
MEGAN OWEN, University of Waterloo

Statistics in tree space

We introduce new notions of mean and variance for a set or distribution of phylogenetic trees. These definitions of mean and variance are analogous to those for a weighted set of points in Euclidean space, but with the underlying space being the space of phylogenetic trees constructed by Billera, Holmes, and Vogtmann (2001). A property of this space (non-positive curvature) ensures there is a unique shortest path between any two trees. Furthermore, this path can be computed in polynomial time, leading to a practical algorithm for computing the mean and variance. I will compare the mean and variance to existing consensus tree and summary methods, as well as present applications to such biological problems as the reconstruction of phylogenetic trees and the classification of lung airway scans.