

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

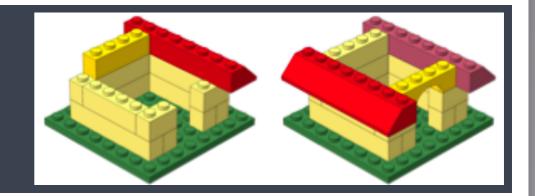
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

https://tinyurl.com/hbc-rnaseq

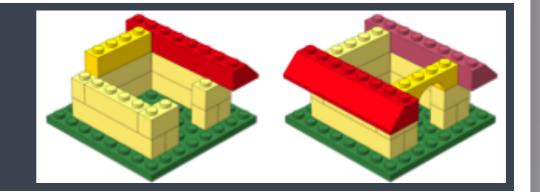
Learning Objectives



- ✓ 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

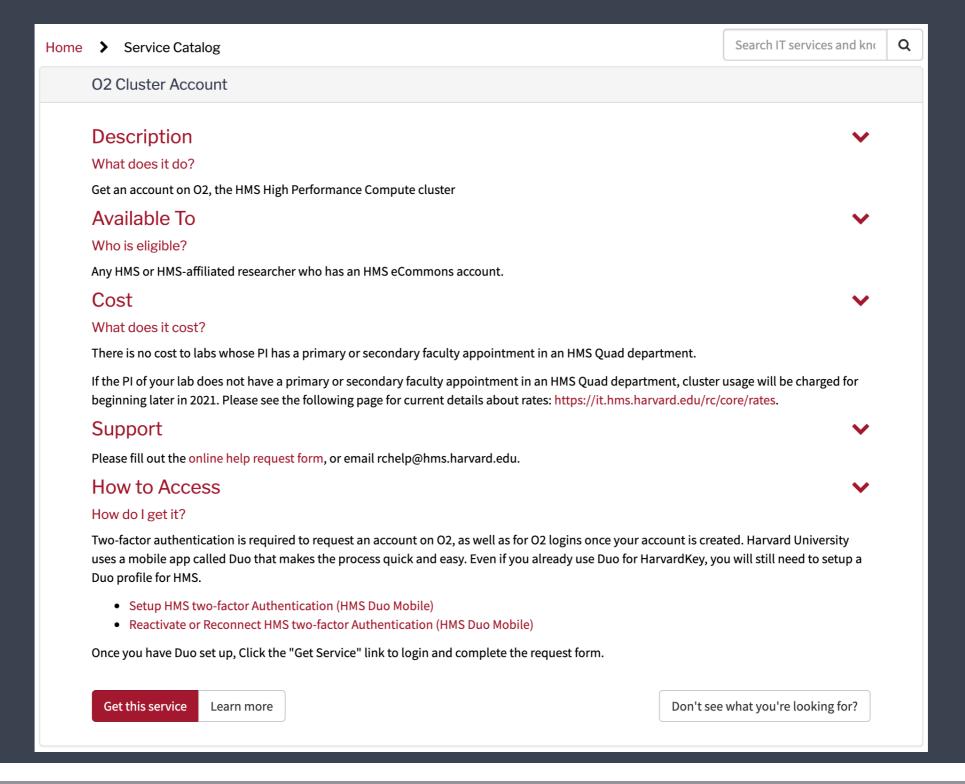


Workshop registration opens about 3 weeks prior to workshop date(s). Register by clicking on the class title.

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!



Thanks!

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

These materials have been developed by members of the teaching team at the <u>Harvard Chan Bioinformatics Core (HBC)</u>. These are open access materials distributed under the terms of the <u>Creative Commons Attribution license (CC BY 4.0)</u>, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.



Contact us!

HBC training team: hbctraining@hsph.harvard.edu

02 (HMS-RC): rchelp@hms.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

HBC: @bioinfocore

HMS-RC: @hms_rc