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Bret Larget* (bret.larget@wisc.edu), 430 Lincoln Avenue, Department of Botany, Madison, WI 53706. *Recent Advances in Bayesian Concordance Analysis.*

Bayesian concordance analysis, as implemented in the software BUCKy, is a method to simultaneously estimate multiple gene trees with prior information that trees from different genes relating the same set of taxa are likely to be similar, if not identical. Information is shared between genes, but discordance among genes is allowed. Recent advances include a cluster model where discordant gene trees are expected to be topologically similar, as many biological processes that create gene tree discordance predict. We review recent advances in this research area. (Received August 10, 2015)