

University of Maine QIIME Workshop

Oct 3-4 2014

Acadia National Park



This schedule is tentative.

Workshop details at <http://bit.ly/acadia-rcn-qiime> (we'll have you open this link during the workshop).

October 3: Introduction to QIIME

08:00 - 09:50 Intro to microbial community analysis and the QIIME input files (demultiplexing through OTU picking) [Greg]

09:50 - 10:05 Break, "office hours" (instructors will be available for one-on-one discussion of more specific topics)

10:05 - 11:00 OTU picking protocols, diversity analysis [Greg]

11:00 - 11:15 Options for using QIIME: Amazon Web Services, Virtual Box, local installation and the pros and cons of each [Jai]

11:15 - 12:00 Working with AWS, starting an instance and logging in; Getting working versions of ssh, sftp ([Mobaxterm](#), [Cyberduck](#)) Part 1 [Jai]

12:00 - 13:30 Lunch break

13:30 - 14:30 Hands on: Working with AWS: ssh, sftp (students should download and install [Cyberduck](#)) Part 2 [Jai]

14:30 - 17:00 Hands on: QIIME's [Illumina Overview Tutorial](#) [Greg and Jai]

19:30 - 20:30: Hands-on: exploring core diversity analysis results [Greg and Jai]

October 4: Advanced QIIME

8:00 - 9:15 Methods for clustering (see discussion [here](#)) [Greg]

9:15 - 10:30 Hands on: Working with OTU tables (sorting, filtering, splitting, etc) [Jai]

10:30 - 11:00 Coffee/snack break/office hours

11:00 - 12:00 Office hours

12:00 - 13:30 Lunch break

13:30 - 14:15 Detailed overview (but not hands-on) of working with alternative reference databases; discussion of PCR chimeras [Greg]

14:15 - 15:00 Intro: PICRUST [Greg]

15:00 - 15:15 Break, “office hours” (instructors will be available for one-on-one discussion of more specific topics)

15:15 - 16:00 PICRUST [Greg]

16:00 - 17:00 “Office hours” (instructors will be available for one-on-one discussion of more specific topics)

19:30 - 20:30: Reproducible bioinformatics; Future directions: QiiTA, QIIME 2.0 [Jai and Greg]

Notes

Students will log into AWS directly, rather than use an IPython Notebook. We will make all commands that we run available in a reference IPython Notebook.