Introduction to ChIP-seq using HPC
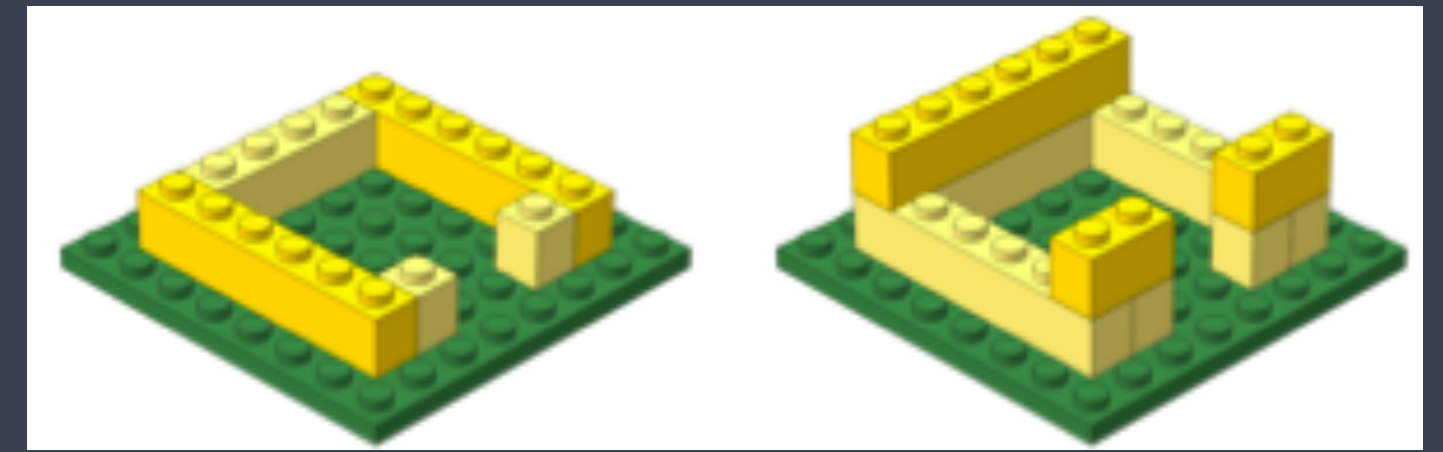
Harvard Chan Bioinformatics Core

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
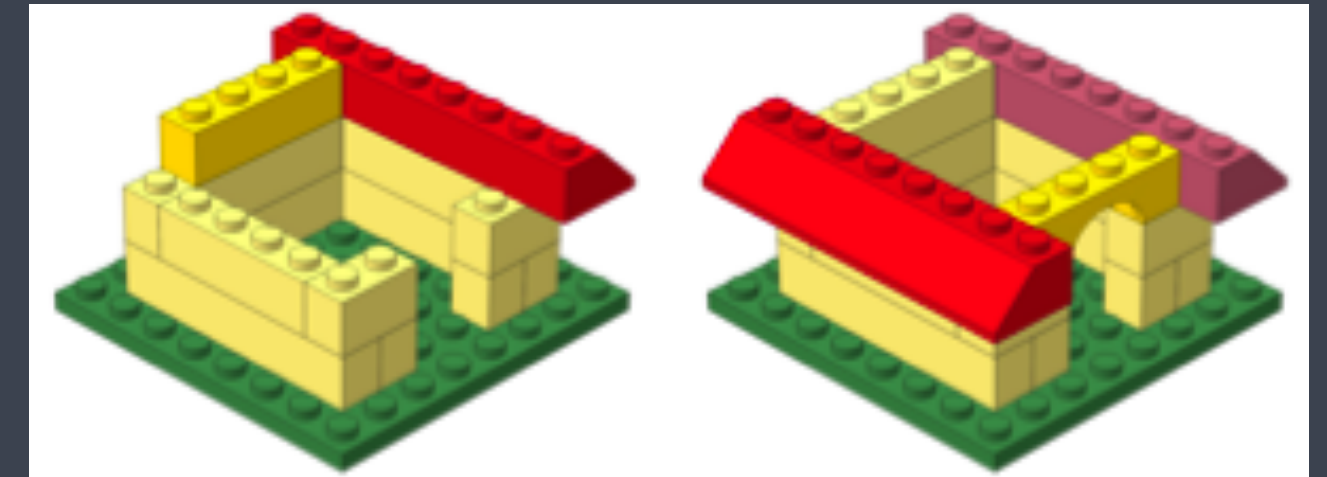
✓ Describe best practices for designing a ChIP-seq experiment

✓ 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?

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More Information..

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

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

HBC twitter: @bioinfocore