BP 35: SYBE: Statistical Physics and Biological Evolution

Time: Friday 10:30–12:30 Location: TRE Ma

Invited Talk BP 35.1 Fri 10:30 TRE Ma

Microbial evolution in spatially-structured environments — •Arjan de Visser — Laboratory of Genetics, Wageningen University, The Netherlands

The theory of evolution is increasingly powerful in explaining the diversity of life by looking back, but is still largely unable to predict the future course of evolution. One problem with the development of a predictive theory of evolution is the lack of direct experimental tests of evolutionary models, which are constrained by the slow pace of evolution. Microbial experimental evolution offers a promising tool in this respect. Microbes, such as bacteria and fungi, allow relatively rapid evolutionary changes under controlled conditions that can be replicated. Moreover, they can be temporarily stored in non-evolving state in the freezer and molecular tools allow the manipulation of their genotypes and identification of evolved genetic changes. One limitation of these studies so far has been the use of unstructured well-mixed environments, while natural environments are spatially structured. Spatial environmental structure has several consequences for the process of evolution, including (i) increased environmental heterogeneity allowing more diverse adaptive opportunities, (ii) fragmentation of populations into small semi-isolated subpopulations with a greater role of genetic drift, and (iii) decreased access to nutrients due to slow diffusion leading to inefficient local resource competition among clone mates. I will introduce the approach of experimental evolution, and present examples of studies addressing various consequences of spatial environmental structure for microbial evolution.

Invited Talk BP 35.2 Fri 11:00 TRE Ma

Correlated mutations: Facts or artifacts? — •Amnon Horovitz — Weizmann Institute, Rehovot, Israel

Mutations that affect protein function by structural perturbation at one site are often compensated for by mutations at other sites. Such correlated mutations are thought to occur since there is greater selective pressure to conserve protein structure and function than sequence. Correlated mutation analyses have indicated that distant sites in proteins are often coupled to each other. It has not been clear, however, whether such correlations between distant positions reflect real long-range interactions or common ancestry. In order to address this question, lattice models of proteins were subjected to mutation and selection for greater stability and long-range correlations that arose as a result were characterized. Our results show that long-range correlations with non-zero coupling energies do exist in lattice models [1] and that they are more common when the stability of the native state is achieved by negative design, i.e. by destabilizing non-native contacts [2]. The implications of these findings for real proteins will be discussed.

[1] O. Noivirt-Brik, R. Unger and A. Horovitz, BMC Struct. Biol. **9**, 4 (2009).

[2] O. Noivirt-Brik, A. Horovitz, and R. Unger, PLoS Comput. Biol. **5**, e1000592 (2009).

Invited Talk BP 35.3 Fri 11:30 TRE Ma

Macroscopic laws in bacterial genome evolution — •Erik van Nimwegen — Biozentrum, Universität Basel, Switzerland

Over the last century an enormous effort has been invested into the modeling of evolutionary dynamics, but validation of these models with real data have been limited for several reasons: Until the 1950s it was simply not known what the substrate of natural selection was and until recently data was limited to small fractions of the genomes of a small number of organisms. In addition, none of the existing evolutionary models capture all the complexities of evolution in the real world, so that it is generally unclear which predictions of evolutionary models one would expect to observe in real world data.

However, recently the number of publically available complete genome sequences has grown from one (in 1995) to currently almost 1500. This has offered researchers, for the first time, a chance to identify 'laws' of genome evolution not from general theoretical considerations, but directly by analysis of the available genome data. Indeed such studies have recently uncovered several remarkable macroscopic laws in genome structure and evolution. These quantitative laws concern features such as the distribution of evolutionary rates and gene family sizes, the distribution of genes across different functional categories, and large-scale properties of regulatory networks. In this talk I will discuss some of these laws and their implications for our understanding of genome evolution in prokaryotes.

Invited Talk BP 35.4 Fri 12:00 TRE Ma

The role of horizontal gene transfer in the evolution of bacterial genomes — •Paul Higgs — McMaster University, Hamilton, Ontario, Canada

For a set of related genomes, the core is the set of genes found in every genome, and the pan-genome is the set found in at least one genome. The pan-genome is usually much larger than the core. Genes can be lost by deletion and they can be gained by duplication, by *de novo* evolution of a new sequence, or by horizontal gene transfer (HGT) from another organism. We analyze clusters of related genes from a large number of complete genomes in order to estimate the relative rates of these processes. If the rate of HGT is very high, the traditional tree-like picture of evolution breaks down. It has been argued that the HGT rate was so high in the earliest cells that there were no separate lineages of organisms. Only when the HGT rate began to fall would lineages begin to emerge with their own distinct sets of genes. This phenomenon has been called the Darwinian Threshold. We study a model for genome evolution that incorporates both beneficial and detrimental effects of HGT and show that the model predicts the occurrence of a Darwinian Threshold.