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Barbara Holland, Peter D. Jarvis, Jeremy G. Sumner and Amelia Taylor*
(amelia.taylor@coloradocollege.edu). *Developing a Statistically Powerful Measure for
Phylogenetic Tree Inference using Phylogenetic and Markov Invariants*. Preliminary report.

In the late 1980's Cavendar and Felsenstein and Lake introduced the idea of phylogenetic invariants; a class of polynomials useful in the study of phylogenetic trees. Allman and Rhodes renewed interest in these polynomials taking the point of view of algebraic geometry and giving a comprehensive description of the set of polynomials which lead to their use studying numerous analytical questions like identifiability. As part of this renaissance Casanellas and Fernandez – Sanchez provided one of the first simulation studies exploring the use of the polynomials for tree inference, leaving many open questions about using the polynomials directly for tree inference. Around the same time Sumner and coauthors suggested an alternative perspective using group representation theory. We briefly present the two perspectives for the two-state general Markov model on quartet trees and then describe our study of using polynomials from each perspective to build a statistically powerful measure for tree inference, and argue for one particular measure including simulation results. (Received July 15, 2015)