# Jacobson

**Systems Biology Models of the Interactions Between Host, Phytobiome and Environment**

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We have created Parakraken, a parallelized kmer profile-based taxa identification approach that uses full kmer profiles from every publicly available genome sequence (including bacteria, archae, fungi, viruses, nematodes, insects, protists, etc.). This allows us to detect the cryptic phytobiome in the DNA or RNA sequence of any host tissue. We are using Parakraken as well as OTU-based amplicons to identify taxa in different host tissues across a genome wide association study (GWAS) population of Populus trichocarpa. We also have other independent layers of data across this population, including metabolomics, transcriptomics, phenology, pyMBMS and many climactic phenotypes measured across the original locations of the genotypes in the population. In addition, we have developed new methods for GWAS that allow us to achieve considerable sensitivity and use rare alleles found in the population. Furthermore, we have developed explainable-AI approaches to find complex epistatic architectures responsible for the host's ability to detect and modulate its microbiome and other phenotypes. The result is a comprehensive systems biology model of a plant and its regulation of its microbiome, its adaptation to its climactic environment and the metabolic intermediaries involved therein. We believe that many of the genes responsible for host-phytobiome association have orthologs across the plant kingdom. Thus, we combine the results of these approaches in Populus with many orthogonal layers of information in order to score each hypothesis supported by multiple lines of evidence in order to prioritize specific mechanisms for cross species experimental validation.