

Introduction to RNA-seq using HPC

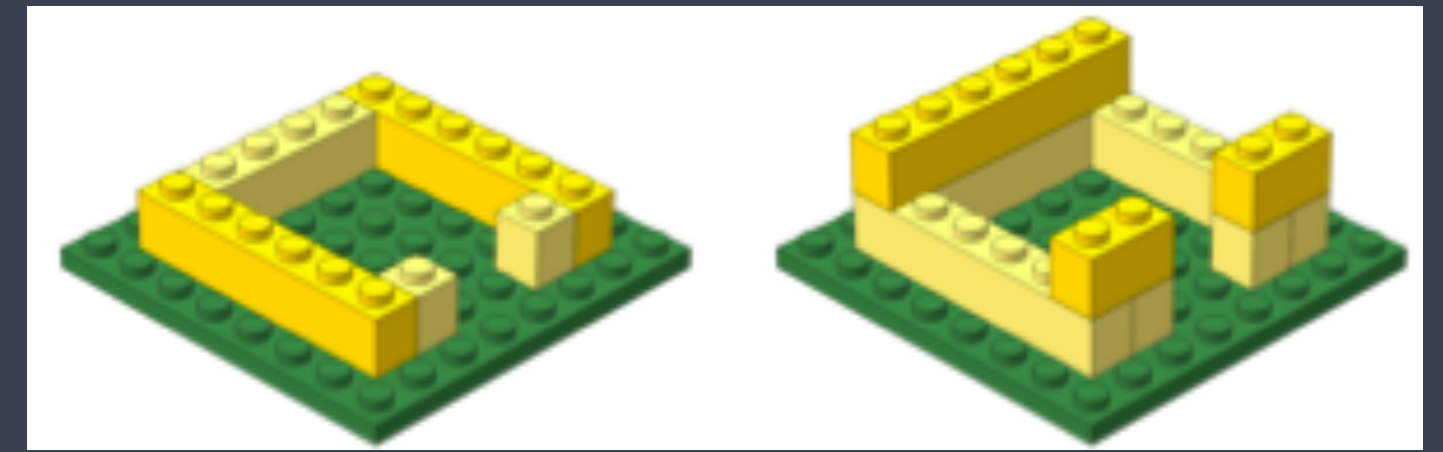
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

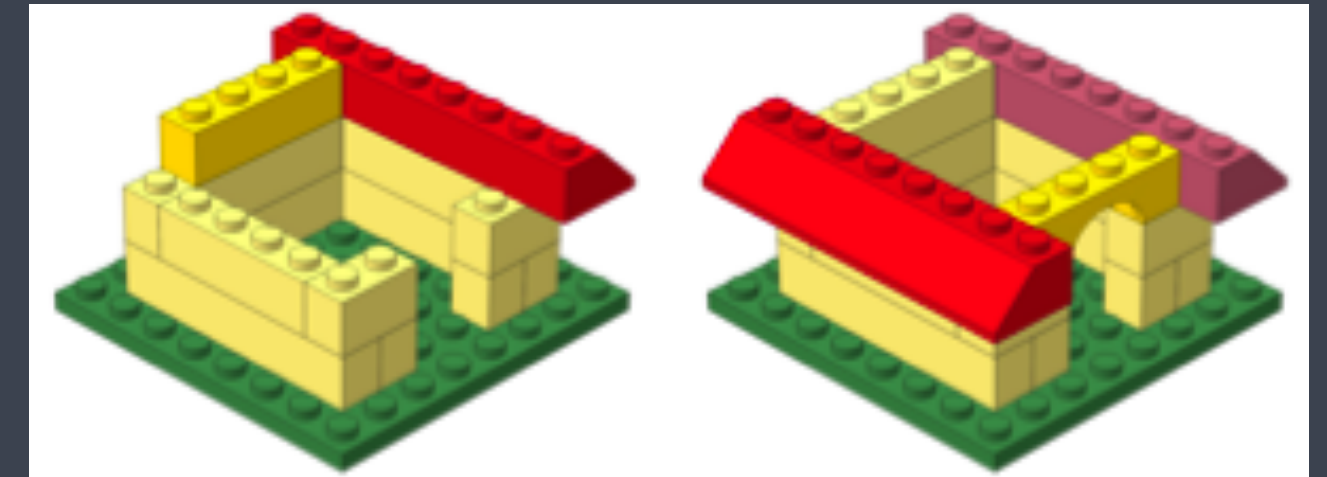
Wrap up

Learning Objectives



- ✓ Learn what a “shell” is and become comfortable with the command line interface
 - Find your way around a filesystem using the command line
 - Work with small and large data files
 - Become more efficient when performing repetitive tasks
- ✓ Understand what a computational cluster is and why we need it
 - Independently access the O2 cluster
 - Perform analysis using the cluster (run programs, pipelines, etc.)

Learning Objectives



- ✓ Describe best practices for designing a ChIP-seq experiment
- ✓ Describe steps in a typical ChIP-seq analysis workflow
- ✓ Use HMS-RC's O2 compute cluster to efficiently run the ChIP-seq workflow from sequence reads to peak calls, including QC and visualization.

Some steps in the ChIP-seq workflow require a working knowledge of R, and we won't be covering these in much detail.

Survey...

<https://tinyurl.com/chipseq-survey>

Talk to us early

Involvement in study design to optimize experiments



Questions?

HBC training team: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu



More Information..

HBC training materials: <https://hbctraining.github.io/main>

HBC website: <http://bioinformatics.sph.harvard.edu>

HBC twitter: @bioinfocore

