

# Mathematical & Computational Biology Seminar

Organizer: Valerie Hower

Wednesday, 2:00–3:00pm, 939 Evans

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Nov. 4      **Luay Nakhleh**, Rice University

*Techniques for inferring phylogenetic relationships of species from multi-locus data*

Accurate inference of species phylogenies and understanding of their relationships with gene trees are two central themes in molecular and evolutionary biology. Traditionally, a species tree is inferred by sequencing a genomic region of interest from the group of species under study, reconstructing its evolutionary history, and declaring it to be estimate of the species tree. However, recent analyses of the increasingly available whole-genome data from various groups of organisms have demonstrated that different genomic regions have evolutionary histories that may disagree with each other as well as with that of the species, calling into question the suitability of the traditional approach to inferring evolutionary histories of species. As a result, a new, post-genomic paradigm has emerged, in which multiple genomic regions are analyzed simultaneously, and their evolutionary histories are reconciled in order to infer the evolutionary history of the species. In this talk, I will present recent efforts for developing efficient computational techniques for accurate reconciliation of gene trees and inference of species phylogenies—trees and networks.