are the average of cells with different ages. We introduce a C14-structured population model to predict the average C14 content and accounting for cell division, cell inflow from a fast cycling stem cell population and cell death. Additionally, a priori knowledge such as tissue growth has to be considered resulting in constrains for the model solution. We use variations of this model to analyse C14 data from human liver and muscle tissue.

30 min. Meet the Speaker