

BIOLOGY 848: PHYLOGENETIC METHODS – HOMEWORK #2

At <http://phylo.bio.ku.edu/slides/Preston-Martinez-Hileman-2011-newick.tre> you should find a text file containing two trees.

The trees are expressed in the [Newick](#) file format. If you save the file of trees to your computer and open the file in [FigTree](#) then you should be able to see the trees.

The trees are taken from Preston, J. C., C. C. Martinez and L. C. Hileman. 2011. “Gradual disintegration of the floral symmetry gene network is implicated in the evolution of a wind-pollination syndrome.” *Proceedings of the National Academy of Sciences, USA* 108(6): 2343-2348. ([pdf](#))

The first tree is a phylogeny. The second tree is a gene family tree of the DIVARICATA (DIV) family of genes.

Reconcile the trees by drawing the DIV tree inside the phylogeny (similar to the depiction of the evolution of the globin genes in the lecture slides).

Use a square at a node to indicate a gene duplication event. Use an X to indicate the loss of a gene (either by gene deletion or lack of sampling for that gene).

Your reconciliation need not be an optimal reconciliation (it does not need to be the reconciliation which minimizes the number of duplication/deletion events, for example). It should be a valid representation of both trees.