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Visualization of Phylogenetic Tree space

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Abstract

When working with phylogenetic trees and Markov chain Monte Carlo (MCMC) methods it is often of interest to visualize the tree space provided by the MCMC algorithm. First, we need to define a metric so we can get an distance between all trees. However the tree space is an high dimensional space so it needs to be reduced to allow visualization. In this thesis we look at two metrics and four dimension reduction methods. The main conclusion is that metric is much more important than the method used to reduced the dimensions. Different metrics can give almost completely different plots while different dimension reduction methods rarely radically changes the plots.

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