

Spring 2013 GNET 742 –

Introduction to UNIX and Perl Programming for biomedical data analysis

An introductory course designed to present the fundamentals of UNIX operating system followed by introduction to Perl programming with an emphasis on analysis of bio-medical data. Class will utilize a combination of lectures complemented with practical computer instruction.

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Calendar

Date (2013)		Instructor	Topic
14-Jan	M	Hemant Kelkar	Intro to UNIX operating system
15-Jan	Tu	Hemant Kelkar	Cluster computing resources
22-Jan	Tu	Joel Parker	Intro to Perl
28-Jan	M	Joel Parker	Variables and variables types
29-Jan	Tu	Joel Parker	File processing
4-Feb	M	Joel Parker	Program control
5-Feb	Tu	Joel Parker	Complex data structures
11-Feb	M	Joel Parker	Regular expressions and subroutines
12-Feb	Tu	Joel Parker	Review and application

Location and time

Time: 10 am – 11:30 am, MTue

Lectures and computer lab: Biogen Idec Classroom 307, Health Sciences Library.

Materials: All learning materials will be posted on “Sakai” at Sakai <https://sakai.unc.edu>.

Instructors

Hemant Kelkar, Ph.D.

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TBD

Teaching Assistant for GNET742

Class description

This class is designed to teach the fundamentals of UNIX operating system and Perl programming using practical “hands-on” computer instruction. This module will concentrate on applications of Perl programming to biomedical data/analysis.

Class Syllabus

(HK) Lecture 1 – Introduction to UNIX operating system

Accessing UNIX account using the secure shell (SSH) program. Basic UNIX commands followed by navigation of the UNIX file system. Transferring files from local desktop to the UNIX server using secure file transfer protocol. Introduction to the X-Windows interface and graphical output from the UNIX server.

(HK) Lecture 2 – UNIX computing resources at UNC-CH.

Using cluster computing resources at UNC-CH. Introduction to the “kure” compute cluster and the load sharing facility (LSF) used for cluster job management. Basic bioinformatics tools (NCBI blast/BLAT).

(JP) Lecture 3 – Introduction to Perl including history, advantages, and disadvantages of the language.

(JP) Lecture 4 – Definition of a variable and basic uses. Understanding of variable types including scalars, strings, arrays, and hashes.

(JP) Lecture 5 - Reading and writing files and processing of command line arguments.

(JP) Lecture 6 – Understanding basic logic, and program control with conditional statements and loops

(JP) Lecture 7 – Complex data structures focused on processing large genomic data

(JP) Lecture 8 – Subroutines, regular expressions and modules.

(JP) Lecture 9 – Review and knowledge application.

Class grade (subject to change)

100 % Assignments

There will be NO FINAL EXAM for this class.

Auditing and class size

Class is limited to twenty four (24) students. Auditing will not be allowed.

Recommended readings

General readings

Tisdall, J. (2001) Beginning perl for bioinformatics. O'Reilly and associates.

Homework assignments

Homework assignments will be due by 6 pm on Friday of the following the week they were originally assigned in. You can generally expect to have the grades for the assignments available a week after the due date.

Class Examinations

There will be **NO FINAL EXAM** for this class.

Linux server access for class

A compute solution will be provisioned for this class with assistance from ITS-Research Computing and will make use of the "kure" cluster. If you are registered student for this module then an account will be automatically added for you on the "kure" cluster. Logins will be based on your "onyen". Access to this server will remain available through the duration of the course and will allow you to work outside the class hours for assignments/projects.