

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

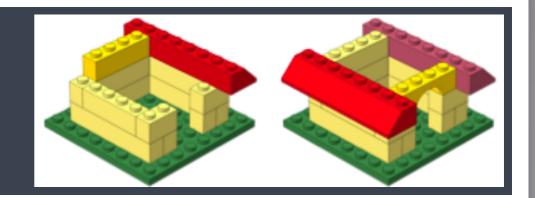
Harvard Chan Bioinformatics Core

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.

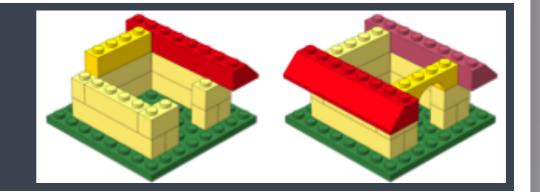
DGE and scRNA-seq



Topic	Category	Date	Duration	Prerequisites
Introduction to RNA-seq Part I	Advanced	March 17th, 21st, 24th	Three 2.5h sessions	Shell
Introduction to R	Basic	April 28th, May 2nd, 5th, 9th	Four 2h sessions	None
Introduction to RNA-seq Part II	Advanced	May 16th, 19th, 23rd, 26th	Four 2h sessions	R
Introduction to Shell	Basic	June 20th, 23rd, 27th	Three 2.5h sessions	None
Variant Calling	Advanced	TBD	TBD	TBD
Introduction to Shell	Basic	TBD	Three 2.5h sessions	None

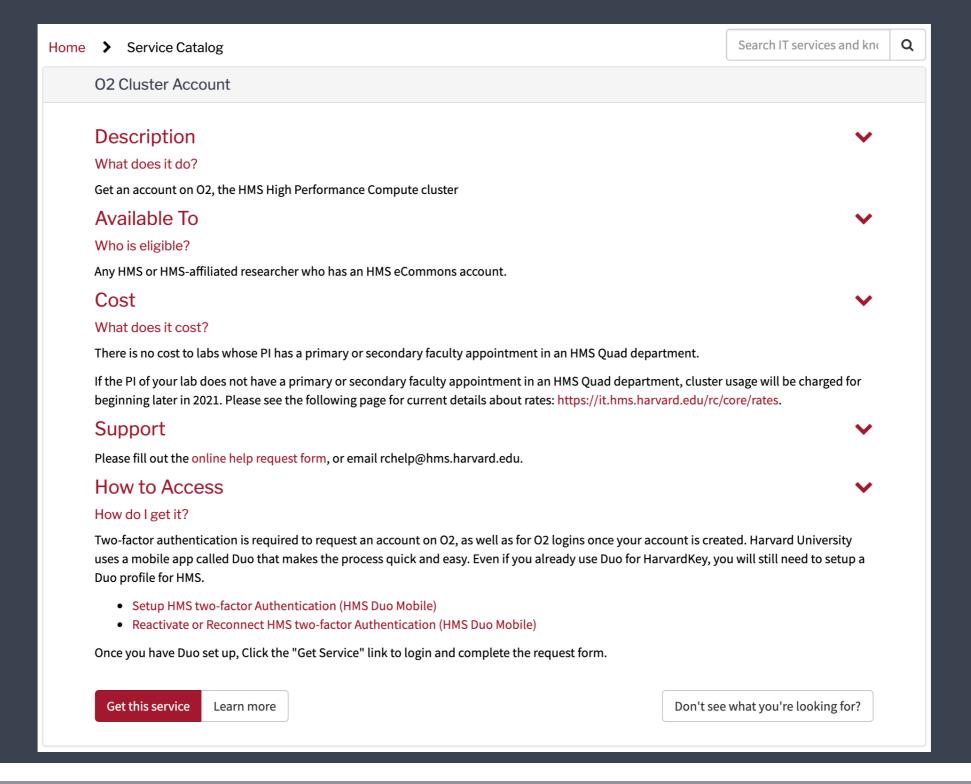
https://bioinformatics.sph.harvard.edu/upcoming-workshops

Survey



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

Get an O2 account!



Interested in additional training?

https://hbctraining.github.io/Training-modules/

- Workshops on bioinformatics methods & related skills.
- Once a month for 3 hours
- · Hands-on workshops be prepared with your MAC or Windows computer
- · Free and open to everyone at Harvard University and its affiliates
- Will typically meet the third Wednesday of the monthfrom 1-4 online via Zoom (meeting time is subject to change-please check)

Topic	Pre-requisites	Date/Time	Time	Registration
Advanced Shell	Intermediate Shell	3/15/2023	1 – 4pm	<u>Register!</u>
Git/Github	Shell	4/19/2023	1 – 4pm	<u>Register!</u>
ML4Bio	TBD	TBD	TBD	Coming soon
Python basics	None	6/21/2023	1 – 4pm	<u>Register!</u>

Interested in additional training?

All workshop materials available at:

https://hbctraining.github.io/main

Upcoming relevant courses from our partners at Countway Library

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