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James H Degnan* (jamdeg@unm.edu), Department of Mathematics and Statistics, 311 Terrace NE, Albuquerque, NM 87131, and **Sha Zhu**, Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, United Kingdom. *Displayed Trees Do Not Determine Distinguishability Under the Network Multispecies Coalescent*. Preliminary report.

Recent work in estimating species relationships from gene trees have included inferring networks assuming that past hybridization has occurred between species. Probabilistic models using the multispecies coalescent can be used in this framework for likelihood-based inference of both network topologies and parameters, including branch lengths and hybridization parameters. A difficulty for such methods is that it is not always clear whether, or to what extent, networks are identifiable — i.e., whether there could be two distinct networks that lead to the same distribution of gene trees. We present a new representation of the species network likelihood that represents the probability distribution of the gene tree topologies as a linear combination of gene tree distributions given a set of species trees. This representation makes it clear that in some cases in which two distinct networks give the same distribution of gene trees when sampling one allele per species, the two networks can be distinguished theoretically when multiple individuals are sampled per species. This result means that network identifiability is not only a function of the trees displayed by the networks. (Received August 03, 2015)