

A tutorial on perfect phylogenies

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A phylogeny is a tree whose leaves are bijectively labeled by the elements of a set of taxa (genes, species, etc.). The topology of the tree represents a hypothesis about the evolutionary relationships between the taxa. A central problem in the field of computational phylogenetics is to assemble a phylogeny from a set of characters (partitions of the set of taxa) such that each character is convex on the phylogeny (the collection of subtrees induced by the leaves labeled by taxa in the same part of the character are node-disjoint). The problem of determining whether such a phylogeny exists has been studied by systematians since the mid-1960's and is called the perfect phylogeny problem. In this tutorial our goal is to give a brief introduction to the mathematical and algorithmic structure of the perfect phylogeny problem.