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Elizabeth Allman, Sonja Petrovic, John Rhodes and Seth Sullivant*, Department of Mathematics, Box 8205, North Carolina State University, Raleigh, NC 27695. *Identifiability of Phylogenetic Mixture Models.*

Phylogenetic data arising on two possibly different tree topologies might be mixed through several biological mechanisms, including incomplete lineage sorting or horizontal gene transfer in the case of different topologies, or simply different substitution processes on characters in the case of the same topology. Recent work on a 2-state symmetric model of character change showed such a mixture model has non-identifiable parameters, and thus it is theoretically impossible to determine the two tree topologies from any amount of data under such circumstances. Here the question of identifiability is investigated for 2-tree mixtures of the 4-state group-based models, which are more relevant to DNA sequence data. Using algebraic techniques, we show that the tree parameters are identifiable for the JC and K2P models. We also prove that generic substitution parameters for the JC mixture models are identifiable, and for the K2P and K3P models obtain generic identifiability results for mixtures on the same tree. This indicates that the full phylogenetic signal remains in such mixtures, and that the 2-state symmetric result is thus a misleading guide to the behavior of other models. (Received January 13, 2010)