



Epidemiology and Population Health Summer Institute at Columbia University



WEEK 4: JUNE 28-29 8:30AM - 5:30PM

Microbial Communities Profiling via QIIME2 and Qiita

DESCRIPTION

This course will provide a theoretical, analytical and practical introduction to QIIME 2 (canonically pronounced 'chime two'), which stands for Quantitative Insights into Microbial Ecology 2, and Qiita (canonically pronounced 'cheetah'), a multiomics and multi-study online tool. QIIME 2 and Qiita are open source software packages for comparison and analysis of microbial communities, primarily based on high-throughput amplicon sequencing data (such as SSU rRNA) generated on a variety of platforms, but also supporting analysis of other types of data (such as shotgun metagenomic, metabolomics or proteomics). The main Qiita deployment (<http://qiita.microbio.me/>) allows users to manage and analyze large studies, their metadata and the multiple data types generated from the same samples. Additionally, it allows users to combine their samples with other published and public studies available in the system. QIIME 2 is a stand-alone environment for the analysis of individual microbiome data sets that can be used on your laptop, university computational resources, and cloud computing resources.

INSTRUCTORS

- **J. Gregory Caporaso, PhD**
- **Antonio Gonzalez, PhD**

OBJECTIVES

By the end of the course, participants will be able to

- Understand the most recent QIIME2 and Qiita features for microbial community analysis
- Select the best workflow and parameters to perform the different steps for microbial community analysis
- Understand and apply on their own datasets different phylogenetic and non-phylogenetic metrics to compare microbial diversity samples
- Upload and analyze their own datasets using Qiita and compare their studies with other public studies

EARLY DISCOUNTS
AVAILABLE UNTIL
APRIL 1, 2017

REGISTRATION OPEN
THROUGH MAY 1, 2017

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