

T-BAS: A Tool for Real-time Tracking of Biodiversity Across the Tree of Life

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The Tree-Based Alignment Selector (T-BAS) toolkit is a unique phylogenetic analytic tool that integrates complex microbial biodiversity data and the rich metadata being continuously produced by biologists. This metadata may include metagenomics data on microbial associations with other organisms, phenotypic data, and abiotic or environmental data generated from new sensing technologies. Although tracking the spread of plant pathogens through complex agricultural landscapes remains exceedingly difficult, recent advances in our ability to sequence large numbers of pathogen isolates and analyze population genomic data is providing new insights into pathogen movement. Inspired by the tree of life, the structure of our Plant Aid database will reflect the phylogenetic relationships among sampled taxa, allowing researchers to use the evolutionary insights provided by the tree of life to understand the web of biotic and abiotic interactions and parameters underlying plant performance and resilience.