EPIC

Epidemiology and Population Health Summer Institute at Columbia University

WEEK 1: JUNE 3-4   8:30AM - 5:30PM

Microbial Communities Profiling via QIIME2 and Qiita

DESCRIPTION

This course will provide a theoretical, analytical and practical introduction to QIIME2 (canonically pronounced 'chime'), which stands for Quantitative Insights Into Microbial Ecology, and Qiita, a multiomics and multi-study on-line tool. QIIME2 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 deploy (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.

INSTRUCTORS

- **Antonio Gonzalez, PhD**
- **Yoshiki Vázquez-Baeza, 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, 2019

REGISTRATION OPEN THROUGH MAY 1, 2019

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