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James H. Degnan*, jamdeg@unm.edu, and **Huan Jiang**. *Trait evolution on two or more trees.*

In trait evolution models in phylogenetics, the mean value of a trait for a species evolves along the branches of a phylogeny. This process leads to correlated traits values at the tips of a phylogenetic tree, where tips that are more closely related tend to have more similar mean trait values. An implicit assumption in these models is that the mean trait value is evolving on a single tree. We consider a more general perspective in which trait values can be modeled as arising on a combination of trees. This is motivated by consideration of traits that are strongly influenced by a small number of genes, in which case it makes sense to think of the traits as evolving on the gene trees, which reflect the ancestry for gene orthologs sampled from different populations, as opposed to the species tree, which reflects the ancestral relationships for populations. The multiple genes contributing to a trait can be related to the species tree through the multispecies coalescent, for example, but we consider a model which allows arbitrary contributions from two or more gene trees to a trait value. In this model, the correlation structure for the observed traits is a linear combination of the correlation structures that arise on each of the contributing gene trees. (Received January 21, 2018)