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
  - 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/
  - Ryan’s Tutorials
    - http://ryanstutorials.net/linuxtutorial/

- Linux Books
  - UNIX and Perl to the RESCUE! by Keith Bradnam & Ian Knorf
  - 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/](http://mobaxterm.mobatek.net/)
- **PuTTY**: [http://www.putty.org/](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**

**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**