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).

Survey

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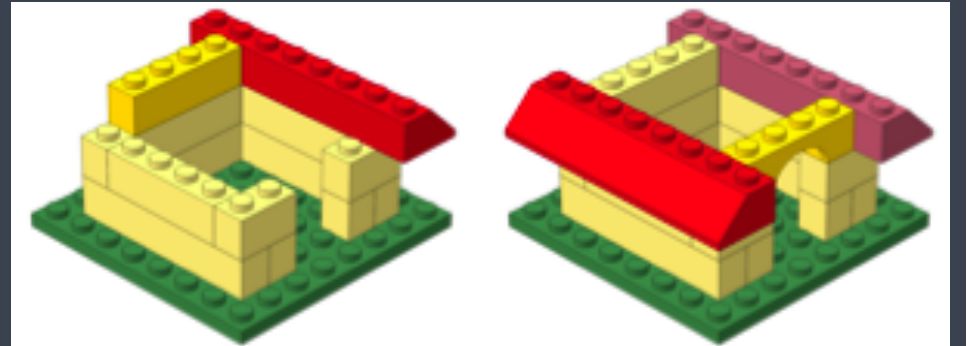
Upcoming workshops

- **March 6th:** *Gene annotations and functional analysis of gene lists (3 hr)*

- **March 12th and 13th:** *Introduction to R*

- **April 1st and 2nd:** *Introduction to differential gene expression analysis (bulk RNA-seq)*

- **April 3rd:** *Generating research analysis reports with RMarkdown (3 hr)*

- **April 29th and 30th:** *Introduction to ChIP-seq analysis*

Useful Resources

- *Creating shortcuts or aliases in Bash*

- *Copying files from other remote locations to O2*

- *Creating symbolic links*

- *Obtaining reference genomes or transcriptomes*

Thanks!

- Andy Bergman from HMS-RC

- Data Carpentry

Contact us!

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