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Elizabeth S Allman (esallman@alaska.edu), **John A. Rhodes** (jarhodes2@alaska.edu) and **Hector Banos*** (hbassnos@gmail.com). *Identifiability of species network topologies from genomic sequences using the logDet distance.*

Hybridization plays an important role during the evolutionary process of some species. In such cases, phylogenetic trees are insufficient to describe species-level relationships. We show that most topological features of a level-1 species network (a network with no interlocking cycles) are identifiable under the network multi-species coalescent model using the logDet distance between aligned DNA sequences of concatenated genes. (Received August 30, 2021)