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Averages in the space of phylogenetic trees

The space of metric phylogenetic trees is a polyhedral complex, as constructed by Billera, Holmes, and Vogtmann (2001). This space is also non-positively curved, so there is a unique shortest path between any two trees and a well-defined notion of an average or mean trees for a given set of trees. Finding either of these is a convex optimization problem. We will describe how a polynomial time algorithm for computing the shortest path can be used in computing the mean tree. We will also discuss how the mean tree can be used in some applications, such as reconstructing species trees from gene trees and comparing the topology of blood vessels in the brain.

Joint work with Ezra Miller (Duke) and Scott Provan (UNC).