1139-14-294 Colby Long* (long.1579@mbi.osu.edu) and Laura Kubatko. *Identifiability of Species Phylogenies Under a Modified Coalescent.*

Coalescent models of evolution account for incomplete lineage sorting by specifying a species tree parameter which determines a distribution on gene trees. Each gene tree gives a DNA site pattern probability distribution and the site pattern probability distribution from the coalescent model is obtained by integrating over all possible gene trees. Using rank conditions on certain flattening matrices, it has been shown that the unrooted topology of the species tree parameter of the multispecies coalescent is generically identifiable from DNA site pattern frequencies. Moreover, a statistically consistent reconstruction method called SVDQuartets has been developed to recover this parameter. In this talk, we describe a modified multispecies coalescent model that allows for different effective population sizes and violations of the molecular clock. We show that the unrooted topology of the species tree for these models is generically identifiable and that SVDQuartets is still a statistically consistent method for inferring this parameter. (Received February 14, 2018)