1056-92-1415   **Katherine Isaacs*** (`katherine.isaacs@students.sjsu.edu`). *A Statistical Method for Environmental Prediction in Metagenomic Samples.* Preliminary report.

A metagenome is a sampling of genetic sequences from the entire microbial community within an environment. Examining the functional diversity represented by these sequences gives insight into the biological processes within the environment as well as the biological differences between environments. Most research has focused on single specific environments and the few comparative analyses have been based only on small homogeneous fractions of the metagenomic data which is currently available. We explore a technique using supervised Random Forests and canonical discriminant analysis to study over 200 metagenomes from varied environments. Our findings confirm this method differentiates and predicts environments accurately using only a subset of key functional hierarchies. (Received September 21, 2009)