

Working in a command line environment is becoming increasingly essential for biologists to analyze their complex datasets. This hands-on workshop will be an excellent starting point for biologists who want to learn basic UNIX commands to perform simple tasks. This workshop will also serve as a “background” for our subsequent advanced workshops offered in later part of this semester.

This workshop will include three sections, each addressing different levels of UNIX computing. The first section will introduce users to basic UNIX environment skills; the second section teaches necessary skills to perform routine file manipulations and the third section will serve as an introduction to the servers and computational resources available at RCAC/ITaP at Purdue as well as utilizing them to run some simple next generation sequence analysis programs.

Prerequisites for this workshop include: RCAC account (you will be given an account when you register for the workshop if do not already have one).

The intended audience for this presentation is scientists and students who want to start using bioinformatics tools at Purdue but who have little or no experience working with Unix servers at the command line.

Some references and suggested reading:

UNIX and perl for biologists: http://korflab.ucdavis.edu/Unix_and_Perl

Gibas, Cynthia and Per Jambeck. "Developing bioinformatics computer skills" O'Reilly Media, Inc., 2001.

<http://www.ee.surrey.ac.uk/Teaching/Unix/>

Bioinformatics Core

Basic UNIX for Biologists

(Registration required)

Thursday, August 29, 2013

9:00 AM to 3:00 PM

Stanley Coulter Hall (SC) 283

Purdue University

Contact for details: bioinformatics@purdue.edu

Please register by 5 PM on Sunday, August 25, 2013 by sending an email to bioinformatics@purdue.edu with the following information:

Name and email (only @purdue.edu will be accepted):

Advisor's Name:

Level of familiarity with UNIX/LINUX:

Basic or Intermediate