1172-92-196   **Gleb Zhelezov*** (`gzhelezov@unm.edu`) and **James H. Degnan**. *Trying out a million genes to find the perfect pair with MTrip.*

Consensus methods can be used for reconstructing a species tree from several gene trees which exhibit incompatible topologies due to incomplete lineage sorting. Motivated by the fact that there are no anomalous rooted gene trees with three taxa and no anomalous unrooted gene trees with four taxa in the multispecies coalescent model, several contemporary methods form the gene tree consensus by finding the median tree with respect to the triplet or quartet distance—i.e., estimate the species tree as the tree which minimizes the sum of triplet or quartet distances to the input gene trees. These methods reformulate the solution to the consensus problem as the solution to a recursively-solved dynamic programming problem. We present an iterative, easily-parallelizable approach to finding the exact median triplet tree. By taking advantage of the fact that gene trees associated with the same species tree often have distinct bipartitions of identical taxa subsets, this implementation finds the exact median tree of many gene trees faster than comparable methods, has better scaling properties with respect to the number of gene trees, and has a smaller memory footprint. (Received August 27, 2021)