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**Anthea Monod\*** ([am4691@cumc.columbia.edu](mailto:am4691@cumc.columbia.edu)). *Tropical Statistics & Geometry of Phylogenetic Tree Space*. Preliminary report.

Phylogenetic trees are the fundamental representation of evolutionary processes, and are particularly essential in modeling many important and diverse biological phenomena, such as speciation, the spread of pathogens, and the evolution of cancer. Trees may be compared with one another in a moduli space, whose geometry is determined by a metric. The classical representation of this space is the BHV tree space, endowed with the geodesic metric. In this talk, I will discuss an alternative distance function, known as the tropical metric. I will present a comparison of geometric and topological properties of tree spaces under the two metrics that are particularly relevant for statistical analysis. I will make the case that the tropical moduli space of phylogenetic trees is a natural setting for probability and statistics, because it allows for a tropical interpretation of linear algebra, which is the basis of classical statistical analysis. This is joint work with Bo Lin and Ruriko Yoshida. (Received September 23, 2018)