1146-05-534   **Bo Lin***, School of Mathematics, Georgia Institute of Techlonogy, Atlanta, GA 30332, and **Anthea Monod**, **Qiwen Kang** and **Ruriko Yoshida**. *Tropical Statistics for Phylogenetic Trees.*

Phylogenetic trees are the fundamental mathematical representation of evolutionary processes in biology. As data objects, they are characterized by the challenges associated with "big data," as well as the complication that their discrete, geometric structure results in a non-Euclidean phylogenetic tree space, which poses computational and statistical limitations. We propose a novel framework motivated from tropical geometry for the statistical analysis of evolutionary biological processes represented by phylogenetic trees. Our framework allows for the definition of probability measures, expectations, variances, and other fundamental statistical quantities. In addition, our setting exhibits analytic, geometric, and topological properties that are desirable for rigorous, theoretical treatment in probability and statistics, as well as increased computational efficiency over the current state-of-the-art. We demonstrate our approach on seasonal influenza A viral data. (Received January 29, 2019)