Metaboverse: Metabolic network pattern recognition tools contextualize multi-omic data and reveal disease-relevant signatures

Jordan A. Berg, Youjia Zhou, Yeyun Ouyang, T. Cameron Waller, Sara M. Nowinski, Tyler Van Ry, Ian George, James E. Cox, Bei Wang, Jared Rutter

Due to the scale and complexity inherent in metabolism, systems approaches that are easily accessible to the general researcher are necessary. We developed Metaboverse, a user-friendly, interactive, and cross-platform analysis and visualization tool for data layered on metabolic networks. Metaboverse offers the ability to integrate multi-omic, multi-condition, time course, and metabolomics tracing datasets on over ninety model organisms. We developed a search engine that comprehensively searches and analyzes the network for complex regulatory patterns within the sequencing, proteomics, and metabolomics data, integrating enzyme information into the metabolic network to create a robust search space. This framework will be foundational in allowing users to analyze their data in a more holistic manner that integrates all measured information of their biological system to rapidly identify interesting regulatory patterns within the global metabolic network.

View interactive poster



View pre-print for novel biological insights found by Metaboverse

