

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

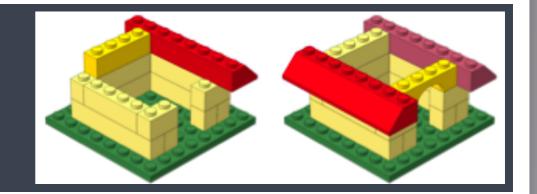
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

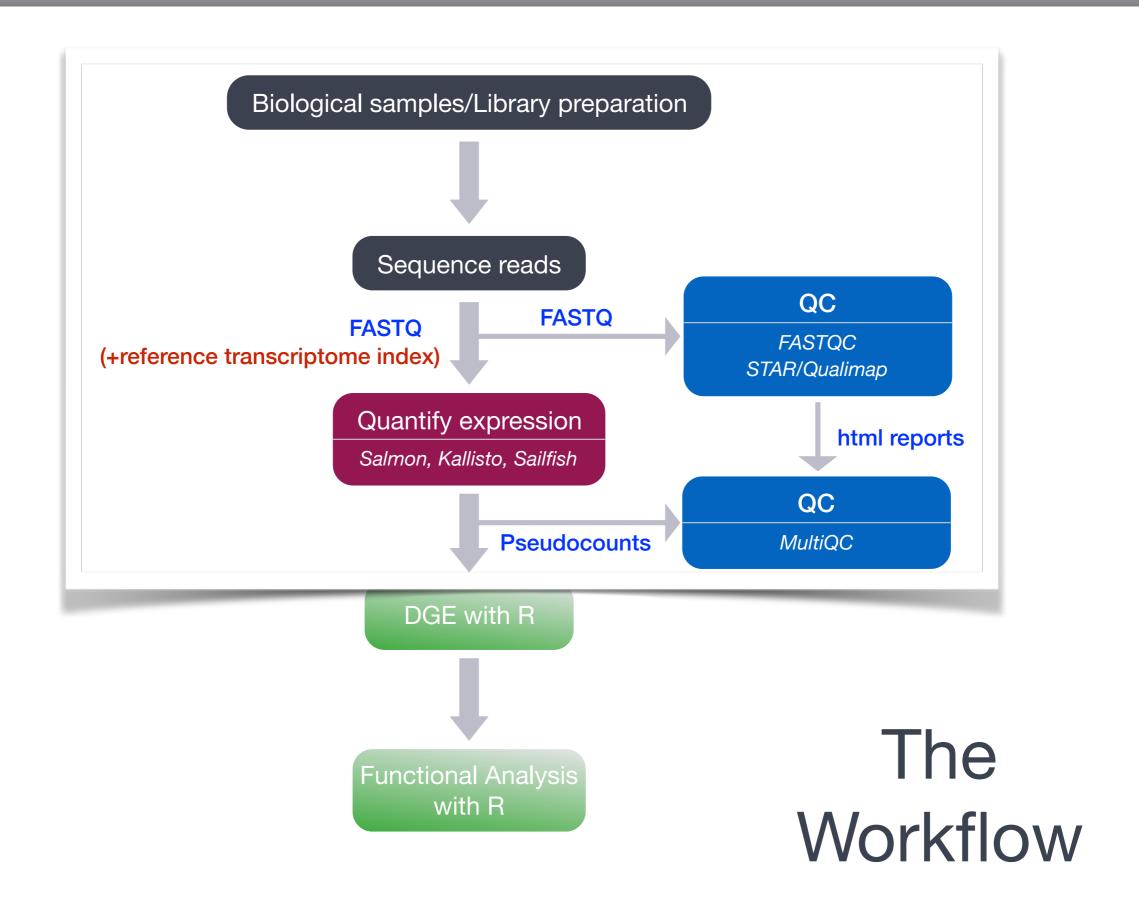
https://tinyurl.com/hbc-rnaseq

Learning Objectives

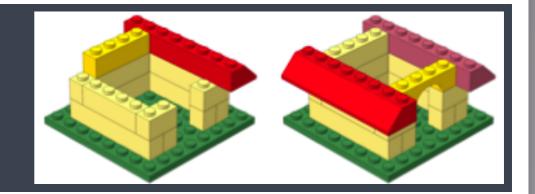


- ✓ Describe best practices for designing a bulk RNA-seq experiment
- ✓ Describe steps in an RNA-seq analysis workflow (from sequence data to expression quantification).
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps.

We won't be covering how to perform differential gene expression (DGE) analysis on count data in this workshop. A DGE workshop will be held on April 1st/2nd and the pre-requisite for it is a working knowledge of R (March 12th/13th).



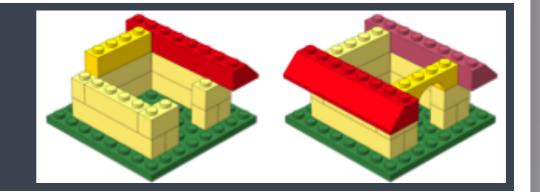
Learning Objectives



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Survey



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

R and DGE



Upcoming workshops

Workshops for HSCI, on-quad HMS, and DF/HCC researchers*:

Please note that until further notice, all workshops will be taught remotely via Zoom.

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 R	Basic	November 2nd, 5th, 9th & 12th	Four 2h sessions	None
Bulk RNA-seq Part 2 (Differential Gene Expression on expression counts)	Advanced	December 3rd, 7th, 10th & 14th	Four 2h sessions	R

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

Harvard Chan Bioinformatics Core & The Cancer Data Sciences Program at DF/HCC

Workshop Series Details:

- Leaders in single-cell genomics at Harvard present their latest tools (including demo or tutorial)
- Once a month for 2-3 hours
- Free and open to everyone at Harvard University and its affiliates

Fall 2021 schedule:

Speakers	Date	Time	Registration			
October Topic: scRNA-seq						
Peter Kharchenko						
 Ilya Korsunsky 	10/13/2021	1 – 4pm	Sign up!			
 Soumya Raychaudhuri 						
November Topic: scATAC-seq						
Luca Pinello, Huidong Chen, Jayoung Ryu (SIMBA)Gali Bai (MAESTRO)	11/10/2021	12 – 3pm	Sign up!			
December Topic: single cell multimodal analyses						
Cliff Meyer (SHARE-seq)	TBD	TBD	TBD			

Thanks!

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

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