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*Phylogenetic Networks*

Phylogenetic trees are central to evolutionary biology and have been the focus of much research in mathematics, statistics, and computer science for several decades. Though appropriate for several groups of taxa, a phylogenetic tree may be inadequate for other groups. In particular, horizontal gene transfer is ubiquitous in bacteria, hybridization is very common in many groups of eukaryotes, and recombination is a hallmark of sexual species. All these processes result in reticulate evolutionary histories best modeled with phylogenetic network. I will describe phylogenetic networks, approaches to their inference, and mathematical and computational challenges that arise in their inference and analysis.