BP 24: Systems biology

Time: Wednesday 9:30–11:15 Location: ZEU 250

Topical Talk BP 24.1 Wed 9:30 ZEU 250

Collaboration between biomolecules: A physical analysis — •Ulrich Gerland — Ludwig Maximilians Universität, München, Germany

In biology, different molecules often collaborate on a common task, creating functionalities far beyond what a single type of molecule could accomplish. The physical principles underlying this synergism are only beginning to be understood and exploited in engineered systems. I will present a theoretical study that focuses on enzymes which collaborate to catalyze multi-step biochemical reactions. Cells often coordinate the spatial arrangement of such enzyme teams, into intra- or extracellular clusters, or co-localize them on the cell membrane. We study the impact of the spatial arrangement on the reaction efficiency within reaction-diffusion models [1,2]. Remarkably, although the study of reaction-diffusion systems has a long history, many questions about systems with localized reaction centers remain largely unexplored.

[1] A. Buchner, F. Tostevin, and U. Gerland (2013) Clustering and optimal arrangement of enzymes in reaction-diffusion systems. *Phys. Rev. Lett.* 110, 208104.

[2] A. Buchner, F. Tostevin, F. Hinzpeter, and U. Gerland (2013) Optimization of collective enzyme activity via spatial localization. *J. Chem. Phys.* 139, 135101.

BP 24.2 Wed 10:00 ZEU 250

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 specific environmental stresses, the cell activates several stress-specific molecules called sigma factors. They bind the core RNA polymerase 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 developed a theoretical model based on earlier work from the Gross lab. Within this framework, we inspect the effects of some factors that modulate the competition such as anti-sigma factors, small RNA, active transcription and non-specific binding. The model shows that a passive regulation of the transcription of the alternative sigma cognate genes is feasible and a more effective upregulation is achieved in competition regime. We also 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. Our model matches well to in vitro and in vivo measurements here analyzed. The theory supports evidence for a passive global switch of the transcriptional program and gives new insights into RNAP partitioning in the cell.

BP 24.3 Wed 10:15 ZEU 250

Centrosomes are autocatalytic droplets of pericentriolar material organized by centrioles — •David Zwicker[1], Markus Decker[2], Steffen Jaensch[2], Anthony A. Hyman[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

During cell division, the mitotic spindle is organized with the help of two centrosomes located at the spindle poles. Centrosomes consist of centrioles that are surrounded by pericentriolar material. The physical nature of centrosomes and in particular of the pericentriolar material remain unclear. We describe centrosomes as liquid-like droplets and study their assembly using a general theoretical description. Our model is based on two forms of the centrosome components: A soluble form in the cytoplasm and a form that tends to phase separate and forms droplets. We show that an autocatalytic chemical transition between these forms can account for the experimentally observed growth dynamics of centrosomes. Such autocatalytic growth requires an initial trigger, which we propose is provides by a catalytic activity of the centrioles. This activity provides a nucleation mechanism that puts centrosome formation under the reliable control by centrioles. Spontaneous homogeneous or heterogeneous nucleation is strongly suppressed in this scenario. Autocatalytic growth can explain rapid centrosome assembly from material provided in the cytoplasm while the control of nucleation by centrioles is reliable. Our theory highlights the role of phase separation in the spatial organization of cells.

BP 24.4 Wed 10:30 ZEU 250

A Biophysical Taxonomy of Quorum Sensing Networks — •Bastian Drees and Ilka Bischofs — BioQuant, Center for Quantitative Analysis of Molecular and Cellular Biosystems at Heidelberg University, Heidelberg

Bacteria control their collective behavior in response to population size by encoding information about cell density into a concentration of signaling molecules. To carry out this process, called quorum sensing (QS), bacteria use signaling networks that vary in their organization between different organisms. This diversity in the physical organization (transport mechanism, receptor location, etc.), potentially gives rise to classes of different QS architectures. To introduce a classification scheme we systematically studied the encoding properties of a comprehensive set of 116 generic signal generating network topologies focusing on their sensitivity and noise characteristics. Intimate relationships between architecture and encoder function can be employed to rationalize a hierarchical network classification scheme. Our model shows that almost all signal generating architectures are able to mediate QS. The resulting taxonomic scheme consists of two layers: One layer containing three basic encoder classes that are defined by a characteristic "core network motif" and that share the same qualitative noise and sensitivity behavior, independent of system parameters. The second layer contains five classes of architectures that are composed out of two core motifs and as a result can express complex and counter-intuitive encoding behaviors. Our analysis indicates that different QS systems might enable bacteria to conduct different types of QS.

Invited Talk BP 24.5 Wed 10:45 ZEU 250

Gene expression in embryos: from single molecules to network dynamics — •Thomas Gregor — Joseph Henry Laboratories of Physics and Lewis Sigler Institute for Integrative Genomics, Princeton University, Princeton, USA

The nodes of the pattern forming segmentation network in the early fly embryo are transcription factors, i.e. proteins that cross-regulate each other via activating or repressive interactions. Hence, in order to answer questions about the physical underpinnings of this network, obtaining quantitative access to the transcription processes is key. In particular, in addition to proteins, quantitative handles to other molecular species such as RNA-polymerases and mRNA molecules are crucial to understand the transition from one network node to the next. I will report on our recent progress in developing methods to count individual molecules of mRNA in intact embryos, and to monitor the transcriptional activity of nascent mRNA at their site of production on the DNA in living fly embryos. Initial results using these methods will be discussed.