

CASE STUDY

NIMBioS Investigative Workshop: Computational Advances in Microbiome Research

Overview

Top thought leaders in computational microbial community analysis techniques partnered with NIMBioS to provide the first modern forum to integrate novel bioinformatic techniques from diverse areas of microbial community research, ranging from the human microbiome to extremophiles and agriculture. J. Banfield (Earth and Planetary Science and Environmental Science, Policy and Management, University of California, Berkeley) and Curtis Huttenhower (Biostatistics, School of Public Health, Harvard University) co-organized the two-day meeting in 2015, which brought together 41 other individuals from a wide range of backgrounds.

"The most valuable aspect was meeting potential co-authors in the field to plan new informatics experiments and discovering knowledge gaps that my informatics team could help fill."

-Todd DeSantis, Co-founder, Second Genome



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Problem

Recent years have seen a tremendous growth in microbial community research, ranging from studies of the human microbiome to investigations of biogeochemical cycling in global soil, oceans and coral mucus ecosystems. Current research trends have been triggered by the decreasing cost, increasing ubiquity, and democratization of analysis methods for high-throughput sequencing, which has made both amplification-based and shotgun metagenomic profiling of microbial communities accessible to diverse research fields. Microbial community studies have a long history derived from a variety of research areas, including ecology, soil and ocean biochemistry, human and environmental toxicology, air quality and environmental monitoring, agriculture, and biodefense. As the methods necessary for modern data



analysis have become more complex, new computational approaches have developed independently in many subfields, but there have been few opportunities to integrate knowledge and bioinformatic techniques across microbial community research areas. Until now, no scientific gatherings have focused exclusively on computational and bioinformatic considerations.

Outcomes

- Microbial community analysis techniques from diverse fields were identified.
- Gaps in computational and statistical techniques not currently addressed in any subfields were identified, as were gaps in biological knowledge that could be addressed by new quantitative methods.
- New collaborations and funding opportunities were explored, and future work in microbial community bioinformatics was identified.

For more information, visit www.nimbios.org/microbiome

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