Introduction to bulk RNA-seq Data Analysis (Part I) (2022)

(Experimental design -> Raw data -> Count matrices)

Note: Until further notice, workshops will be taught online via Zoom. However, we anticipate returning to in-person teaching in 2022.

**Next workshop dates and times:**

- **Tuesday, March 29th:** 9:30 AM - 12 PM
- **Friday, April 1st:** 9:30 AM - 12 PM
- **Tuesday, April 5th:** 9:30 AM - 12 PM

Before registering for this workshop, please note that the instruction for this workshop will require workshop participants to spend between 3-5 hours between classes on reading and exercises! This "self-learning" is mandatory if you want to follow along in the next online session. Online and in-person classes will focus on discussions, exercises and some instruction.

**Description:**

This hands-on workshop will instruct participants on how to design a bulk RNA-seq experiment, and how to efficiently manage and analyze the data using the command-line interface and high-performance computing. The workshop will cover the first part of the bulk RNA-seq data analysis workflow, from experimental design to the generation of a count matrix.

Note: Differential gene expression analysis on the count matrix will be covered in a separate workshop (Introduction to bulk RNA-seq data - Part II).

**Prerequisites?**

This is one of our advanced workshops, and requires registrants to have attended the following Basic workshop offered by our training team within the last 6-8 months: Introduction to command-line interface workshop.

**FAQ** - I am fluent in command-line interface and running jobs on the cluster, but have not attended the above prerequisite workshop, can I still register?

**Answer** - Yes, you can register but please do the following:

- Complete the registration first
- Then email us directly at hbctraining@hsph.harvard.edu with a detailed description of your knowledge/experience in command-line interface. **Failure to do this step will prevent or delay you from being accepted into this advanced workshop.**

**Who Should Attend?**

Eligible* Harvard researchers who want to learn:

1. How to design a bulk RNA-seq experiment
2. The steps involved in taking raw RNA-sequencing data (Illumina) and generating a count (gene expression) matrix
3. How to compute and assess QC metrics at every step in the workflow
4. How to automate a simple workflow on the cluster using shell scripting
5. How to effectively use HMS-RC's O2 cluster for analysis

**Cost and Registration:**

There is a non-refundable and non-transferable $50 registration fee for this advanced workshop.

We will be accepting 35-45 participants on a first-come, first-served basis:

- If you are one of the first 35-45 eligible* registrants, you will receive an email with a link to pay the (non-refundable & non-transferable) $50 registration fee.
- If you are not among the first 35-45 eligible* registrants, you will be added to the waitlist and notified when we open registration for the next iteration of this workshop.

NOTE: You will not have a reserved seat for this workshop until you pay the registration fee. Please make sure you pay within the time stated in that email, else you will lose your spot to someone on the waitlist.
Eligibility requirements:

* To be eligible to attend this workshop you should fulfill **at least one** of the following criteria:

  * Harvard Medical School researcher in a lab on the Quad, with grants administered by Gordon Hall
  * Harvard School of Dental Medicine researcher, with grants administered by Gordon Hall
  * Graduate student at the Harvard Medical School
  * Researcher affiliated with the Dana-Farber / Harvard Cancer Center (DF/HCC).
  * Harvard researchers whose PIs are associated with the HSCI as Principal or Affiliated faculty

If you are unsure of your eligibility, please register anyway and we will get back to you.

**Registration is closed.**

*(Please check the eligibility requirements above prior to registering)*

**NOTE: We do *not* record our training sessions.**

**Questions?**

Please contact us at hbctraining@hsph.harvard.edu with any questions.