

NeighborNet

The NeighborNet algorithm is an algorithm based on [neighbour joining](#) to construct phylogenetic networks. Like neighbor joining, this method takes a [distance matrix](#) as input and starts with a completely unresolved [tree](#) (i.e. a tree connecting all [nodes](#) individually to a single [root](#)). It determines which two [edges](#) (or taxa/branches) may be connected to a new intermediate node because they are the least distant ones compared to any of the other branch combinations in the network. This process is repeated until there are no 'unprocessed' edges left. The difference to neighbour joining is that NeighborNet allows for collections of clusters that overlap and do not form a hierarchy. The [SplitsTree](#) software package implements several phylogenetic algorithms amongst which NeighborNet.

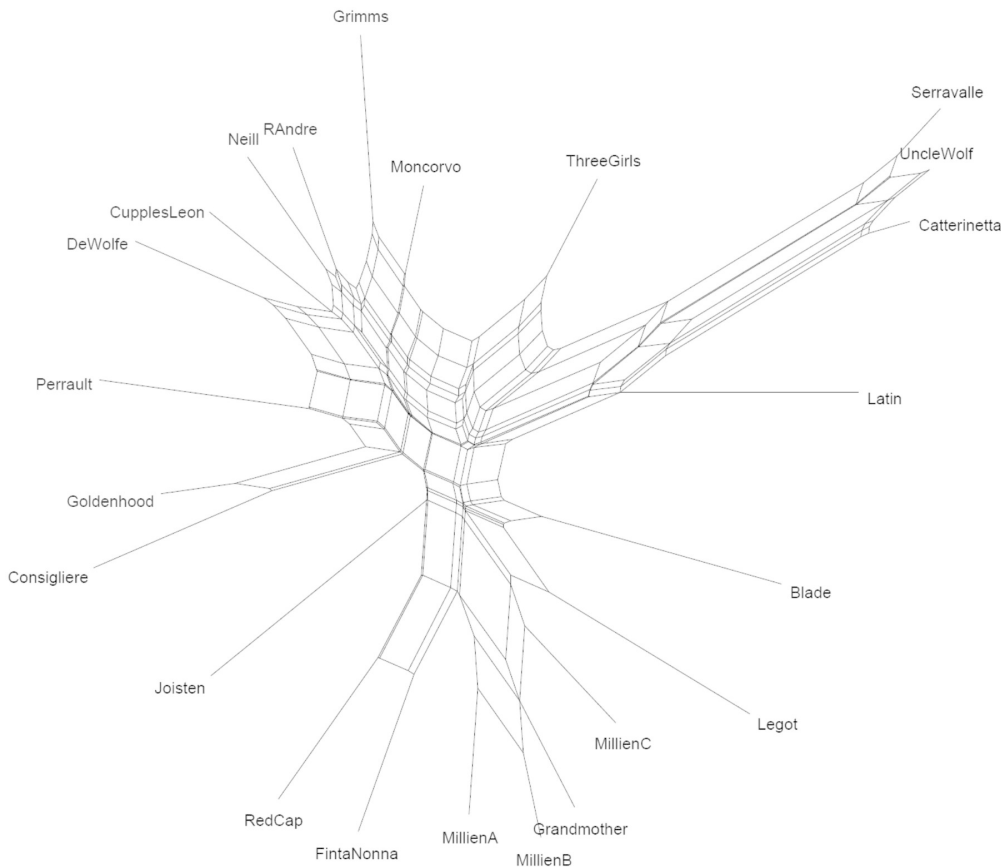


Fig. 1: NeighborNet representation of different versions of Red Riding Hood (Tehrani et al. 2015)

References

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