AKB 20 Systems Biology and Bioinformatics

Zeit: Freitag 14:00–15:30 Raum: TU H2013

Hauptvortrag AKB 20.1 Fr 14:00 TU H2013

Conflict and Cooperation in Biological Systems — •Peter Hammerstein — Humboldt Universitaet

In biology, the components of a living organism are often compared with parts of a well designed machine, assuming that the evolutionary process acts somewhat like a human engineer. This picture has been used many times as a powerful heuristic tool but it can be misleading. The wheels of a machine have no "incentive"to act improperly, but parts of an organism can be under selection to actively undermine the performance of that organism. Mitochondria, usually regarded as the cell's "power plant", are subject to selective forces under which they would in principle benefit by suppressing male function. The same is true for intracellular symbiotic bacteria found in many insect species. These bacteria kill males or turn them into females or effectively sterilize them. Medicine needs to recognize that there are enemies within.

Hauptvortrag AKB 20.2 Fr 14:30 TU H2013

Systems Biology of the JAK-STAT signalling pathway — •Jens Timmer[1] and Ursula Klingmüller[2] — [1]Centre for Data Analysis and Modelling, University of Freiburg, Eckerstr. 1, 79104 Freiburg — [2]German Cancer Research Center, Im Neuenheimer Feld 280, 69120 Heidelberg

Considerable progress has been made in identifying the molecular composition of cellular signalling networks. However, to reveal the systems' properties, quantitative models based on experimental data have to be developed. To demonstrate this Systems Biology approach, we investigate the core module of the JAK-STAT pathway of the Epo-receptor. Based on time resolved quantitative measurement of the involved proteins, we estimate the parameters in differential equations describing the pathway. The results show that the so far believed assumption of a feed-forward cascade to describe the pathway does not hold. A generalization of the model that includes nucleocytoplasmatic cycling is suggested and validated by successfully predicting the outcome of a new experiment. From this model, we infer the time courses of the unobserved STAT populations and show that, on a systems level, fast nucleocytoplasmatic cycling of STAT serves as a remote sensor to closely couple gene activation to receptor activity.

AKB 20.3 Fr 15:00 TU H2013

A Solvable Sequence Evolution Model and Genomic Correlations — •Philipp W. Messer[1,2], Peter F. Arndt[2], and Michael Lassig[1] — [1]Institute for Theoretical Physics, University of Cologne, Zuelpicher Str. 77, 50937 Koeln, Germany — [2]Max Planck Institute for Molecular Genetics, Ihnestr. 73, 14195 Berlin, Germany

We study stochastic sequence evolution processes whose elementary steps are duplication, mutation, insertion, and deletion of single letters. Such processes are found to generate long-range correlations in the frequencies of letters as long as the sequence length is growing, i.e., the combined rates of duplications and insertions are higher than the deletion rate. For constant sequence length, on the other hand, all initial correlations decay exponentially. These results are obtained analytically and are supported by simulations. Their implications for explaining the long-range correlations in genomic DNA are discussed.

AKB 20.4 Fr 15:15 TU H2013

Dynamics of Multi-Allele Evolution on a Fitness Landscape — •Julia Schwartz and Ulrich Gerland — Department für Physik, LMU München

The evolution of a populations genotype can be represented by the motion of a cluster through sequence space. The Wright-Fisher model is a widely accepted way to describe its dynamics. It includes mutation, selection, and random genetic drift due to the finite population size. However, simulations based on this model are not feasable for large populations or high mutation rate due to the enormous number of mutations, most of which are quickly lost from the population. We have developed a method to approximate the dynamics of the Wright-Fisher model, so that simulations in these regimes become possible. The method is based on a combination of the continuum approximation with a heuristic truncation scheme for the cluster dynamics. The latter incorporates an adjustable parameter which controls the tradeoff between accuracy and computational effort.