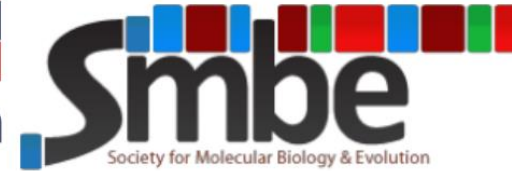


Evolution &
Comparative Genomics



Friday, May 2nd 11:00 AM EDT

Billera-Holmes-Vogtmann (BHV) Phylogenetic Tree Space: Algorithms and Applications to Evolutionary Biology

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A continuous phylogenetic tree space is a geometric space whose points correspond to phylogenetic trees with branch lengths. Such a space provides a framework for analyzing both the tree topology and branch lengths together, which is important for processes such as the multi-species coalescent which depend on tree branch lengths. This talk will introduce the most well-known such space, the Billera-Holmes-Vogtmann (BHV) tree space. BHV tree space has several nice properties, including unique shortest paths (geodesics) between pairs of trees, and a unique tree (the Fréchet mean) minimizing the sum of the squared distances to a set of trees. I will discuss some recent work on algorithms and applications of BHV tree space, including using the geodesics to explore and visualize phylogenetic landscapes and to find relevant high likelihood trees.