Introduction to the command-line interface (shell)
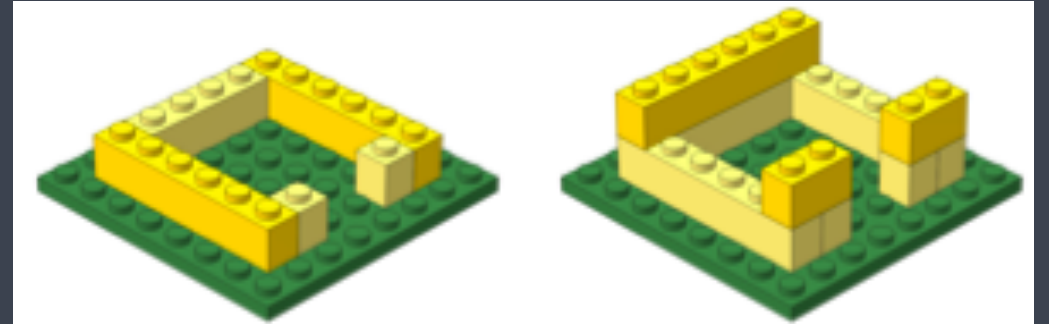
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing
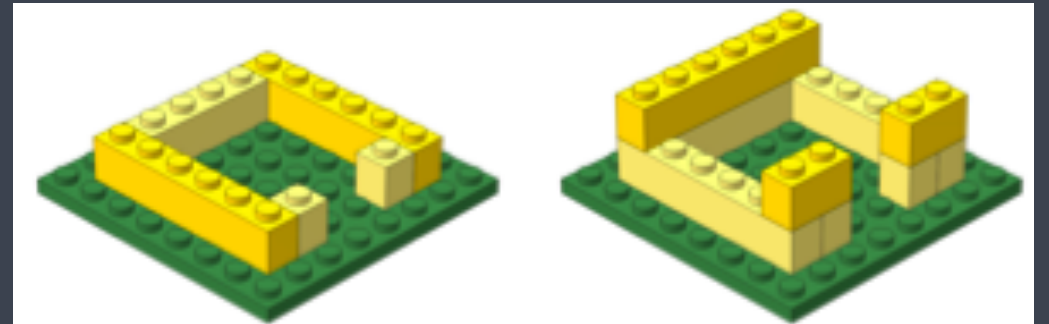
https://tinyurl.com/hbc-shell

Learning Objectives

✓ Learn what a "shell" is and become comfortable with the command-line interface

- Find your way around a filesystem using written commands

- 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

Setting up…

✓ Introduction to the command-line interface (shell, Unix, Linux)

- Dealing with large data files

- Performing bioinformatics analysis

  - Using tools

  - Accessing and using compute clusters

✓ R

- Parsing and working with smaller results text files

- Statistical analysis, e.g. differential expression analysis

- Generating figures from complex data

Exit survey

https://tinyurl.com/intro-shell

Consulting

- RNA-seq, small RNA-seq and ChIP-seq analysis

- Genome-wide methylation

- WGS, resequencing, exome-seq and CNV studies

- Quality assurance and analysis of gene expression arrays

- Functional enrichment analysis

- Grant support
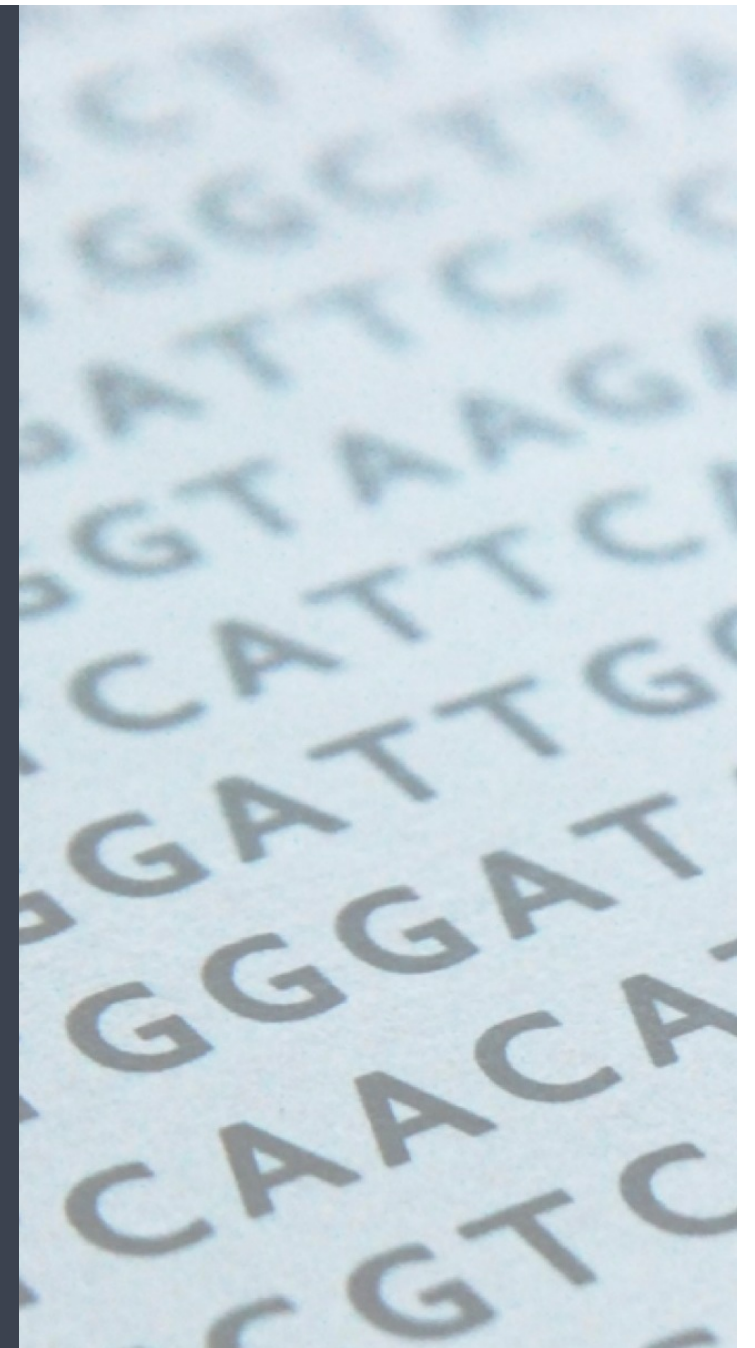
Data Management

- HMS Data management -

  Webpage: https://datamanagement.hms.harvard.edu/

  Click here to sign up for data management related emails

- Harvard-wide Research Data Management -

  https://researchdatamanagement.harvard.edu/

Contact us!

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

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

HBC workshop listserv: https://tinyurl.com/hbc-mailing-list

Training email: hbctraining@hsph.harvard.edu

Consulting email: bioinformatics@hsph.harvard.edu

O2 (HMS-RC): rchelp@hms.harvard.edu

Twitter

@bioinfocore

Thanks!

- Kathleen Keating and Andy Bergman from HMS-RC

- [Data Carpentry](#)