PICRUSt

Back to

All of the code in this page is meant to be run on the command line unless otherwise specified.

Install PICRUSt (MSI/Unix)

These instructions assume that you are installing PICRUSt on MSI or another computer where you do not
have root access. However, even if you do have root access, using Anaconda as a python environment manager
can be very useful and can prevent a lot of headaches.

First, install Anaconda and set up an environment using Python 2.7. See the HUMAnN2 page for Anaconda
installation and setup instructions.

After you have created a "python2" environment in Anaconda as described on the HUMAnN2 page, you can
load that environment with `source activate python2`.

```
# These commands are for running on MSI

# activate your python2 Anaconda environment
source activate python2

# clone the repository
git clone git://github.com/picrust/picrust.git picrust

# enter the data directory
cd picrust/picrust/data

# download the precalculated picrust files
wget ftp://ftp.microbio.me/pub/picrust-references/picrust-1.0.0/16S_13_5_precalculated.tab.gz
wget ftp://ftp.microbio.me/pub/picrust-references/picrust-1.0.0/ko_13_5_precalculated.tab.gz

# enter the top-level directory
cd ../../
python setup.py install
```

Now you should be able to run PICRUSt.

Run PICRUSt

```
# load a slightly older version of QIIME
module load qiime/1.8.0

# Normalize OTU counts by 16S copy number
normalize_by_copy_number.py -i otu_table.biom -o normalized_otus.biom

# Predict metagenomes
predict_metagenomes.py -i normalized_otus.biom -o picrust.biom

# Collapse functions to level 3 KEGG pathways
```

```
categorize_by_function.py -i picrust.biom -c KEGG_Pathways -l 3 -o picrust_L3.biom

# (optional) convert to txt
biom convert -i picrust_L3.biom -o picrust_L3.txt --to-tsv
```