1057-92-323 **David Haws*** (`dchaws@gmail.com`), UNIVERSITY OF KENTUCKY, Department of Statistics, 817 PATTERSON OFFICE TOWER, Lexington, KY 40506-0027, and **Eric M O'Neill**, **Peter Huggins**, **David Weisrock** and **Ruriko Yoshida**. *Identifying Outlier Gene Trees: Gene Tree Distributions and Support Vector Machinery.*

The increased use of multi-locus data sets for species tree reconstruction has strengthened the need to identify particular loci with gene tree patterns that deviate from those generated under neutral processes. Gene trees reconstructed from neutral unlinked loci are expected to be correlated with one another through evolution within a single shared species tree history. Identifying outlier gene trees that significantly deviate from the general genome-wide distribution is, therefore, important in meeting assumptions of species tree reconstruction, and in the identification of genes with unique evolutionary properties. One approach for identifying outlier genes is to statistically test for deviations from an overall distribution of neutrally-evolving gene trees. Here, we propose a methodology for using support vector machine (SVM) as a statistical tool for testing for differences between distributions of gene trees sampled from different underlying histories, applying either the dissimilarity or path-difference map to vectorize trees. We first apply our GeneOut algorithm to two known distributions of coalescent trees each simulated within two different specie tree histories. We then apply our algorithm to the analysis of gene trees reconstructed from simulated DNA sequence data. (Received January 25, 2010)

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