

NIMBioS Interdisciplinary Seminar

3:30 p.m.*, Tuesday, March 25, 2014

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Generalization of the Central Models of Molecular Evolution in the (Post)Genomic Era

The advances of comparative genomics and phylogenomics call for replacement of the key models of molecular evolution by a new generation of more general models. The traditional view of a genome of an individual organism or species has been supplanted by the pangenome concept. It has become apparent that the rates of gene loss and gain far exceed the rates of nucleotide substitution, at least in prokaryotes. Therefore, the pangenome, i.e. the entirety of the genes available to a given species, is typically is much larger than any individual genome, extremely dynamic and variable between different groups of microbes. I will present an overview of the genome dynamics and pangenome size estimates across the microbial world. The dynamic genome evolution and the dominance of horizontal gene transfer (HGT) in the evolution of prokaryotes also undermines the classical Tree of Life (TOL) concept. The notion of a single TOL is giving way to the model of a phylogenetic network that, however, can be shown to encompass a tree-like central trend. Further, genome-wide comparison of phylogenetic trees bears on the Molecular Clock model. It has been long known that the Molecular Clock is substantially overdispersed. I will show that the new model of Universal Pacemaker of genome evolution that only requires the conservation of relative rates of gene evolution, in contrast to the conservation of absolute rates inherent in Molecular Clock, yields a better fit to the phylogenomic data for diverse organisms. The new, general models of evolution do not refute the classic models but include them as extreme cases, in a pattern that appears common in the history of science.

Location: Tom Hallam Auditorium, Room 206 at NIMBioS, Claxton Education Bldg, 1122 Volunteer Blvd.

*Join us for refreshments at 3 p.m. in the Auditorium.

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