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/
- PuTTY: http://www.putty.org/

**Biocluster Resources**

- Biocluster 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