Microbial Communities Profiling via QIIME and Qiita

CLASS DURATION
Monday, June 20, 2016 - Friday, June 24, 2016 1:30 PM - 5:30 PM
Location: HSC, Monday, Wednesday, Friday: LL204, Tuesday, Thursday: LL103
Hammer Health Sciences Library (HSC) is located at 701 W. 168th St. New York, NY 10032
Directions can be found here: https://www.cuepisummer.org/contactpage

INSTRUCTORS
Antonio Gonzalez, PhD
Programmer Analyst
University of California, San Diego, Department of Pediatrics
email: antgonza@gmail.com

COURSE DESCRIPTION
This course will provide a theoretical, analytical and practical introduction to QIIME (canonically pronounced 'chime'), which stands for Quantitative Insights into Microbial Ecology, and Qiita, a multimics and multi-study online tool. QIIME 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.

PREREQUISITES
1. Bring your own laptop computer with relevant software installed.
   a. QIIME is open source software, as are most of its dependencies. The recommended installations by operating system are:
      • Mac OS X: MacQiime http://www.wernerlab.org/software/macqiime
      • Windows: VirtualBox http://qiime.org/install/virtual_box.html. As a result of the nature of virtualization the kind of hardware specifications you are going to need will increase. Additionally, it will limit the size of datasets you can work with, but it still is a fully functional installation of QIIME.
      • Linux & Mac OS X: http://qiime.org/install/install.html#native-base
         A functioning installation of QIIME is a requirement because otherwise the workshop will be of little value to you (and we will spend a long time trying to troubleshoot installation problems). A way to test your QIIME installation is by running these commands without any errors (warnings are fine):
            $ unzip qiime_overview_tutorial.zip
$ cd qiime_overview_tutorial
$ curl -L -o qiime_tutorial_commands_serial.sh http://goo.gl/vjFIDY
$ chmod +x qiime_tutorial_commands_serial.sh
$ ./qiime_tutorial_commands_parallel.sh

If you are having problems installing QIIME, please be sure to visit http://qiime.org/install/install.html. For further assistance, you can visit the QIIME forum (http://forum.qiime.org).

2. Upload your dataset to Qiita. If you plan to bring your own dataset to the workshop the requirements are that (1) you upload your sample & preparation templates, (2) and raw data to Qiita (http://qiita.microbio.me/). For more information, visit: http://qiita.microbio.me/static/doc/html/index.html. If you run into any issue send an email to qiita.help@gmail.com.

COURSE LEARNING OBJECTIVES
By the end of the course, participants will be able to:
1. Understand the most recent QIIME and Qiita features for microbial community analysis
2. Select the best workflow and parameters to perform the different steps for microbial community analysis
3. Understand and apply on their own datasets different phylogenetic and non-phylogenetic metrics to compare microbial diversity samples
4. Upload and analyze their own datasets using Qiita and compare their studies with other public studies

COURSE READINGS
Due to the QIIME installation and Qiita upload requirements, there are no required readings but the following references should give some basic background:

- Lozupone, Catherine A., and Rob Knight. 'Species divergence and the measurement of microbial diversity.' FEMS microbiology reviews 32.4 (2008): 557-578.
## COURSE SCHEDULE

<table>
<thead>
<tr>
<th>Session 1 – Introduction to QIIME, Qiita and microbiome analysis</th>
<th>June 20</th>
<th>Tools background and introduction to the microbiome analysis. Quick overview of the command line interface. Setting up studies in Qiita.</th>
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<tbody>
<tr>
<td>Session 2 – Study design and initial processing steps</td>
<td>June 21</td>
<td>Study design and setup with QIIME and Qiita. Understand primer selection, picking Operational Taxonomic Units (OTUs) methods, representative set selection, building a phylogenetic tree, assigning taxonomy and finishing with a BIOM table. Process your own studies in Qiita.</td>
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<tr>
<td>Session 3 – Downstream analysis with a BIOM table</td>
<td>June 22</td>
<td>Possible analyses with QIIME of a BIOM table. Overview of alpha, beta, and taxonomy analyses, their statistical methods and metrics. Tools to generate time series and spatial visualizations of your samples.</td>
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<tr>
<td>Session 4 – Working with Qiita, other tools and visualizations</td>
<td>June 23</td>
<td>Analyses in Qiita, combine private and public studies. Other tools: supervised learning, source tracking, Il, among others. Review and interpretation of the methods section of published articles.</td>
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<tr>
<td>Session 5 – Future of QIIME and final remarks</td>
<td>June 24</td>
<td>Have an overview of what we can expect of the future and open discussion.</td>
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