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Chicago, IL 60657. *SVDquartets and Numerical Algebraic Geometry*.

Phylogenies are mathematical models of the evolutionary history of a set of taxa. The SVDquartets method (Chifman-Kubatko 2014) assigns a numerical score to each of the three possible four-taxon (quartet) trees within a larger dataset. Lowest-scoring quartets are combined via quartet-agglomeration methods such as Quartets Max Cut (Snir-Rao 2012), producing a phylogeny on the entire dataset. The theory (Chifman-Kubatko 2015) behind this method is that the lowest-scoring quartet is generically identifiable assuming the multi-species coalescent model (MSC): the score represents the distance to an algebraic variety corresponding to matrices for time-reversible models of nucleotide substitution. This score enables the SVDquartets method to bypass the problem of gene tree estimation error that is a major issue in MSC-based methods. A comparative study showed that SVDquartets performed unevenly in comparison with other MSC-based methods on many datasets. In this talk we address (1) interaction of the SVDquartet score with quartet-agglomeration methods, (2) the distance computation to the algebraic variety representing the substitution model, and (3) strategies to boost the performance of this approach and expand the theory behind it. (Received September 18, 2016)