E. S. Allman, H. Banos* (hdbanoservantes@alaska.edu) and J. A. Rhodes. Species network identifiability under the coalescent model.

Hybridization sometimes plays an important role in evolution, so that phylogenetic networks are necessary to describe species-level relationships. In this talk, we prove that most topological features of a level-1 species network are identifiable from gene tree topologies under the network multispecies coalescent model (NMSC). A new approach to proving this identifiability result depends on understanding the expected frequencies of gene topologies for subsets of 4 taxa under the NMSC, an intertaxon distance built from 4-taxon networks, and the circular network algorithm of Huson and Dress for constructing split graphs. Importantly, the line of argument points the way to a practical inference algorithm. (Received January 27, 2019)