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**Emily Castner, Brent Davis and Joe Rusinko\*** (rusinko@hws.edu), NY. *Nearest Point Phylogenetic Reconstruction using Numerical Algebraic Geometry.*

We propose a phylogenetic reconstruction algorithm which uses the distance to the nearest point on the phylogenetic model to select the tree of best fit. Our implementation is currently for quartet trees which can be then used to reconstruct larger trees using a quartet amalgamation algorithm. This algorithm allows for data dependent hypothesis testing which helps identify when trees have been accurately reconstructed an important feature since quartet amalgamation algorithms are sensitive to error in input trees but do not require a complete set of quartet trees as inputs. We present initial findings for the Jukes-Cantor, Kimura 2 and 3 parameter models and the general Markov model of evolution. (Received August 09, 2015)