

Workshop on Microbiomics, Metagenomics, and Metabolomics

Soha Hassoun

Department of Computer Science
Tufts University
Medford, MA, USA
soha@cs.tufts.edu

Yasser El-Manzalawy

Department of Biomedical and
Translational Informatics
Geisinger Health System
Danville, PA, USA
yelmanzalawi@geisinger.edu

Georg Gerber

Department of Pathology
Harvard Medical School
Boston, MA, USA
ggerber@bwh.harvard.edu

David Koslicki

Computer Science and Engineering, Biology
Pennsylvania State University
State College, PA, USA
dmk333@psu.edu

Gail Rosen

Department of Electrical and Computer Engineering
Drexel University
Philadelphia, PA, USA
glr26@drexel.edu

ABSTRACT

The past decade has witnessed a revolution in microbiology through the advent microbiomics: investigating entire microbial ecosystems in and around us as opposed to studying single microbes in isolation. Recent technological advances in high throughput sequencing technology has enabled these studies, significantly improving our capacity to explore the composition and dynamics of these microbial communities. A key goal of microbiome research is defining the structure of and functional relationships between various organisms constituting microbiota under different conditions (e.g., health and disease states and/or environmental factors). These efforts stand to significantly improve human and environmental health since many physical processes are regulated by or interact with microbial organisms. Large scale collaborative efforts in this direction, such as the Human Microbiome Project and the Earth Microbiome Project, have generated unprecedented amounts of metagenomic data. To decipher this resulting data, novel computational algorithms and tools are rapidly being developed to identify organisms (taxonomic classification of microbiome sequences), assemble bacterial genomes from these in situ experiments (metagenome assembly), functionally and metabolically profile microbiomes, and identify taxonomic and functional biomarkers.

Against this background, the main goal of this workshop is to highlight recent advances in computational methods for metagenomics and metabolomics and to discuss remaining key challenges and promising future research directions. Topics include methods to identify microbes and their functions, measure similarity of samples, identify biomarkers, provide functional profiling, and enable efficient real-time analysis of ubiquitous microbiome samples and studies.

CCS CONCEPTS

- Life and medical sciences

KEYWORDS

Microbiomics; Metagenomics; Metabolomics

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