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_Perdcurrent.html#part2](http://korflab.ucdavis.edu/Unix_and_Perdcurrent.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 Knorn
  - *Developing Bioinformatics Computer Skills* by Cynthia Gibas & Per Jambeck
  - *Linux Pocket Guide* by Daniel 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/

- **Biocluster Resources**
  - Biocluster help page
  - Campus cluster help page
  - How to submit a cluster job
  - qsub script generator

- **Class Video**
- **Detailed QIIME tutorial**

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**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

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**Class Materials:**

**Slides:**

- **Statistical Analyses in QIIME - updated**

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**Additional Links**

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