



CDB SEMINAR

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14:00~15:00 C1F Auditorium

Phylogenomics in the light of ever-growing sequencing data

Summary

A pressing challenge in phylogenomics is the need to cope with the massive production of complete genomic sequences, especially after recent technological developments. Problems that are particularly affected by the increasing flow of genomic data and that require continuous update are: i) the establishment of evolutionary relationships between species (the so-called Tree Of Life (TOL)), ii) the inference of orthology and paralogy relationships across genomes, and iii) the study of the evolution of large, widespread super-families that evolved through complex patterns of duplications and losses. To face such challenges we have developed two sophisticated pipelines that allow high scalability and continuous update, while achieving highest levels of accuracy. The first such pipeline automatically reconstructs entire species-centric collections of gene phylogenies (the so-called phylome), and combines this with phylogenetic information from various other sources to derive unique orthology and paralogy predictions. The second pipeline, which we apply to the superfamily and the Tree of Life assembly problems, is able to reconstruct large phylogenies by means of an iterative strategy that provides scalable resolution and allows continuous update. In this talk, I will illustrate the use of such approaches in the context of the assessment of the evolution of important traits in fungi, and the reconstruction of a genome-based, eukaryotic tree of life.

Host:

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