



生物信息学研究中心

Center of Bioinformatics

学术报告

题目： Two Birds with One Stone: A Tool for Gene Duplication Inferences via Reconciliation and Species Tree Reconstruction

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Abstract: Millions of genes in the modern species belong to only thousands of gene families. A gene family includes instances of the same gene in different species and duplicate genes in the same species. Two genes in different species are ortholog if they diverged when the most recent common ancestor of the species speciated. Orthologs are used to infer signaling pathway evolution and correspondence between genotype and phenotype and hence ortholog identification is a basic task in comparative genomics. Because of complex gene evolutionary history, however, ortholog identification is extremely difficult. One key method for it is to use an explicit model of the evolutionary history of the genes subject to study, called the gene (family) tree. It compares the gene tree with the evolutionary history of the species in which the genes reside, called the species tree, using a procedure known as the tree reconciliation. Tree reconciliation presents challenging problems when species trees are not binary in practice.

Here, non-binary gene and species tree reconciliation is studied in a binary refinement model, which unifies gene duplication inference through tree reconciliation with reconstruction of species tree from gene trees. The study produces an automatic tool for inferring gene duplication events through tree reconciliation and for reconstructing species tree from gene trees.

The tool supports quick automated analysis of large data sets.