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

Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

https://tinyurl.com/intro-to-rnaseq-adv

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).

Useful Resources

- *Creating shortcuts or aliases in Bash*

- *Copying files from other remote locations to O2*

- *Creating symbolic links*

- *Obtaining reference genomes or transcriptomes*

Survey

https://tinyurl.com/rnaseq-adv-exit-survey
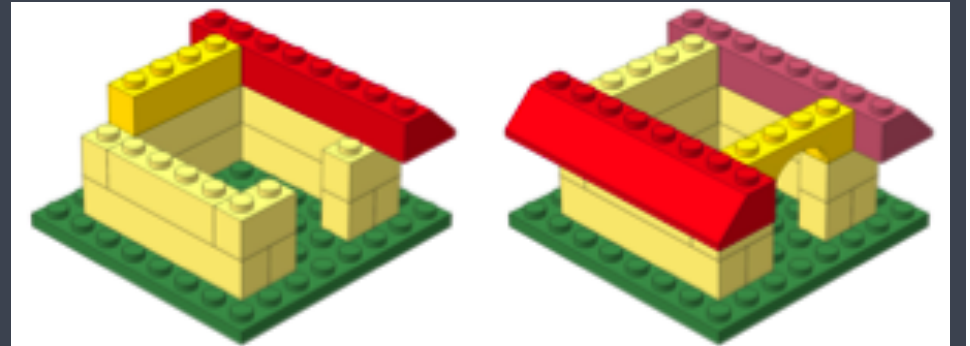
Upcoming workshops

- July 17th & 18th: Introduction to single-cell RNA-seq

- July 29th & 30th: Introduction to R

- August 15th & 16th: Introduction to differential gene expression analysis (bulk RNA-seq)

Bioinformatics Community Networking Breakfast!

- ***Free and open*** *to the LMA community*

- *Food and seats are* **first-come-first-served**

- ***Last Wednesday*** *of every month*

Date: June 26th, 2019

Time: 9:00 to 10:30 am

Venue: Kresge 201 (HSPH)

Thanks!

- Andy Bergman from HMS-RC

- [Data Carpentry](#)

Contact us!

HBC training team: hbctraining@hsph.harvard.edu

O2 (HMS-RC): rchelp@hms.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

HBC: @bioinfocore

HMS-RC: @hms_rc