

# Introduction to RNA-seq using High-Performance Computing (HPC)

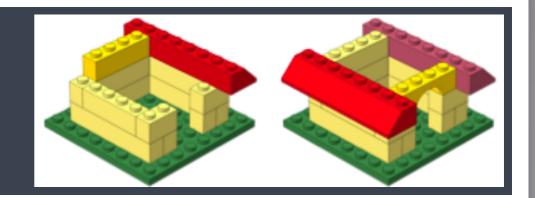
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

https://tinyurl.com/hbc-rnaseq

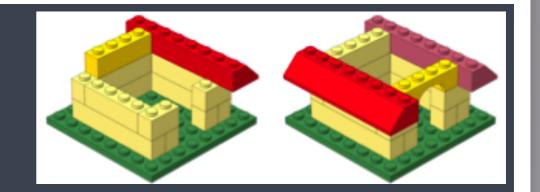
# Learning Objectives



- ✓ Describe best practices for designing a bulk RNA-seq experiment
- ✓ Describe steps in an RNA-seq analysis workflow (from sequence data to expression quantification).
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps.

We won't be covering how to perform differential gene expression (DGE) analysis on count data in this workshop.

# Survey



https://tinyurl.com/hbc-rnaseq-exit

## R and DGE

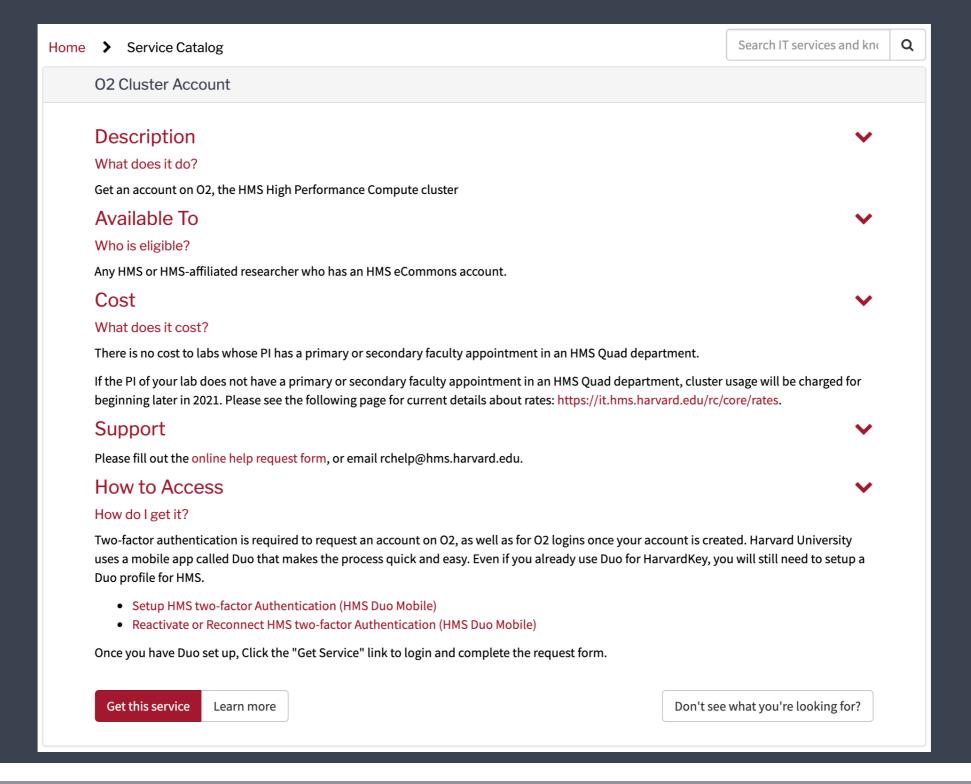


Workshop registration opens about 3 weeks prior to workshop date(s). Register by clicking on the class title.

Topic	Category	Date	Duration	Prerequisites
Introduction to RNA-seq Part I (Experimental design -> Raw data -> Count matrices)	Advanced	March 29th, April 1st & 5th	Three 2.5h sessions	Shell
Introduction to R	Basic	April 19th, 22nd, 26th & 29th	Four 2h sessions	None
Bulk RNA-seq Part 2 (Differential Gene Expression on expression counts)	Advanced	May 6th, 10th, 13th & 17th	Four 2h sessions	R

https://bioinformatics.sph.harvard.edu/upcoming-workshops

#### Get an O2 account!



### Interested in additional training?

All workshop materials available at:

https://hbctraining.github.io/main

Upcoming relevant courses from our partners at Countway Library:

- 1. Writing a Data Management Plan (April 13th)
- 2. Introduction to Data Repositories (April 27th)
- 3. How and Where to Publish your Data (May 11th)

#### Office hours

- Office hours for trainees
- Every other Wednesday, 11am noon
- 4 x 30 minute slots available

#### Thanks!

- Kathleen Chappell and Andy Bergman from HMS-RC
- Data Carpentry

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#### Contact us!

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