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We will present a geometric model of a space which parametrizes phylogenetic trees using both combinatorics and geometry. The geometry of the space gives a way of measuring a distance between phylogenetic trees as well as a way of ‘averaging’ or ‘combining’ several trees whose leaves are identical. The convex hull of a set of trees can also be defined, thus making possible a “peeling” procedure which finds the most central trees in a set, called the tree of greatest depth. This geometric model of tree space provides answers to questions concerning the number of ‘neighbors’ to a given tree and the ‘curvature’ of the boundaries between regions defining different trees that have been posed by biologists and statisticians over the last decade. It also provides a justification for disregarding portions of a collection of trees that agree, thus simplifying the space in which comparisons are to be made. (Received September 24, 2000)