

A two days mini course by Prof. Eugene Koonin will be given at Apr 23-4 at the Inst. of Evolution and the Department of Evolutionary and Environmental Biology at the Univ. of Haifa

The mini course will include two meetings, three hours each. Talks are targeted not necessarily and specifically at evolutionary biologists, rather at the wider spectrum of biologists and even exact scientists. People wishing to participate in specific talks are welcome.

Please find specific details below.

Further information can be obtained from Sagi Snir

Course Title: Chance and Necessity in Genome Evolution

Speaker: Eugene V. Koonin, National Center for Biotechnology Information, NIH, Bethesda, USA

Time: April 23-4, 10:00-13:00.

Location: The seminar room in the new labs complex (located at the former Student Union offices, no 11 in the map) http://multimedia.haifa.ac.il/campus_map/

The course will be broken down into six lectures, so people unable to attend all lectures can choose based on interest/availability

Day 1 (Tuesday)

1. Overview of comparative and evolutionary genomics
2. The "laws" of genome and phenome evolution
3. The Tree of Life, the three domains, and the origin of eukaryotes

Day 2 (Wednesday)

4. Evolution of viruses and virus-host arms race as a fundamental factor of evolution
5. Evolution of genomic complexity
6. The interplay of randomness and adaption in genome evolution and the overhaul of the theory of evolution

Abstract:

These lectures aim at presenting a panoramic view of today's Evolutionary Biology in light of the results of Comparative Genomics and Systems Biology. I will attempt to demonstrate that the concepts

of evolution based on the Neo-Darwinian Modern Synthesis are to be substantially amended in the post-genomic era. Fundamental novelties that change our ideas of evolution come to a large extent from comparative genomics of microbes and viruses on which I will primarily focus.

When Darwin formulated the central principles of evolutionary biology in the *Origin of Species* in 1859 and the architects of the Modern Synthesis integrated these principles with population genetics almost a century later, the primary if not the sole objects of evolutionary biology were multicellular eukaryotes, above all animals and plants. Before the advent of efficient gene sequencing, all attempts to extend evolutionary studies to microbes have been futile. In the 1980s, sequencing of the rRNA genes in thousands of microbes allowed the construction of the three domain 'ribosomal Tree of Life' that was widely thought to have resolved the evolutionary relationships between microbes. However, subsequent massive sequencing of numerous, complete microbial genomes revealed novel evolutionary phenomena, the most fundamental of these being: i) pervasive horizontal gene transfer, in large part mediated by viruses and plasmids, that shapes the genomes of archaea and bacteria and renders Darwin's concept of the Tree of Life largely obsolete, and ii) Lamarckian-type inheritance that appears to be critical for antiviral defense and other forms of adaptation in prokaryotes. In the other, non-cellular part of the microbial world, the study of the evolution of viruses reveals extreme genomic diversity and modularity as well as high rate of sequence change that translates into the quasispecies modality of evolution. It is also becoming increasingly clear that the incessant arms race between viruses and their cellular host is one of the major forces that shapes the evolution of all genomes. Thus, microbial phylogenomics adds new dimensions to the fundamental picture of evolution even as the principles discovered by Darwin remain among the central tenets of evolutionary biology.

Taken together, these findings should compel us to reconsider the contributions of chance and "necessity" (quoting the famous book by Jacques Monod) at different stages of the evolutionary process. I will argue that the process of genomic and phenotypic mutagenesis is far from being completely random but instead includes important adaptive aspects. Conversely, the process of fixation of mutations is far from being fully deterministic and includes substantial randomness. I will further expand this perspective but considering the importance of rare random events such as endosymbiosis in major evolutionary transitions.

Finally, I will discuss reductive evolution as a major evolutionary trend and evolution of complexity as a “genomic syndrome”.