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Luay Nakhleh* (nakhleh@rice.edu), Houston, TX 77005. *Statistical Inference of Reticulate Evolutionary Histories Using Data from Unlinked Loci.*

The multispecies coalescent (MSC) model has emerged as a major stochastic process that helps capture the intricate relationship between species trees and gene trees. Combined with models of sequence evolution, the MSC can be viewed as a generative model of genomic sequence data in the context of a (species) phylogenetic tree. A significant outcome of the use of genome-wide data has been the increasing evidence, or hypotheses, of reticulation (e.g., hybridization) during the evolution of various groups of eukaryotic species. Reticulate evolutionary histories are best represented as phylogenetic networks. I will describe the multispecies network coalescent (MSNC) model, which extends the MSC model so that it operates within the branches of a phylogenetic network. This extended model naturally allows for modeling vertical and horizontal evolutionary processes acting within and across species boundaries. In particular, it simultaneously accounts for gene tree incongruence across loci due to both hybridization and incomplete lineage sorting. I will then describe a likelihood function for this model, as well as a method for Bayesian sampling of phylogenetic networks and their parameters using reversible-jump Markov chain Monte Carlo (RJMCMC). (Received January 21, 2018)