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Laura Kubatko* (kubatko.2@osu.edu), **Julia Chifman**, **Paul Blischak** and **Andrea Wolfe**.

An Invariants-based Method for Efficient Identification of Hybrid Species From Genomic Data.

Coalescent-based species tree inference has become widely used in the analysis of genome-scale multilocus and SNP datasets when the goal is inference of a species-level phylogeny. However, numerous evolutionary processes are known to violate the assumptions of a coalescence-only model and complicate inference of the species tree. One such process is hybrid speciation, in which a species shares its ancestry with two distinct species. We propose a method that can examine genome-scale data for a large number of taxa and detect those taxa that may have arisen via hybridization, as well as their potential “parental” taxa. The method is based on a model that considers both coalescence and hybridization together, and uses phylogenetic invariants to construct a test that scales well in terms of computational time for both the number of taxa and the amount of sequence data. We demonstrate the utility of the method using both simulated and empirical data. (Received January 22, 2018)