

Introduction to High-Performance Computing (HPC) for RNA-seq data

Harvard Chan Bioinformatics Core

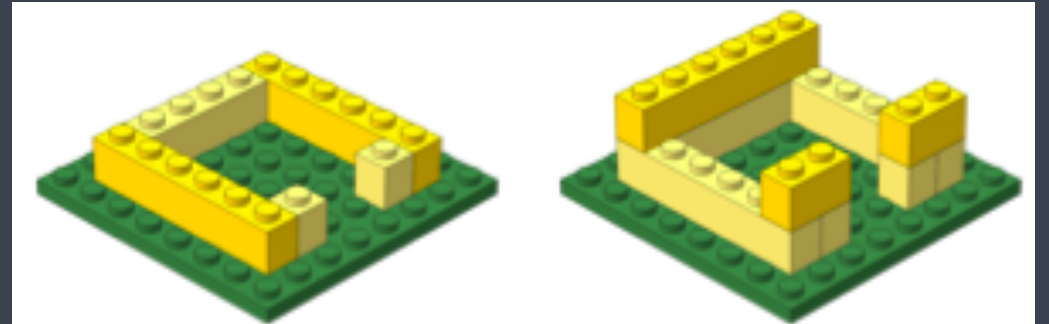
in collaboration with

HMS Research Computing

May 30 & 31, 2018

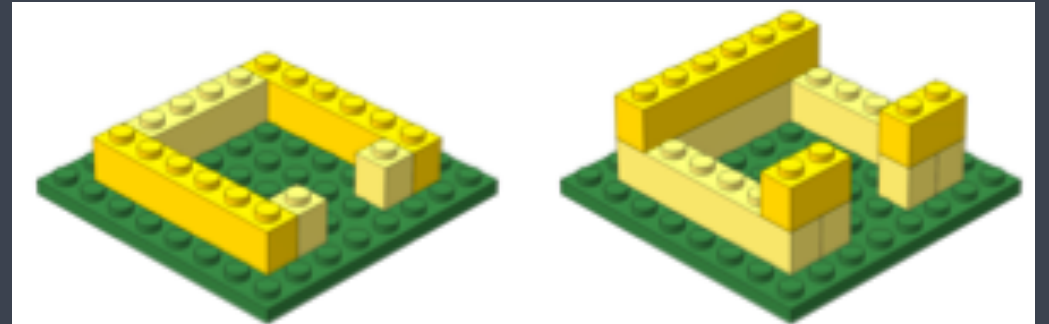
<https://tinyurl.com/hbc-unix-may>

Learning Objectives



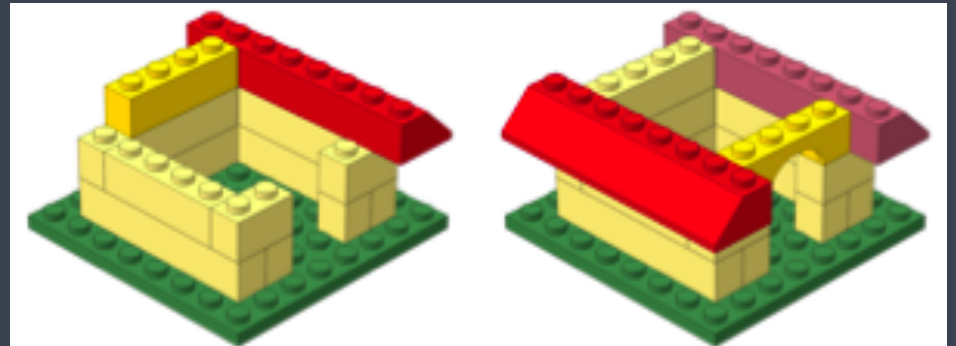
- ✓ Learn what a “shell” is and become comfortable with the command line interface
 - Find your way around a UNIX filesystem
 - Work with small and large data files
 - Become more efficient when performing repetitive tasks

Learning Objectives



- ✓ Learn what a “shell” is and become comfortable with the command line interface
 - Find your way around a UNIX filesystem
 - 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 an RNA-seq experiment
- ✓ Describe steps in an RNA-seq analysis workflow

We won't be covering how to perform differential gene expression analysis on count data in this workshop, since it requires a working knowledge of R.

FAS-RC's Odyssey cluster

<https://www.rc.fas.harvard.edu/training/introduction-to-odyssey-online/>

<https://www.rc.fas.harvard.edu/resources/running-jobs/>

<https://portal.rc.fas.harvard.edu/apps/modules>

<https://www.rc.fas.harvard.edu/upcoming-training/>

Survey...

<http://tinyurl.com/intro-rnaseq-exit-survey>

Talk to us early

Involvement in study design to
optimize experiments



Questions, information?

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Resources:

<http://bioinformatics.sph.harvard.edu/resources/>

