

Introduction to UNIX and RNA-seq Analysis

REQUEST FOR APPLICATIONS

Course description:

This three-day hands-on workshop will cover how to efficiently manage and analyze data using the UNIX/Linux command line interface and high-performance computing (HPC). These methods form the foundation of high-throughput sequencing data analysis and are critical for researchers looking to improve efficiency when performing computational tasks. All hands-on activities will be performed in the context of an RNA-seq workflow. Ideal participants for this workshop are researchers who want to build a foundation for analyzing sequencing data

In this workshop, participants will learn the basics of UNIX/Linux and gain experience using the HMS compute cluster (Orchestra), as well as learn the workflow (tools and parameters) to generate gene counts (expression data) from RNA sequencing data, and design considerations for an RNA-seq experiment.

Target audience:

Researchers who want to perform computational tasks more efficiently and/or who want to build a foundation for analyzing sequencing data. Preference will be given to applicants with limited sequencing experience and those interested in RNA-seq analysis.

Date applications are due: 5:00pm on August 16, 2017

Applicant Endorsements are due: 5:00pm August 21, 2017

Date by which applicants will be notified: 5:00pm on September 6, 2017

Selection process and criteria:

Harvard Catalyst's Education Program offers first priority to applicants who are current Harvard students, faculty, or current employees of Harvard University, its ten schools, and its seventeen Academic Healthcare Centers (AHC), or that of Boston College School of Nursing, MIT, or Harvard Pilgrim Health Care. A complete list of participating institutions can be found on the Harvard Catalyst website: <http://catalyst.harvard.edu/about/>.

The next level of priority is awarded to members of the national Clinical Translational Science Award (CTSA) consortium. A complete list of participating institutions (CTSCs) can be found on the CTSA website: <https://www.ctsacentral.org/institutions>

Applicants who are external to the groups listed above are accepted for a fee when space is available.

It is strongly recommended that applicants accepted into the UNIX workshop also apply for the November 2017 iteration of the Introduction to R: Basics, Plots, and RNA-seq Differential Expression Analysis workshop. The Introduction to R workshop will show participants how to

use gene count data generated in the UNIX course to generate lists of differentially expressed genes.

~~Application-~~The application for the Introduction to R workshop will open July 20, and accepted applicants of the UNIX workshop will have priority admission.

Tuition/fee for external participants:

The expectation is that by accepting a seat in one of the Education Program courses, the participant is agreeing to attend the entirety of the course. As part of the application process, a supervisor's endorsement for course attendance, granting the applicant permission to be away from the lab or clinical duties for the duration of the course, will be automatically generated. If a participant must be absent for any portion of the course, it is the participant's responsibility to notify course coordinators, since attendance is taken at all sessions. If the participant cannot be reached, the coordinators will then be obliged to notify the endorsing supervisor of the unexplained absence. Since the Education Program courses are expensive to produce, but are offered to Harvard and CTSC affiliates free-of-charge, including meals and Continuing Medical Education (CME) credits, the only obligation of participants is to attend and participate fully.

Please also note that participants seeking CME credits must attend all course sessions and complete each daily evaluation. No partial CME credits are offered.

If you have any questions about the course or information above, please don't hesitate to ask. The course coordinators can be reached at PGE_Bioinformatics@catalyst.harvard.edu