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A phylogenetic tree models the common evolutionary history of a group of species. A tree metric is a distance function on a set of species realized by a tree with edge weights. Distance-based phylogenetic algorithms attempt to solve the NP-hard least-squares phylogeny problem by mapping an arbitrary dissimilarity map representing biological data to a tree metric. The set of all dissimilarity maps is a Euclidean space properly containing the space of all tree metrics as a polyhedral fan. Outputs of distance-based tree reconstruction algorithms such as UPGMA and Neighbor-Joining are points in the maximal cones in the fan. Tree metrics with polytomies, or internal vertices of degree higher than three, lie at the intersections of maximal cones. A phylogenetic algorithm divides the space of all dissimilarity maps into regions based upon which combinatorial tree is reconstructed by the algorithm. We use polyhedral geometry to compare the local nature of the subdivisions induced by least-squares phylogeny, UPGMA, and Neighbor-Joining. Our results suggest that in some circumstances, UPGMA and Neighbor-Joining poorly match least-squares phylogeny when the true tree has a polytomy. (Received August 09, 2013)