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**Luay Nakhleh\*** ([nakhleh@rice.edu](mailto:nakhleh@rice.edu)), 6100 Main Street, Houston, TX 77005. *Gene trees in phylogenetic networks.*

Phylogenetic networks model reticulate evolutionary histories arising due to processes such as horizontal gene transfer in prokaryotes and hybridization in eukaryotes. The topology of a phylogenetic network (the "evolutionary" version of networks) is a rooted, directed, acyclic graph, whose leaves are bijectively labeled by a set of taxa and in which each node (except for the root) has in-degree 1 or 2. Each edge in the network has parameters that include the population size and length in generations along that edge. Furthermore, given a gene, or genomic region of interest, we associate with each edge in the network a function to capture the probability that the gene has evolved inside that edge. This model constitutes a generative model of gene trees under the multi-species coalescent model with reticulation. In this talk, I will describe the model, the distribution of genes under it, and a maximum likelihood framework for inferring phylogenetic networks from genome-wide data. This is joint work with James Degnan, Jianrong Dong, Kevin Liu, and Yun Yu. (Received July 23, 2015)