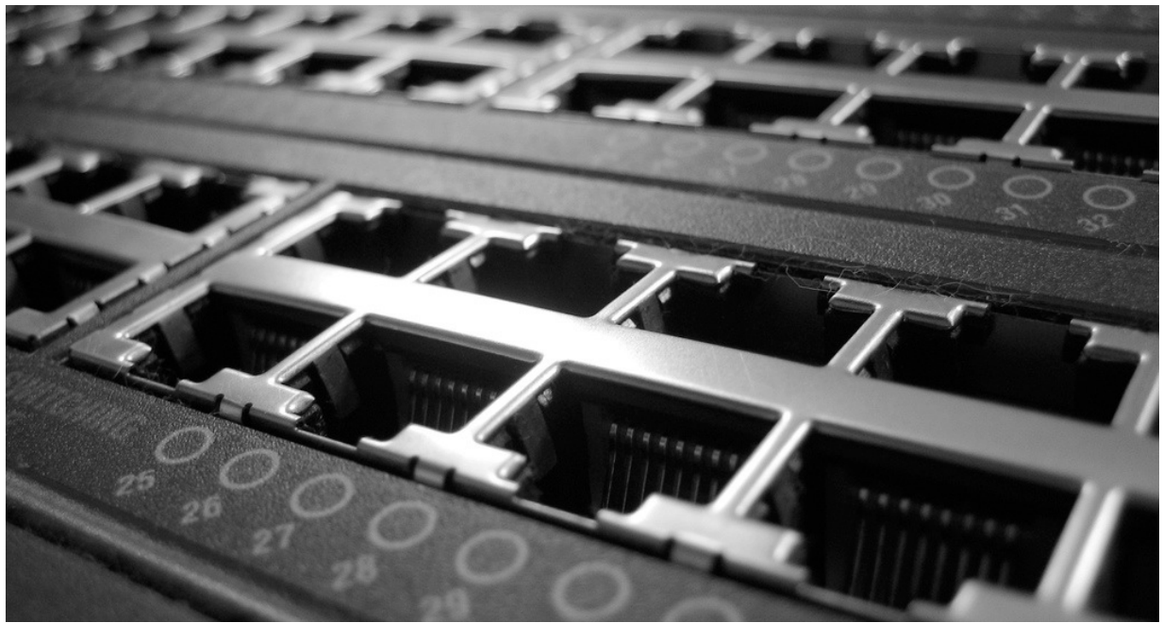


Introduction to RNA-seq using High-Performance Computing (HPC)

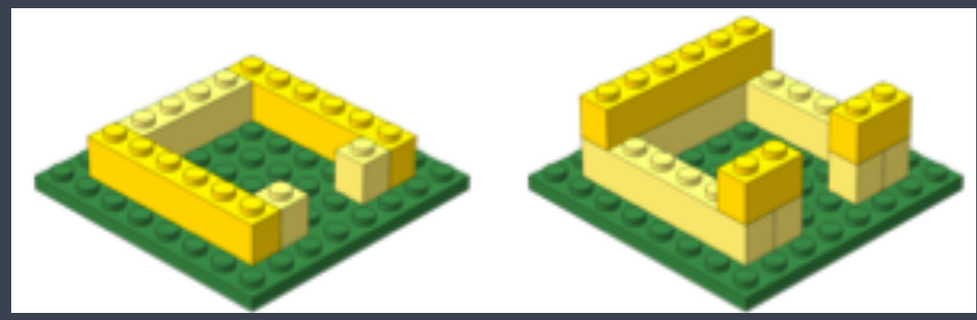
Bioinformatics Core at the

Harvard T.H. Chan School of Public Health

April 23-24, 2018

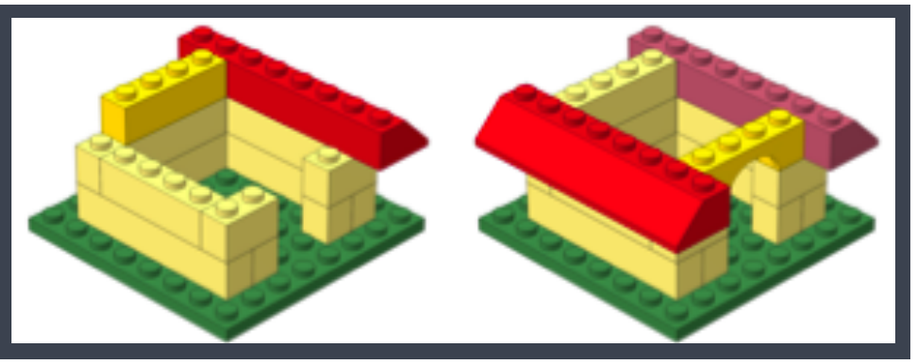
https://tinyurl.com/intro-rnaseq-gt

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 local 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
- ✓ Use the local compute cluster to efficiently run the RNA-seq workflow from sequence files to count matrices.

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.

More information?

Training materials: https://hbctraining.github.io/main/

HBC training: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

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