

GNET PHCO 749

Short title: Practical RNA-Seq

Long title: Practical RNA-Seq

Effective term: Spring 2018

Course units/hours: 2 credit hours

Grading basis: (GRAD – H, P, L, F)

Course Component: lecture, lab

Meeting time: 1:30 – 3pm M/W/F March 18th through April 26th, 2019

Location: 307 Biogen Idec Classroom - Health Sciences Library

Course Coordinator: Mauro Calabrese (jmcalabr@med.unc.edu, room 4093 GMB)

Lectures will be posted on the Sakai site.

Course Description

This graduate-level course is designed to familiarize students with everything needed to run one complete RNA-Seq experiment, including the concepts behind experimental design, how to prepare samples, running them on a NextSeq 500, and analyzing data. There will be minimal emphasis on theory and heavy focus on practical aspects. There are **no** formal prerequisites required for this course and **no** prior experience with UNIX or the command line interface is expected. Students interested in taking the class should prepare a 250-word essay describing how they plan to use RNA-Seq in their own research and email the essay to Dr. Calabrese (jmcalabr@med.unc.edu). Registration will be by consent of Dr. Calabrese and will be limited to 20 students.

Registration

Students interested in taking the class should prepare a 250-word essay describing how they plan to use RNA-Seq in their own research and email the essay to Dr. Calabrese (jmcalabr@med.unc.edu). Registration will be by consent of Dr. Calabrese and will be limited to 20 students.

Short Description

This course will take students through one complete RNA-Seq experiment, from data production to analysis. No prerequisites are required.

Course objectives (learning outcomes):

The objective of this course is to provide students with a base of knowledge so that they can apply RNA-Seq to problems in their own research. Students will become familiar with experimental design, the Illumina sequencing technology, sample preparation, and how to perform simple data analyses that include visualizing RNA-Seq data on the UCSC genome browser and performing differential gene expression analysis.

Course Assignments

Short assignments will be given to familiarize students with basics of the UNIX/command-line interface and running computational processes on the Kure Computer cluster.

Lab component

After the first four lectures, students will attend a demonstration in which previously prepared samples will be prepped for loading into the NextSeq 500. These samples will then be sequenced on the NextSeq, and the data returned are what will be analyzed during the final four lectures of the course.

Assessments

Student evaluation and individual grades will be determined from class participation and a final take home exam.

Lectures:

- 1) Introduction to RNA-Seq
- 2) Basics of Illumina platform
- 3) Molecular Biology of Library preparation
- 4) Running the NextSeq and processing data
- 5) *Lab demonstration – sample quality control and NextSeq run*
- 6) Using Unix
- 7) Data processing (Kure)
- 8) Data processing (Kure)
- 9) Data processing, visualization (Kure, IGV/UCSC)
- 10) Data processing (R)
- 11) Data processing (R)
- 12) Data processing (R)
- 13) Data processing (R)
- 14) Data processing (R)