AKB 26 Cellular Computation and Gene Regulation

Time: Friday 11:00–12:00 Room: ZEU 255

Invited Talk AKB 26.1 Fri 11:00 ZEU 255

The physics of cellular computation — •Pieter Rein ten Wolde — FOM Institute for Atomic and Molecular Physics (AMOLF), Kruislaan 407, 1098 SJ, Amsterdam, The Netherlands

Gene regulatory networks are the central processing units of life. They orchestrate cell development, control the cell cycle and allow the cell to integrate different signals and thereby allow the cell to recognize patters in, for instance, the food supply of the organism. While gene regulatory networks can perform computations analogous to electronic circuits, their design principles are markedly different. We use database analyses, theory and computer simulations to unravel the design principles of gene regulatory networks. We show that the molecular character of the components makes gene regulatory networks intrinsically stochastic and thus prone to biochemical noise, yet also allow them to process information in a very sophisticated manner.

AKB 26.2 Fri 11:30 ZEU 255

Optimal target search on a fast folding DNA with volume exchange — •Ralf Metzler, Michael Lomholt, and Tobias Ambjoernsson — NORDITA, Blegdamsvej 17, DK-2100 Copenhagen

We study the search process of a target on a rapidly folding DNA by an ensemble of proteins, whose search combines 1D diffusion along the chain, Lévy type diffusion [1] mediated by chain looping, and volume exchange. A rich behavior of the search process is obtained with respect to the physical parameters, in particular, for the optimal search. Thus, it turns out that the Lévy search component leads to much more efficient target search and under certain conditions renders 3D volume diffusion obsolete [2]. The model includes the special cases of the 'standard' 3D/1D exchange [3] as well as pure 1D search [4]. The model is expected to pertain to typical in vivo studies of genetic regulation, and predicts significantly higher targeting rates than previous models. It is suggested that the Lévy contribution can be studied experimentally under low salt conditions disfavouring protein unbinding from the DNA.

[1] R. Metzler and J. Klafter, Phys. Rep. 339, 1 (2000); J. Phys. A 37 R161 (2004).
[2] M.A. Lomholt, T. Ambjörnsson, and R. Metzler, subm. to Phys. Rev. Lett.; E-print cond-mat/0510072.
[3] M. Coppey, O. Benichou, R. Voituriez, and M. Moreau, Biophys. J. 87, 1640 (2004).
[4] I. M. Sokolov, R. Metzler, K.Pant, and M. C. Williams, Biophys. J. 89, 895 (2005).

AKB 26.3 Fri 11:45 ZEU 255

Stepwise bending of DNA by a single TATA-box Binding Protein — •Simon F. Tolic-Norrelykke[1,2,3], Mette B. Rasmussen[2], Francesco S. Pavone[3], Kirstine Berg-Sorensen[2,4], and Lene B. Oddershede[2] — [1]Max-Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [2]The Niels Bohr Institute, DK-2100 Copenhagen O, Denmark — [3]European Laboratory for Non-linear Spectroscopy, 50019 Sesto Fiorentino (Fl), Italy — [4]Dept. of Physics, Technical University of Denmark, DK-2800, Kgs. Lyngby, Denmark

The TATA-box binding protein (TBP) is required by all three eukaryotic RNA polymerases for the initiation of transcription from most promoters. TBP recognizes, binds to, and bends promoter sequences called "TATA-boxes" in the DNA. We present results from the study of individual Saccharomyces cerevisiae TBPs interacting with single DNA molecules containing a TATA-box. Using video microscopy, we observed the Brownian motion of beads tethered by short surface-bound DNA. When TBP binds to and bends the DNA, the conformation of the DNA changes and the amplitude of Brownian motion of the tethered bead is reduced compared to that of unbent DNA. We detected individual binding and dissociation events and derived kinetic parameters for the process. Dissociation was induced by increasing the salt concentration or by directly pulling on the tethered bead using optical tweezers. In addition to the well defined free and bound classes of Brownian motion we observed another two classes of motion. These extra classes were identified with intermediate states on a three-step, linear, binding pathway. Biological implications of the intermediate states are discussed.