Lecture 1: Analysing non standard data: distances for trees and networks.

Inferential summaries of tree estimates are useful in the setting of evolutionary biology (phylogenetic trees), psychometrics (decision trees) and data mining (hierarchical clustering). Practitioners need to consider the stability and `generalizability' of these summaries. Geometric distance between trees were developed by Billera, Holmes and Vogtmann (2001) [BHV] who showed that the space of trees is negatively curved (a CAT(0) space), thus enabling statistical inference on all types of binary rooted trees.