

Combining Phylogenetic Trees Using Consensus Network Methods

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DNA and protein sequences are available for a vast number of genes from a multitude of different species, and phylogenetic trees are routinely constructed to show the evolutionary relationships between species for individual genes. However, these gene trees are single snapshots of relationships between species which may not be constant across all of the genes studied. Consensus network methods have been developed to represent the overall inter-relationships within a group of species across a number of genes, and to allow the representation of the incongruities between individual gene trees.

The Consensus Network algorithm does not use the sequence data directly, but instead uses the collection of splits (the division of the taxa on a tree into two groups by a single line) present in the input trees to create a consensus 'tree' that represents the splits found across the data set.

However, it is often the case that not all of the species in a group are represented in each individual gene tree. The Consensus Network requires that all the input trees contain identical taxa and those taxa that do not have sequences for all of the genes in the data set have to be discarded from the analysis, resulting potentially in considerable loss of information. The Supernet method addresses this limitation and the algorithm creates a consensus network from the splits present in gene trees with either complete taxon coverage or where there are overlapping sets of species, although the accuracy of the results may be impaired if there are many gaps in the coverage.

In this paper we will present a non-mathematical overview of these consensus network methods and extend their use to textual data sets with complete or incomplete manuscript coverage. We will invite discussion as to whether these methods may be of any practical value with textual material.