Benjamin K Hollering* (bkholler@ncsu.edu) and Seth Sullivant. Identifiability in Phylogenetics and Algebraic Matroids.

A statistical model is identifiable if the parameters that produce a probability distribution in the model can be recovered from the distribution. In phylogenetics, the identifiability of the tree parameter is of particular interest. In this talk, we discuss a new computational strategy for proving the identifiability of the tree parameters that utilizes the matroids associated to the vanishing ideals of these models. This method allows us to avoid the computation of the vanishing ideal itself which is typically quite expensive. Specifically, we will discuss an application of this method to 2 tree mixtures for the CFN model and to phylogenetic networks for the Jukes-Cantor and CFN models. (Received July 15, 2019)