QIIME (+ Linux) Workshop 2016

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Day 1: Introduction to Linux

**Date:** July 8th, 2016, 9 am – 1 pm

**Instructors:** Jessica Kirkpatrick (HPCBio), Jenny Drnevich (HPCBio)

**Assistant:** Shoham Das

**Location:** 607 IGB

**Class Materials:**

- Presentation
- Linux cheat sheet
- Getting on a UNIX-based terminal
- Appendix
- Class Video

**Additional Linux Resources:**

- Beginner Linux - self-guided tutorials for extra practice
  - Tutorial from the book *UNIX and Perl to the RESCUE!*
  - Parts 1 and 2 cover UNIX
    - [http://korflab.ucdavis.edu/Unix_and_Perl/current.html#part2](http://korflab.ucdavis.edu/Unix_and_Perl/current.html#part2)
  - SIB tutorial
    - If it asks you to log in, just log in as a "guest user"
    - Click on "UNIX elearning module" at the bottom to get started
  - University of Surrey tutorial
    - [http://www.ee.surrey.ac.uk/Teaching/Unix/](http://www.ee.surrey.ac.uk/Teaching/Unix/)
  - Ryan's Tutorials
    - [http://ryanstutorials.net/linuxtutorial/](http://ryanstutorials.net/linuxtutorial/)

- Linux Books
  - *UNIX and Perl to the RESCUE!* by Keith Bradnam & Ian Knowl
  - *Developing Bioinformatics Computer Skills* by Cynthia Gibas & Per Jambeck
  - *Linux Pocket Guide* by Danial J. Barrett
  - *Beginning Shell Scripting* by Eric Foster-Johnson, John C. Welch, & Micah Anderson
  - *Learning the bash Shell* by Cameron Newham
  - *bash Cookbook* by Carl Albing, JP Vossen, & Cameron Newham

- Linux-related Software

Day 2: Introduction to QIIME & Preprocessing

**Date:** July 11th, 2016, 9 am – 1 pm

**Instructors:** Jessica Kirkpatrick (HPCBio), Chris Wright (CBC), Jenny Drnevich (HPCBio)

**Assistant:** Shoham Das

**Location:** 607 IGB

**Class Materials:**

- Slides:
  - Chris Wright’s presentation
  - Introduction to QIIME and pre-processing: [presentation](#)

- Example dataset files:
  - Condensed sequencing report
  - FASTQC report for forward reads of archaea dataset

**Additional Files**

- Upstream analysis homework
- Class Video
- Detailed QIIME tutorial

Day 3: Basic QIIME Analyses

**Date:** July 13th, 2016, 9 am – 1 pm

**Instructors:** Jessica Kirkpatrick (HPCBio), Jenny Drnevich (HPCBio)

**Assistant:** Shoham Das

**Location:** 607 IGB

**Class Materials:**

- Slides:
  - Basic analyses in QIIME: presentation

**Additional Files**

- Full analyses homework
- Full analyses homework [ANSWER KEY](#)
The following software allows remote access from a Windows computer to a Linux based terminal. Mac already has a UNIX-based terminal pre-installed. You can find it in Applications -> Utilities -> Terminal

- MobaXterm: http://mobaxterm.mobatek.net/
- PuTTY: http://www.putty.org/

### Biocloud Resources
- Biocloud help page
- Campus cluster help page
- How to submit a cluster job
- qsub script generator

### Day 4: Statistical Analyses

Date: July 15th, 2016, 9 am – 1 pm

Instructors: Jenny Drnevich (HPCBio), Jessica Kirkpatrick (HPCBio)

Assistant: Shoham Das

Location: 607 IGB

### Class Materials:

Slides:

- Statistical Analyses in QIIME - updated

### Additional Links

- Class Video
- QIIME 2.0 site; blog announcement
- McMurdie and Holmes, 2014
- Bioconductor workflow for full microbiome analyses