

In the pursuit of questions related to eco-evolutionary principles governing microbial communities, he has garnered ample experience on genomic and metagenomic analyses in environmental, clinical, agricultural, and engineered settings, including the description, characterization, modeling, and simulation of microbial communities and populations. He has explored and discussed both theoretical and practical problems on microbiome analysis including the development and application of methods on phylogenomics, taxonomy of prokaryotes, metabolic modeling, statistical techniques, and sequence analyses.

He is the author of over 50 papers and book chapters, has presented multiple workshops, seminars, and symposia on microbiome analysis for researchers and undergraduate educators.

Since new ideas need implementation, throughout his research he has made it a point to implement those ideas in efficient, high-quality, well-documented, and user-friendly software. He has developed tens of bioinformatic tools and web interfaces in a variety of programming languages and frameworks (Ruby, Rails, Perl, R, C++, etc)