Introduction to Linux & High Performance Computing

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September 2 - Introduction to Linux

Date: September 2nd, 2016, 9 am – 1 pm
Instructors: Jessica Kirkpatrick, Jenny Drnevich (HPCBio)
Teaching Assistant: Shoham Das
Location: 607 IGB

Class materials

- Presentation
- Linux cheat sheet
- Getting on a UNIX-based terminal
- Linux commands appendix

Linux resources

- Beginner 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#part1](http://korflab.ucdavis.edu/Unix_and_Perl/current.html#part1)
  - 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
  - Coursera course on Command Line Tools for Genomic Data Science
    - [https://www.coursera.org/learn/genomic-tools/](https://www.coursera.org/learn/genomic-tools/)

- 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, &

Please note that you will be learning how to use the Biocluster using a PBS/Torque scheduler. A scheduler manages jobs that you submit to the cluster. The commands you use to submit jobs to a cluster are specific to the scheduler you are using. For example, you would use the command "qsub" to submit a job through a PBS/Torque scheduler, but if your cluster used a SLURM scheduler, you would use the command "sbatch". Keep in mind that the Biocluster will switch over from a PBS/Torque scheduler to a SLURM scheduler by the end of the year. To be consistent throughout our Fall workshops, we will teach PBS/Torque commands, but keep in mind that in 2017 these commands will become irrelevant. CNRG plans to offer free classes on the new SLURM system near the end of the year, and we will let you know when these are.

Class materials

- Presentation
- VIDEO - [link here](#)

Biocluster resources

- Biocluster help page
- How to submit a cluster job
- `qsub` script generator
- PBS/Torque & SLURM comparison chart

September 9 - Introduction to High Performance Computing (w/ PBS/Torque)

Date: September 9th, 2016, 9 am – 1 pm
Instructors: David Slater (CNRG), Jenny Drnevich, Jessica Kirkpatrick (HPCBio)
Teaching Assistant: Shoham Das
Location: 607 IGB

Please note that you will be learning how to use the Biocluster using a PBS/Torque scheduler. A scheduler manages jobs that you submit to the cluster. The commands you use to submit jobs to a cluster are specific to the scheduler you are using. For example, you would use the command "qsub" to submit a job through a PBS/Torque scheduler, but if your cluster used a SLURM scheduler, you would use the command "sbatch". Keep in mind that the Biocluster will switch over from a PBS/Torque scheduler to a SLURM scheduler by the end of the year. To be consistent throughout our Fall workshops, we will teach PBS/Torque commands, but keep in mind that in 2017 these commands will become irrelevant. CNRG plans to offer free classes on the new SLURM system near the end of the year, and we will let you know when these are.

Class materials

- Presentation
- VIDEO - [link here](#)

Biocluster resources

- Biocluster help page
- How to submit a cluster job
- `qsub` script generator
- PBS/Torque & SLURM comparison chart
Software

- Access a Linux terminal remotely through a Windows computer:
  - MobaXterm: http://mobaxterm.mobatek.net/
  - PuTTY: http://www.putty.org/
- Mac already has a UNIX-based terminal pre-installed. You can find it in Applications -> Utilities -> Terminal