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**Elizabeth Allman, Sonja Petrovic, John Rhodes and Seth Sullivant\***  
([smsulli2@ncsu.edu](mailto:smsulli2@ncsu.edu)). *Identifiability of phylogenetic mixture models.*

A statistical model is generically identifiable if the map from parameters to probability distributions is generically one-to-one. We show that tree parameters of two tree phylogenetic mixture models are generically identifiable for the Jukes-Cantor and Kimura 2 parameter models and verify computationally that the stochastic parameters are identifiable. These provide the first positive results on identifiability of phylogenetic mixture models with different trees. Proofs rely on a combination of algebraic geometry and combinatorics.

I will spend most of the talk explaining the background of phylogenetic models, mixture models, identifiability problems, etc. Then I will try to highlight some algebraic surprises that arise in the proofs. (Received July 24, 2009)