Tabu Search for Phylogeny Inference

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Abstract: A phylogeny tree (or evolutionary tree) represents a basic structure of relationship among different species. Morphological characters have traditionally been used for inferring phylogenies. The recent progress in molecular sequences provide a large amount of information that can also be used to infer a likely phylogeny. However, the complexity of the underlying mathematical problem presents a special challenge for designing extremely efficient and effective solution methods. In this talk, We present a tabu search algorithm for solving this problem.