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Elizabeth S. Allman (e.allman@alaska.edu), **James H. Degnan** (jamdeg@unm.edu) and **John A. Rhodes*** (j.rhodes@alaska.edu). *Identifiability of species trees from gene tree clades and splits.*

Due to population genetic effects, trees describing the evolutionary histories of individuals genes may differ from the tree describing the history of the species from which they are drawn. While the multispecies coalescent models this process, model-based inference of a species tree from gene trees remains computationally formidable. An attractive option is to summarize a collection of gene trees through the the clades or splits they display, and base inference on only the clade or split frequencies. But for this to work, it is essential that the species tree be identifiable from these summary statistics. Viewing the spaces of clade and split probabilities as algebraic varieties, we establish this fact. Of particular interest is that while the notion of split is unrooted, split probabilities generally retain enough information to identify not only the species tree topology, but also its root. (Received September 16, 2016)