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Ruth Davidson* (redavid2@illinois.edu), **Siavash Mirarab** (smirarab@cs.utexas.edu) and **Tandy Warnow** (warnow@illinois.edu). *Using Phylogenetic Invariants in Coalescent-Based Methods*. Preliminary report.

A phylogenetic tree represents the common evolutionary history of a collection of genes or species. Phylogenetic invariants are polynomial relationships in probabilities associated to models of evolutionary processes. Thus an invariant can give an algebraic encoding of a tree shape representing a specific evolutionary history. Phylogenetic invariants were first introduced in the biology community in 1987. Their study has led to many beautiful results in algebraic geometry and provided interesting links between this classical field of mathematics and discrete optimization problems. In practice, a biologist may consume a combination of techniques when making trees, and methods for large datasets-those which include large numbers of species and/or large numbers of data samples from various loci in the genome from each species-often combine distinct methods for sub-problems into a pipeline. We investigate the problem of exploiting theoretical results about phylogenetic invariants to improve existing pipelines for tree estimation and propose new approaches, with an emphasis on coalescent-based methods. We give some new confidence bounds for the use of invariants in coalescent-based methods that correspond to properties of real data sets. (Received September 15, 2014)