



# 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>

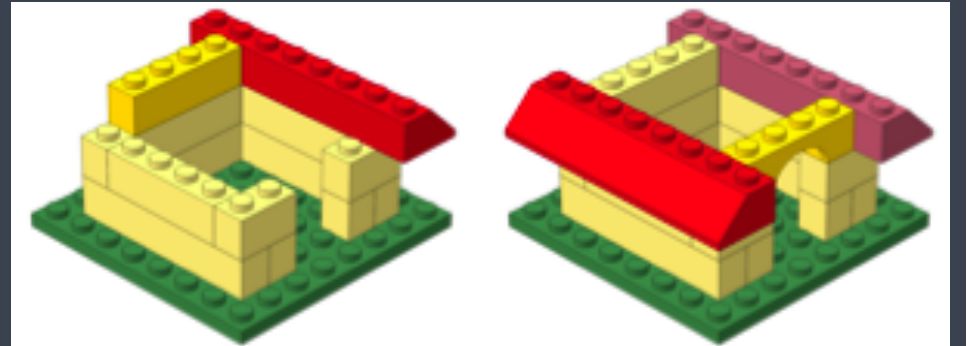
# Learning Objectives



- ✓ 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 1<sup>st</sup>/2<sup>nd</sup> and the pre-requisite for it is a working knowledge of R (March 12<sup>th</sup>/13<sup>th</sup>).

# 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](#)

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