Installing QIIME

Contents

Using QIIME on MSI

1. Connect to MSI using Terminal on Mac/Linux, or putty on Windows, download here: http://www.putty.org/

```
ssh yourusername@login.msi.umn.edu
```

2. Tell MSI where to look for the working QIIME installation
   Run the following commands one time:

```
echo "export PYTHONPATH=/home/knightsd/public/lib/qiime_1.9.1/lib/python:\$PYTHONPATH" >> ~/.bash_profil
echo "export PATH=/home/knightsd/public/lib/qiime_1.9.1/bin:\$PATH" >> ~/.bash_profile
echo "export LD_LIBRARY_PATH=/home/knightsd/public/lib/qiime_1.9.1/lib/qhull-2012.1/lib:\$LD_LIBRARY_PA
```

3. Log in to an interactive node, making sure you have enough time and memory

```
isub -n nodes=1:ppn=4 -m 16GB -w 24:00:00
```

4. Verify that your environmental variables were set correctly.
   You should see that each of these variables has "/home/knightsd/public/lib/qiime_1.9.1/" somewhere in it.

```
echo $PYTHONPATH
echo $PATH
echo $LD_LIBRARY_PATH
```

5. Load the correct python module

```
module load python/2.7.1
```

6. Test QIIME

```
print_qiime_config.py
```

In the future, you only need to do steps 1, 3, and 5.

Helpful tips:
This link shows you the options for different queues and resources at MSI:
http://msi-riss.readthedocs.org/en/latest/msi/msi-queues.html

This link shows current usage of queues at MSI, updated every 15 minutes:
https://s3.msi.umn.edu/pbsnodes/index.html

Installing QIIME on Linux

Tested on Ubuntu MATE 15.10

```
# system dependencies
sudo apt-get install build-essential python-dev python-pip

# Get ready for matplotlib
# http://stackoverflow.com/questions/20533426/ubuntu-running-pip-install-gives-error-the-following-requ
sudo apt-get install libfreetype6-dev

# Get ready to install numpy and scipy
# http://stackoverflow.com/questions/11114225/installing-scipy-and-numpy-using-pip
sudo apt-get install libblas-dev liblapack-dev libatlas-base-dev gfortran

pip install numpy
pip install qiime

# Note: on my installation, the QIIME binaries were placed in $HOME/.local/bin/
# so I added that dir to my PATH environment variable:
echo "export PATH=\$HOME/.local/bin:\$PATH" >> ~/.bashrc
echo "export PATH=\$HOME/.local/bin:\$PATH" >> ~/.bash_profile

# restart terminal then test:
print_qiime_config.py -h
```

Installing QIIME on Mac using macqiime

Tested on Mac OSX El Capitan 10.11.3

```
# extract file
tar xvzf MacQIIME_1.9.1-20150604_OS10.7.tgz

# enter the directory
cd MacQIIME_1.9.1-20150604_OS10.7


# For El Capitan only (not earlier mac OS versions),
# Download the custom install script shown here, and follow the instructions:
https://groups.google.com/d/msg/qiime-forum/N2aZIPrsb_o/SdHXBIylCAAJ
```

```
# run the install script.
# it should request your administrator password.
./install.s

# Try it out
macqiime
print_qiime_config.py
```

Using QIIME virtual machine on Windows/Mac/Linux

1. Download and install VirtualBox: https://www.virtualbox.org/wiki/Downloads
2. Download and open the QIIME virtualbox image: http://qiime.org/install/virtual_box.html
3. Follow instructions at http://qiime.org/install/virtual_box.html
4. Note: to start the QIIME virtual machine you will need to run VirtualBox, and create a "new" virtual machine. The option for "Type" is "Linux". The option for "Version" should be "Ubuntu (64 bit)". If you only see 32-bit options, then visit this web page and try the fix: http://www.fixedbyvonnie.com/2014/11/virtualbox-showing-32-bit-guest-versions-64-bit-host-os. A similar solution is described here: http://qiime.org/install/virtual_box.html
5. Once you have the virtual machine running, you need to make sure the internet is working, that you can cut-and-paste text from your native OS to the virtual machine, and that you can share files between your native OS filesystem and the virtual machine. This means first installing the "Guest Additions", and then performing a few more steps, as described here: https://github.com/biocore/qiime/wiki/QIIME-Virtual-Box:-Before-you-start

Running the QIIME tutorial

Ready to try out QIIME? 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
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. . . ".