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Tandy Warnow* (warnow@illinois.edu), University of Illinois at Urbana-Champaign, Department of Computer Science, Urbana, IL 61801, and **Siavash Mirarab**, **Shamsuzzoha Bayzid** and **Bastien Boussau**. *Species Tree Estimation in the presence of Incomplete Lineage Sorting*.

Estimating the Tree of Life will likely involve a two-step procedure, where in the first step trees are estimated on many genes, and then the gene trees are combined into a tree on all the taxa. However, the true gene trees may not agree with the species tree due to biological processes such as deep coalescence, gene duplication and loss, and horizontal gene transfer. Statistically consistent methods based on the multi-species coalescent model have been developed to estimate species trees in the presence of incomplete lineage sorting; however, the relative accuracy of these methods compared to the usual "concatenation" approach is a matter of substantial debate within the research community.

I will present results showing that coalescent-based estimation methods are impacted by gene tree estimation error, so that they can be less accurate than concatenation in many cases. I will also present weighted and unweighted statistical binning (see Mirarab et al., Science 2014, and Bayzid et al., PLOS One 2015), methods for improving gene tree estimation, and that enable more accurate estimations of species trees in the presence of gene tree conflict due to ILS. (Received August 04, 2015)