

## **Identifiability in Phylogenetics using Algebraic Matroids**

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Identifiability is a crucial property for a statistical model since distributions in the model uniquely determine the parameters that produce them. In phylogenetics, the identifiability of the tree parameter is of particular interest since it means that phylogenetic models can be used to infer evolutionary histories from data. In this paper we introduce a new computational strategy for proving the identifiability of discrete parameters in algebraic statistical models that uses algebraic matroids naturally associated to the models. We then use this algorithm to prove that the tree parameters are generically identifiable for 2-tree CFN and K3P mixtures. We also show that the k-cycle phylogenetic network parameter is identifiable under the K2P and K3P models.

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