

Least Common Ancestors and Decomposition Methods in Phylogenetic Trees

Lifoma Salaam*, Dr Louis Shapiro; Howard University

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Phylogenetic trees are used to model evolutionary relationships between sets of species. In a Phylogenetic Tree, leaves of the tree are associated with extant species, while the internal nodes represent hypothetical ancestral species. Data from the species - genetic, molecular or physical- is used to define a character function from the set of vertices of the tree into the character states. The species (the vertices) are grouped or colored according to their character states- each state is assigned a unique color. Convexity, a key requirement in Phylogenetics, is essentially the condition that all vertices of a given color induce a sub-tree.

We use vertex and leaf generating functions and an interesting tree decomposition method to determine useful combinatorial statistics on convex tree partitions in Phylogenetic Trees. This method is also used with the least common ancestor to count anti-chains of arbitrary size in Binary Trees, Incomplete Binary Trees, Motzkin Trees, and Ordered Trees.