

The geometry of phylogenetic tree spaces
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Phylogenetic trees are the fundamental representation of evolutionary processes, and they are particularly essential in modeling many important and diverse biological phenomena, such as speciation and the evolution of cancer. As trees with weighted edges, they can be embedded in an ambient space \mathbb{R}^n , and the geometry of the tree space depends on the distance function. In this talk, I will introduce a well-studied distance function - the BHV metric, and an alternative distance function - the tropical metric. I will compare the geometric properties of the two metric spaces, including convexity, geodesics and central tendency. These properties have statistical applications, for example, the study of stickiness.