

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

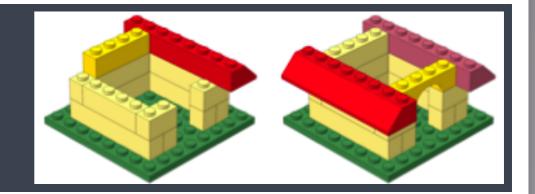
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

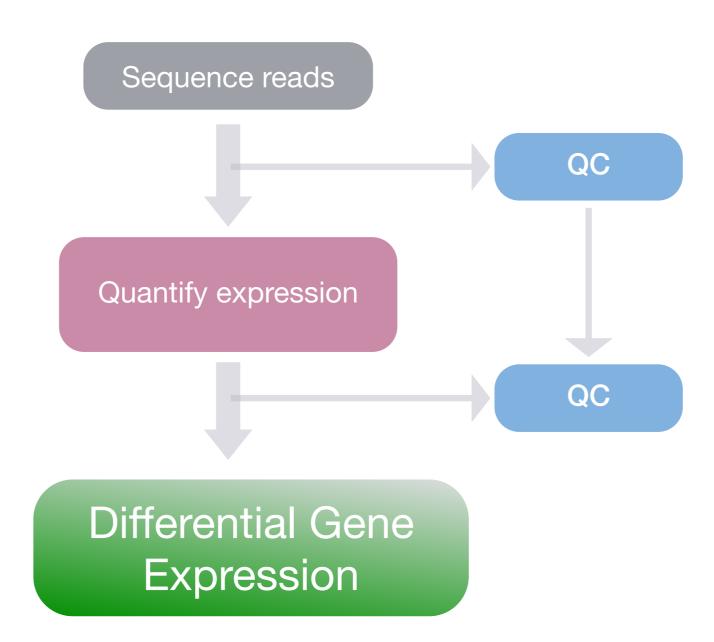
https://tinyurl.com/hbc-rnaseq

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.

What's next?



What's next?



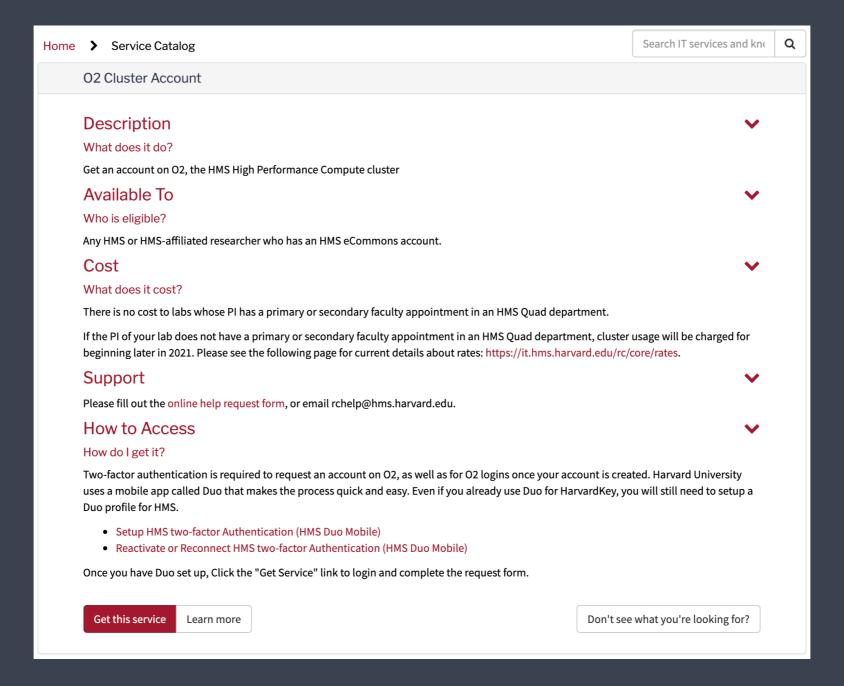
Topic	Category	Date	Duration	Prerequisites
Bulk RNA-seq (Part 1 - FASTQ to counts)	Advanced	March 29, April 2, 5	Three 2.5h sessions	<u>Shell</u>
Introduction to R	Basic	April 9, 12, 16, 19	Four 2h sessions	None
Introduction to Differential Gene Expression (DGE) analysis	Advanced	April 30, May 3, 7, 10	Four 2h sessions	<u>R</u>
Introduction to Command line interface and HPC (Shell)	Basic	May 17, 21, 24	Three 2.5h sessions	None

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

Your feedback matters!

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

How to request an O2 account?



Big data? Big computer! The skill set you need to succeed

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

Spring 2024 schedule - Big data? Big computer! The skill set you need to succeed:

Topic	Pre- requisites	Date/Time	Time	Registration
Accelerate with Automation - Making your code work for you	Basic Shell	3/20/24	1 – 4pm	Register!
Needle in a Haystack - Finding and summarizing data from colossal files	Basic Shell	4/17/24	1 – 4pm	Register!
Shell Tips and Tricks on O2	Basic Shell	5/15/24	1 – 4pm	Register!

Interested in additional training?

All HBC 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

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Contact us!

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