

1047-05-183

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A phylogenetic tree is a binary tree in which the leaves are labelled with different labels. A binary subtree of a phylogenetic tree is obtained by selecting a subset of the leaf vertices, taking their spanning subtree, and in the spanning subtree contracting recursively edges, in which at least one endvertex has degree 2.

A well-known fact is, that given two different phylogenetic trees with there should be a 4-leaf binary tree, which is a binary subtree of one of the phylogenetic trees, but not of the other.

A version of the Maximum Agreement Subtree Problem asks how large common binary subtree must be always there for two phylogenetic trees with n leaves each, using the same label set.

In general, the question is what kind of structures should be shared by any two different phylogenetic trees and what kind of different structures should there be in any two different phylogenetic trees.

These problems show analogy with Ramsey theory and come up naturally in phylogeny reconstruction, and in related questions about testing phylogenetic trees. I'll discuss results on phylogeny reconstruction and phylogeny testing in the framework of the Cavender-Farris-Neyman model.

This is joint work with Mike Steel, Elchanan Mossell and others. (Received January 28, 2009)