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Katherine St. John* (stjohn@lehman.cuny.edu), Department of Mathematics & Computer Science, Lehman College– City University of New York, Bronx, NY 10468. *Spaces of Trees*.

Phylogenies, or evolutionary histories, play a central role in modern biology, illustrating the interrelationships between species, and also aiding the prediction of structural, physiological, and biochemical properties. The reconstruction of the underlying evolutionary history from a set of morphological characters or biomolecular sequences is difficult since the optimality criteria favored by biologists are NP-hard, and the space of possible answers is huge. Phylogenies are often modeled by trees with n leaves, and the number of possible phylogenetic trees is $(2n-5)!!$. Due to the hardness and the large number of possible answers, clever searching techniques and heuristics are used to estimate the underlying tree. We explore the combinatorial structure of the underlying space of phylogenetic trees, under different metrics, in particular the interplay between tree rearrangement metrics and the Billera-Holmes-Vogtmann (BHV) metric. The former yield discrete metrics while the later results in a space that is $CAT(0)$. (Received September 21, 2015)