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*Resolving Gene Trees with Polytomies*

Accurate gene tree reconstruction is a fundamental problem in phylogenetics with many important applications. By reconciling a gene tree with a specie tree, we infer the history of duplications and losses that have shaped the gene family, which reveals the orthology/paralogy relationship between gene copies. However, due to various limitations such as insufficient differentiation between gene sequences, alignment ambiguity or inconsistency with gene order or other genome-level information, it is often difficult to support a single gene tree topology with high confidence. In this case, it may be more appropriate to collapse weakly supported internal nodes or remove dubious nodes, leading to a non-binary gene tree, with polytomies representing non-resolved parts of the tree. The question is then to resolve polytomies, based on appropriate criteria. In this presentation, I will review various optimization criteria for inferring a most parsimonious resolution of a polytomy in term of duplications and losses induced by the reconciliation with a given binary gene tree. I will more specifically deal with the problem of finding a resolution leading to a minimum number of non-apparent duplications, which are those annotated as dubious in the Ensembl database. I will present algorithmic and complexity results for this problem, based on interesting properties on the graph representing the speciation and duplication relationships between the leafs of the polytomy.