BRIGHAM AND WOMEN'S HOSPITAL
HARVARD MEDICAL SCHOOL

181 Longwood Avenue
Boston, Massachusetts 02115-5804

Department of Medicine
Channing Division of Network Medicine

Channing Microbiome Seminar

March 3 (Friday), 2023, 9AM (ET)

Zoom: https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09
Meeting ID: 810 7095 9105
Passcode: 984617

Zheng Sun, PhD

Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School

Eliminating false positives in metagenomic profiling based on type IIB restriction sites

Abstract: Accurate species identification and abundance estimation are critical for the interpretation of whole metagenome sequencing (WMS) data. Numerous computational methods, broadly referred to as metagenomic profilers, have been developed to identify species in microbiome samples by classification of sequencing reads and quantification of their relative abundances. Yet, existing metagenomic profilers typically suffer from false-positive identifications and consequently biased relative abundance estimation. Indeed, false positives can be accounted for more than 90% of total identified species. Here, we present a new metagenomic profiler MAP2B (MetAgenomic Profiler based on type IIB restriction site) to resolve those issues. We first illustrate the pitfalls of using relative abundance as the only feature in determining false positives. We then propose a feature set to distinguish false positives from true positives. By benchmarking the performance in synthetic data and real WMS data from an ATCC mock community, we illustrate the superior performance of MAP2B over existing metagenomic profilers and its robustness against sequencing depth. Finally, by leveraging WMS data from an IBD cohort, we demonstrate the taxonomic features obtained by MAP2B can better discriminate disease status and predict metabolomic profiles.

Bio: Dr. Sun is an Instructor in Medicine at Harvard Medical School. He obtained his PhD from the Chinese Academy of Sciences, and his research goal is to develop innovative methodology to bridge the gap between the human microbiome and human diseases. His interests in the microbiome include: advancing methods for decoding the taxonomic structure, engineering novel microbial features associated with host status, and investigating the mechanisms underlying dysbiosis diseases. His research has been published in top-tier microbiology journals, e.g., *Nature Methods*, *Genome Biology*, *Microbiome*, *eBioMedicine*, *Gut Microbes*, and *mSystems*. In recognition of his contributions to the field, he has been awarded the Charles A. King Trust Postdoctoral Research Fellowship and the NIH Pathway to Independence Award (K99).

PARTNERS HEALTHCARE