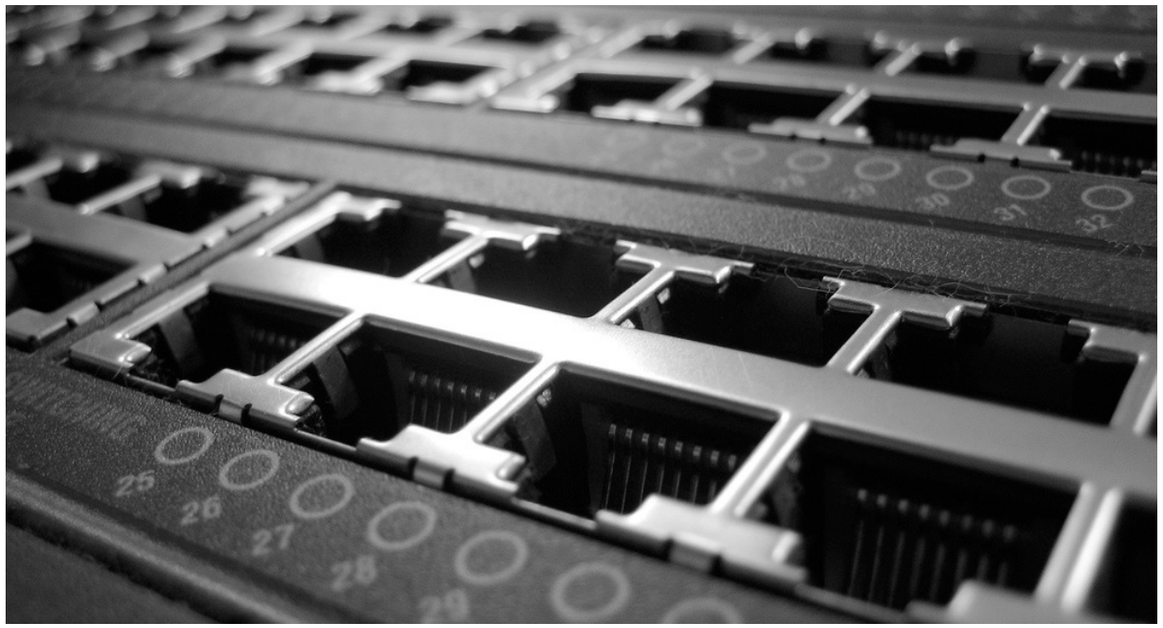


Introduction to RNA-seq using High-Performance Computing (HPC)

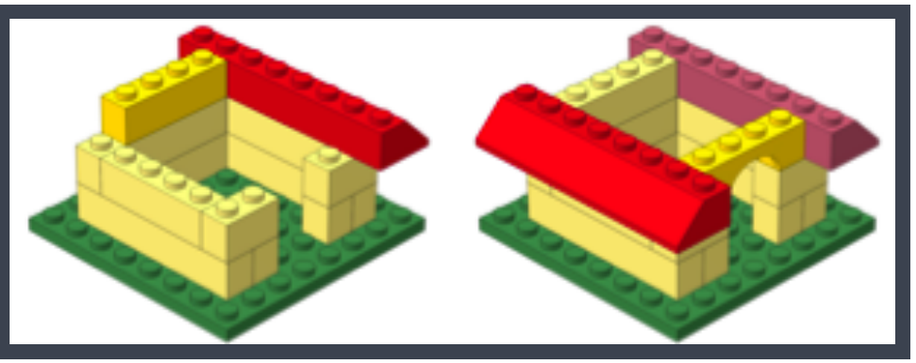
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

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

Learning Objectives



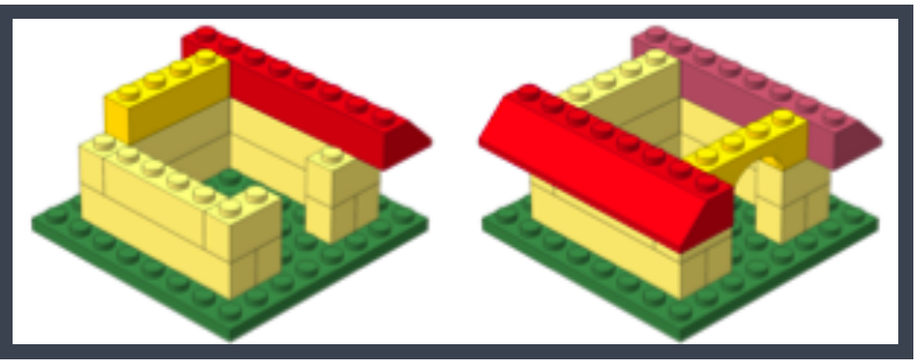
- ✓ Describe best practices for designing a bulk RNA-seq experiment
- ✓ Describe steps in an RNA-seq analysis workflow (from sequence data to expression quantification).
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps.

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

- October 3rd & 4th: Introduction to R *(registration closed)*

- October 21st & 22nd: Introduction to differential gene expression analysis (bulk RNA-seq)

- November 19th & 20th: Introduction to R

- December 2nd & 3rd: Introduction to single-cell RNA-seq

Upcoming free, monthly, 3hr workshops

- **November 15th:**

  Setting up for Success: Everything you need to know to make your data analysis reproducible

  Presented by Julie Goldman from Countway Library

- **December 13th:**

  Setting up for Success: Introduction to Version Control (Git)

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: Sept. 25th, 2019

Time: 9:00 to 10:30 am

Venue: HSPH Building 2, Room 426

Thanks!

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

Contact us!

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