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Cographs: A Mathematical Characterization for Valid Orthology Relations

The divergence of all the genes that descended from a single gene in an ancestral species can be represented as a tree, a gene tree that takes into account both speciation and duplication events. Orthology refers specifically to the relationship between two genes that arose by a speciation event, recent or remote. Comparing orthologous genes is essential to the correct reconstruction of species trees, so that detecting and identifying orthologous genes is an important problem in comparative and evolutionary genomics as well as phylogenetics. In this work, we look at the connection of trees and orthology by trying to answer the following question: How much information about the gene tree, the species tree, and their reconciliation is already contained in the orthology relation among genes? A solution to the first part of this question has already been given by Boecker and Dress in 1998 in a different context. In particular, they completely characterized certain maps which they called symbolic ultrametrics. Semple and Steel [2003] then presented an algorithm that can be used to reconstruct a phylogenetic tree from any given symbolic ultrametric. In this work we investigate a new characterization of orthology relations, based on symbolic ultrametrics for recovering the gene tree. Surprisingly, symbolic ultrametrics are very closely related to cographs, graphs that do not contain an induced path on any subset of four vertices. We will show that the tree corresponding to a symbolic ultrametric can also be recovered using cotrees, trees that can be canonically associated to cographs.