First steps with QIIME

Contents

Back to Table of Contents

Running the QIIME tutorial

After you have gotten QIIME working as described, you are ready to try out QIIME.

A good first step is to follow the QIIME tutorial here: http://qiime.org/tutorials/tutorial.html

Note: you can download files directly to MSI or your Linux computer from the command line with `wget ftp://ftp.microbio.me/pub/qiime-files/qiime_overview_tutorial.zip`.

Running QIIME on class data

You can also run QIIME on the global gut data in the Course repository. First download the repository and data:

```
git clone https://github.com/danknights/mice8992-2016.git repo
```

For example, move to the global gut data directory:

```
cd repo
cd data
cd globalgut
```

Then run OTU picking and core QIIME analyes:

```
# pick de novo OTUs
time pick_de_novo_otus.py -i global_gut_200k.fna -o otus_de_novo

# run core QIIME diversity analyses on de novo OTU table
time core_diversity_analyses.py -i otus_de_novo/otu_table.biom -m map.txt -o corediv_dn -e 1000 --tree_

# pick closed reference OTUs
time pick_closed_reference_otus.py -i global_gut_200k.fna -o otus_closed_ref

# run core QIIME diversity analyses on closed-reference OTU table
time core_diversity_analyses.py -i otus_closed_ref/otu_table.biom -m map.txt -o corediv_cr -e 1000 --tr
```

You can then open the "index.html" file in the output folder in your favorite web browser, and click to see the results of the analysis. In Chrome you may need to open Chrome first, and then choose "File–>Open File. . . ". For the Global Gut data set, click on "index.html" next to PCoA plot (weighted_unifrac). Then click the "Colors" tab in the upper right and select "AGE_GROUP" by which to color the points.