BP 5: Systems biology & gene expression and signaling

Time: Monday 15:00–16:45 Location: H11

Invited Talk BP 5.1 Mon 15:00 H11

Gene transfer between bacteria: from single molecules to genome dynamics — •Berenike Maier — University of Cologne

Horizontal gene transfer (HGT) plays an important role in bacterial genome evolution. Gene transfer between bacteria of different species but also between bacteria and eukaryotes has been reported. A particularly widespread mechanism of gene transfer is transformation which enables bacteria to import and inheritably integrate external DNA. The first part of the presentation will focus on the import of DNA through the cell envelope, a key step to transformation. The proteins forming the DNA uptake machine have been identified. Yet, the biophysical mechanism of the motor pulling DNA from the environment into the bacterial cell remains poorly understood. We used single molecule approaches for studying the molecular mechanism of DNA uptake. Our results are in remarkable agreement with a translocation ratchet model, whereby a periplasmic chaperone rectifies DNA diffusion through the membrane by reversible binding. In the second part, the I will address the question how gene transfer between different bacterial subspecies affects genome dynamics and bacterial fitness. Using laboratory evolution, we show that despite considerable sequence divergence, large portions of the genome are rapidly transferred.

BP 5.2 Mon 15:30 H11

Why E. coli dies exponentially during carbon starvation — •Severin Schink[1,2], Elena Biselli[2], Constantin Ammar[2], Yu-Fang Chang[1], Markus Basan[2], and Ulrich Gerland[1] — [1]Harvard Medical School, Department of Systems Biology, 200 Longwood Ave, Boston 02115 MA, USA — [2]Technical University of Munich, Physics Department, James-Franck-Str 1, 85748 Garching, Germany

While growth of bacteria is well understood and studied, its counterpart death is not. We use the mathematical simplicity of the decay of viability during carbon starvation, a simple exponential function, to uncover how E. coli survives nutrient limitation. We find that survival crucially depends on cannibalistic biomass recycling, where bacteria survive by metabolizing biomass of perished cells. The interdependence of survival and death leads to a negative feedback loop: increased cell death results in more available nutrients, which in turn reduces cell death. As a result, the state of the cells becomes naturally balanced, so that the death rate remains invariant for several days and viability decreases exponentially. This finding permits quantitative insights into how environments and genetic elements affect bacterial survival, as exemplified by a study of the cost of a wasteful enzyme and the benefit of the stress response sigma factor rpoS.

BP 5.3 Mon 15:45 H11

Suppressive antibiotic interactions result from jamming in the translation cycle — •Bor Kavčič[1], Gašper Tkačik[1], and Tobias Bollenbach[2] — [1]IST Austria, Klosterneuburg, Austria — [2]University of Cologne, Cologne, Germany

Translation - synthesis of proteins by ribosomes - is regulated by translation factors and perturbed by certain antibiotics (translation inhibitors). When antibiotics are combined, they interact diversely: the combined effects range from synergistic (combined effect is stronger) to suppressive (one of the drugs loses potency). Such drug interactions are difficult to predict and their underlying mechanisms remain unknown. We systematically measured all pairwise interactions for a set of translation inhibitors. A theoretical model based on ribosomal growth laws explained some of the interactions, but was unable to explain suppression. To further elucidate the origin of these drug interactions, we mimicked antibiotic effects on translation by externally controlling the concentration of one or several key translation factors, which revealed how antibiotic action depends on the translation bottlenecks. Furthermore, if the transition rates are modified, ribosomes can get stuck in traffic jams, leading to a decrease in translation efficiency. We interpret these experiments using a stochastic model of translation based on the TASEP. Our analysis suggests that traffic jams of ribosomes in the translation cycle are at the heart of suppressive interactions between antibiotics that target initiation and translocation.

BP 5.4 Mon 16:00 H11

Towards synthetic cells using peptide-based reaction compartments — Kilian Vogele[1], Thomas Frank[1], Lukas Gasser[1], Marisa A. Goetzfried[1], Mathias W. Hackl[2], Stephan A. Sieber[2], Friedrich C. Simmel[1], and •Tobias Pirzer[1] — [1]Physics of Synthetic Biological Systems - E14, Physics-Department and ZNN, Technische Universität München, 85748 Garching, Germany — [2]Department of Chemistry, Center for Integrated Protein Science Munich (CIPSM), Technische Universität München, Lichtenbergstraße 4, 85748 Garching, Germany

Membrane compartmentalization and growth are central aspects of living cells, and are thus encoded in every cell's genome. For the creation of artificial cellular systems, genetic information and production of membrane building blocks will need to be coupled in a similar manner. However, natural biochemical reaction networks and membrane building blocks are notoriously difficult to implement in vitro.

In this work we utilized amphiphilic elastin-like peptides (ELP) to create self-assembled vesicular structures of about 200 nm diameter. In order to genetically encode the growth of these vesicles, we encapsulate a cell-free transcription-translation system together with the DNA template inside the peptide vesicles. We show in vesiculo production of a functioning fluorescent RNA aptamer and a fluorescent protein. Furthermore, we implement in situ expression of the membrane peptide itself and finally demonstrate autonomous vesicle growth due to the incorporation of this ELP into the membrane.

BP 5.5 Mon 16:15 H11

Membrane diffusion imposes a cell size-dependent polarity switch — •Lars Hubatsch[1,2], Florent Peglion[2], Jacob Reich[2], Nelio TL Rodrigues[2], Nisha Hirani[2], Rukshala Illukkumbura[2], and Nathan W Goehring[2,3] — [1]MPI for the Physics of Complex Systems — [2]The Francis Crick Institute — [3]MRC LMCB, University College London

Reaction - diffusion networks have been established as a ubiquitous way of patterning living systems, bridging between length scales, from single cells to large tissues. Cell polarity, as one of the most fundamental patterns in biology, has been the subject of detailed biological studies, enabling quantitative modelling of the underlying patterning networks. Here, we investigate how cell polarity patterns are influenced by cell size. Many classical types of reaction-diffusion systems exhibit intrinsic length scales, giving rise to a minimum system size below which a pattern returns to uniformity. We show theoretically that such a size threshold is a common feature of current models for polarity. Next, using kinetic parameters measured by single-molecule techniques we quantitatively predict the cell size below which polarity should become unstable in our experimental system, the early C. elegans embryo. Using different mechanical and genetic perturbations in conjunction with 3D live-imaging we show that this size threshold exists in vivo. Cell size-dependent polarity thresholds may explain the commonly observed link between cell size and asymmetric division potential in stem cell lineages.

BP 5.6 Mon 16:30 H11

Modelling the Single Photon Response in Rods — •Charlotte J. Beelen[1], Karl-Wilhelm Koch[1], and Daniele Dell'Orco[2] — [1]Dept. Neuroscience, Biochemistry, University of Oldenburg — [2]Department of Neurosciences, Biomedicine and Movement Sciences, Sect. of Biological Chemistry, University of Verona

Rod cells mediate vision in dim light. After the activation of the pigment molecule rhodopsin, a complex signal transduction cascade leads to an electrical signal, which can then be transmitted further through the retina. This phototransduction cascade can be modelled using differential equations for the relevant molecular species, mainly with mass-action kinetics. It has been tested for a broad range of stimulus conditions in deterministic simulations [1,2].

The phototransduction cascade exhibits a reproducible response to single photons, thus operating at the physical sensing limit. These single photon responses show astonishingly little variability [3]. To investigate the uniformness of the single photon response and find out which reactions are essential for its reproducibility, we perform stochastic simulations of single photon responses. The effect of multiple phosphorylation sites of rhodopsin is studied, as well as single photon responses in different knockout conditions.

[1] D. Dell'Orco et al, Mol. BioSyst. **5** 1232-1246 (2009)
[2] B.M. Invergo et al, Mol. BioSyst. **10** 1481-1489 (2014)
[3] R.D. Hamer et al, J. Gen. Physiol. **122** 419-444 (2003)