Topics in genome rearrangement

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Abstract

This talk covers the probabilistic modeling of prokaryotic genome evolution processes and the consequences of these mechanisms for gene-order based phylogenetics. The modeling of eukaryotic nuclear genome evolution will focus on the quantitative parameters of inversion, transposition, translocation and duplication, and the connection between rearrangements observed at the experimental, clinical, population and evolutionary levels.

These models give rise to statistical analyses and tests for a variety of questions pertaining to functional versus historical versus random proximities of genes. Comparison of the models with empirical data contributes to understanding phenomena as diverse as speciation, infertility due to chromosomal rearrangement, and chromosomal aberrations in neoplasms.