1116-92-2266 **Emily Chae Castner*** (castn22e@mtholyoke.edu), 55 Fire Road 10, Lancaster, MA 01523, and **Brent R Davis** and **Joseph P Rusinko**. *A distance-based method for phylogenetic tree reconstruction using algebraic geometry.* Preliminary report.

Using algebraic geometry and optimization software, we present a new method for phylogenetic quartet reconstruction. Representing tree topologies as varieties and genetic data as points, we determine how well the data fits a Markov model on the associated tree topology by minimizing the distance from the point to the variety. We implement this for the heterogeneous Jukes-Cantor, Kimura 2- and 3-parameter, and general Markov models of evolution. The Kimura 3-parameter model is most accurate on data simulated under the same model. We see that the Jukes-Cantor model is almost as accurate, even with model misspecification on all data, and is by far the fastest. (Received September 22, 2015)