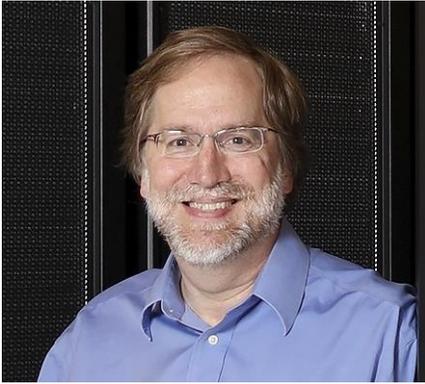


Daniel Jacobson, Ph.D.



Dan's lab was the first group to break the Exascale barrier and is happy to have done so for a biology project. At present, this (2.41 Exaops) calculation is the fastest scientific calculation ever done anywhere in the world. This project led to his team being awarded the 2018 Gordon Bell Prize (the first ever for Systems Biology). His team's work on COVID-19 pathogenesis also led to the 2020 HPCWire Editor's Choice Award for the Top HPC-enabled Scientific Achievement.

Dan's career as a computational systems biologist has included leadership roles in academic, corporate, NGO and national lab settings. His lab focuses on the development and subsequent application of mathematical, statistical and computational methods to biological datasets in order to yield new insights into complex biological systems, including substance use disorders and other neuropsychological conditions. His lab's approaches include the use of Network Theory and Topology Discovery/Clustering, Wavelet Theory, and explainable-AI, together with traditional and more advanced supercomputing architectures. Areas of statistics of particular interest to his lab include the use of both frequentist (parametric and non-parametric) and Bayesian methods as well as the development of new methods for Genome-Wide Epistasis Studies (GWES). These mathematical and statistical methods are applied to various population and (meta)multiomics data sets (Genomics, Phylogenomics, Transcriptomics, Proteomics, Metabolomics, Microbiomics, Viriomics, Phytobiomics, Chemiomics, etc.) individually as well as in combination in an attempt to better understand the functional relationships as well as biosynthesis, signaling, transcriptional, translational, degradation and kinetic regulatory networks at play in biological organisms and communities. His group takes a broad view of biological complexity and evolution that stretches from viruses to microbes to plants to humans. ORNL is home to some of the world's largest supercomputers and thus his lab uses petascale and exascale computing to analyze and model complex biological systems.