

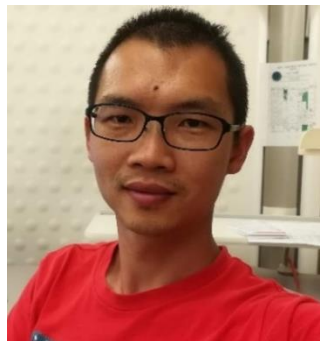
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ASAP 2: A Metagenomic Analytical Tool for Pathogen Detection in the Environment

Tuesday, March 9, 2021

11:00AM-12:00PM (Central Time)



Bio:

Dr. Tian acquired his Ph.D. degree of Environmental Microbiology from Hong Kong University of Science and Technology. After graduation, he worked as a Postdoctoral Research Associate at the University of Oklahoma on several projects, funded by DOE, with a focus on environmental microbiome including soil, groundwater and animal guts. In 2019, he joined the Institute for Food Safety and Health, Illinois Institute of Technology as a Research Scientist. With experience in both experimental and computational biology, Dr. Tian is well versed in studying microbial diversity and function using genomics, metagenomics and metatranscriptomics approaches. His extensive research centers on microbes from a variety of environments including food, soil, groundwater, coastal water, deep-sea water, sediment and animal guts. He takes advantage of state-of-the-art technologies in microbial genomics studies, such as third generation sequencing (e.g. Nanopore) and advanced computational approaches including machine-learning algorithms.

Abstract:

Amplicon sequencing of marker genes such as 16S rDNA, 18S rDNA, ITS and others has been widely used to survey and characterize microbial communities in microbial studies such as pathogen detection. However, the complex data analyses have required many interfering manual steps often leading to inconsistencies in results. Here, we have developed a pipeline, amplicon sequence analysis pipeline 2 (ASAP 2), to automate and glide through the processes without the usual manual inspections and user's interference, for instance, in the detection of barcode orientation, selection of high-quality region of reads, and determination of resampling depth and many more. The pipeline integrates all the analytical processes such as importing data, demultiplexing, summarizing read profiles, trimming quality, denoising, removing chimeric sequences, and making the feature (ASV) table among others, using QIIME 2, Vegan and other tools. The pipeline accepts multiple file formats as input including multiplexed or demultiplexed, paired-end or single-end, barcode inside or outside and raw or intermediate data (e.g. feature table). The outputs include taxonomic classification, alpha/beta diversity, community composition, ordination analysis and statistical tests (variable selection, CCA, RDA, etc.). ASAP 2 supports merging multiple sequencing runs, which helps, integrate and compare data from different sources (public databases and collaborators). The pipeline minimizes hands-on interference and runs amplicon sequencing analysis automatically and consistently and can be efficiently applied in microbial community profiling and pathogen detection in the food safety industry.