BP 9: Focus: Systems Biology of Bacteria (with jDPG)

Time: Tuesday 9:30–12:30 Location: E 020

Invited Talk BP 9.1 Tue 9:30 E 020

Stochastic gene regulation strategies in bacteria — •Ulrich Gerland — LMU, Munich, Germany

The regulatory circuits that control the processing of signals and the transcription of genes in bacterial cells are fascinating nonlinear stochastic systems. They often appear to be optimized by evolution, but they are only beginning to be explored on a quantitative level. I will briefly review some of the developments in this field, and then focus on a small regulatory circuit that controls the production of the machinery required to import and digest a specific sugar in E. coli bacteria. In a population of cells, this remarkably simple circuit leads to heterogeneous dynamic behavior that appears to implement an optimal strategy to deal with unpredictable environments.

Invited Talk BP 9.2 Tue 10:00 E 020

The evolutionary advantage of being round — •Oskar Hallatschek — Max Planck Research Group for Biophysics and Evolutionary Dynamics, MPI-DS, Goettingen, Germany

Bacterial species display an astonishing variety of shapes, such as round, rod-like, comma- or spiral-shaped. Shape is thought to influence several biological functions, such as nutrient take-up, swimming and the attachment to surfaces. Here, we study a possible impact of cell shape on adaptation. We show that, due to a biophysical buckling instability, rod-like bacteria exhibit much higher levels of random number fluctuation (genetic drift) in growing colonies than round microbes. Consequently, the establishment of beneficial mutations is strongly suppressed in colonies of rod-like bacteria. Our experiments and model thus support the hypothesis that shape strongly influences adaptability of growing biofilms.

Invited Talk BP 9.3 Tue 10:30 E 020

Optimal control strategies in living cells — •Markus Kollmann — Department Biologie, Universität Düsseldorf, Germany

Unicellular organisms have evolved an astonishing repertoire to survive in fluctuating environments. To ensure high reproductive success, microorganisms adapt sufficiently fast to new living conditions, such as nutrient availability, osmolarity, and ambient temperature. Such phenotypic adaptation is coordinated by the activity of cellular circuits, whose components are regulated on the level of DNA, RNA, and protein. The question arises whether the observed regulatory strategies of microorganisms can be explained by an optimal tradeoff between precision, timing and resource efficiency of cellular response. Strong evidence for such optimized cellular control can be found within bacteria and the evolved control strategies show striking similarities to predictions from optimal control theory. We give several examples for highly optimized bacterial circuits, their proposed objective functions, and their molecular realizations.

Invited Talk BP 9.4 Tue 11:00 E 020

Bacterial communication systems — •Ilka Bischofs — ZMBH, Heidelberg, Germany

Bacteria interact with each other in multiple ways, e.g. via diffusible signaling molecules. In a process called quorum sensing bacteria produce, secrete, sense and respond to signals, which accumulate with cell density. This allows them to control gene expression in a cell density-dependent manner. For example, frequently they launch specific responses, which are executed more efficiently collectively, upon reaching a "quorum". Interestingly, in nature there exists a variety of different quorum sensing network architectures. In particular, cell density information enters into cellular decision making processes in various ways. By means of simple theoretical models we compare different quorum sensing network architectures. Based on this analysis we begin to derive network design principles that may explain the significance of certain architectural features found in natural networks and we make predictions on how to build synthetic networks with optimized functions.

BP 9.5 Tue 11:30 E 020

A Plausible Mechanism for the Generation of Ultrasensitivity and Bistability in Bacterial Two-Component Systems — •Ronny Straube — Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg

Two-component systems are the simplest signal processing units mostly found in bacteria. They consist of a histidine kinase (HK) and a cognate response regulator (RR) which often acts as a transcription factor. Upon stimulation the HK undergoes autophosphorylation and, subsequently, transfers the phosphate group to the RR. In addition, many HKs also exhibit phosphatase activity towards the phosphorylated form of the RR. The relative activity between autophosphorylation, kinase and phosphatase mode is often regulated by small allosteric effectors. Using a simple mathematical model I show that if the kinase and phosphatase activities are regulated in a reciprocal fashion two-component systems can generate highly sigmoidal responses (ultrasensitivity) quite similar to covalent modification systems in eukaryotes [1]. Under proper kinetic conditions the response can even become hysteretic with an intermediate bistable regime. Hence, despite the bifunctional nature of the HK switch-like all-or-none responses could already be generated at the protein-protein level without genetic regulation. [1] Goldbeter A, Koshland, DE Jr. An amplified sensitivity arising from covalent modification in biological systems. Proc. Natl. Acad. Sci USA 78, 6840-6844 (1981).

BP 9.6 Tue 11:45 E 020

A model for sigma factor competition in bacterial cells — •Marco Mauri and Stefan Klumpp — Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

Bacteria respond to changing environment conditions by switching the global pattern of transcribed genes, making only those products essential for their survival. In response to specif environmental stresses the cell activates several stress-specific molecules called sigma factors. They bind the core RNA polymerase (RNAP) - the machinery of transcription - and direct it towards the appropriate stress response genes. Since more than one sigma species could be present in the cell at the same time, it is believed that the modulation of their availability and competition among them for core RNAP provide important mechanisms for the global switch of the transcriptional program.

To analyze this competition, we have developed a theoretical model based on earlier work from the Gross lab [1]. The model shows that competition occurs only when the number of free sigmas exceeds the number of free cores. Within this framework, we analyzed the effects of some factors that modulate the competition such as anti-sigma factors, small RNA and active transcription. We applied the model to in vitro sigma competition experiments [2] and obtained good agreement. We also used the model to examine under which conditions a stop of transcription of ribosomal RNA as in the stringent response can passively up-regulate transcription driven by alternative sigmas.

[1] Grigorova et al., PNAS. 103, 5332 (2006)
[2] Jishage et al., Genes & Dev. 16, 1260 (2002)

BP 9.7 Tue 12:00 E 020

Unified description of Min protein patterns in vivo and in vitro — •Mike Bonny[1], Elisabeth Fischer-Friedrich[2], Martin Loose[4], Petra Schwille[3], and Karsten Kruse[1] — [1]Theoretische Physik, Universität des Saarlandes, Postfach 151150, 66041 Saarbrücken, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Straße 38, 01187 Dresden, Germany — [3]Biophysics, BIOTEC, TU Dresden, Tatzberg 47/49, 01307 Dresden, Germany — [4]Harvard Medical School, Department of Systems Biology, 200 Longwood Avenue, Warren Alpert Building, Boston, MA 0211

The bacterial proteins MinD and MinE self-organize into a variety of fascinating patterns in the presence of a membrane. In vivo, standing and traveling waves as well as bistable stationary states are observed. In vitro they form plane and spiral waves. Several models explain Min protein pattern formation by cooperative attachment of MinD to the membrane and MinE-induced detachment from the membrane. However, a description reproducing all observed patterns is missing. We have found that MinE can bind by itself transiently to the membrane [1,2]. Analyzing mean field and stochastic models of Min protein dynamics, we find that our description shows all observed in vivo and in vitro patterns if we include the transient membrane interaction of MinE.

[1] M. Loose et al., Struct. Mol. Biol., 18, 577 (2011).
[2] K. Park et al., Cell, 146, 396 (2011).

BP 9.8 Tue 12:15 E 020

Quorum sensing of motile bacteria in spatial confinement — •Jan Ribbe and Berenike Maier — Institut für theoretische Physik, Universität zu Köln, Köln, Germany

Microscopic structures influence the direction of swimming bacteria through hydrodynamic interaction. Thus we hypothesize that the concentration of bacteria in spatially structured environments is heterogeneous and can potentially lead to local accumulation of bacteria. Bacteria in groups often have different lifestyles than individuals. Controlled by quorum sensing and nutrient limitation, a well-defined fraction of cells differentiates into the competent state at high cell density.

Here, we intend to test the hypothesis whether the state of motility impacts on bacterial lifestyle. First we addressed the question whether competence and motility are mutually exclusive. We found that cells of *Bacillus subtilis* that have decided to become competent do not necessarily abolish motility. The rate of motility of competent cells decreases, but remains at 20±10 %. Next, we generated asymmetric microfluidic channels with volumes of 30 pl. We found that motile cells accumulate in the dead ends of the asymmetric channels and exhibit a pronounced concentration gradient. Active swimming promoted accumulation significantly. Using fluorescence reporters for the master regulator of competence, we found that the number of competent cells is strongly increased in dead ends where cell concentration is high. In future experiments we will characterize the spatio-temporal development of competence in microhabitats of different dimensions.