



# Introduction to the command-line interface (shell)

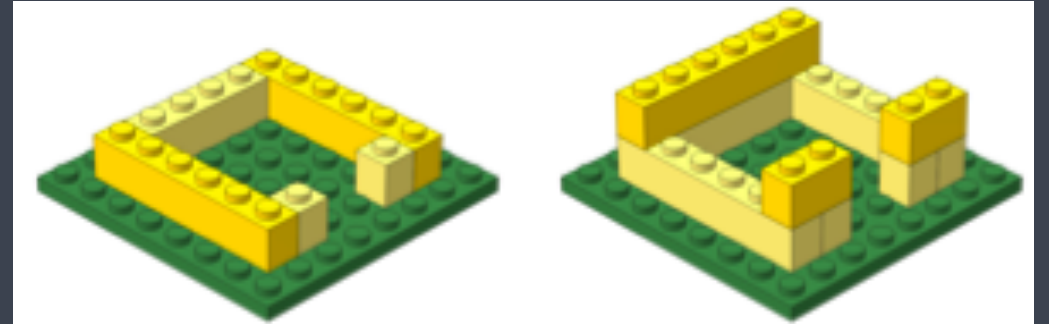
Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

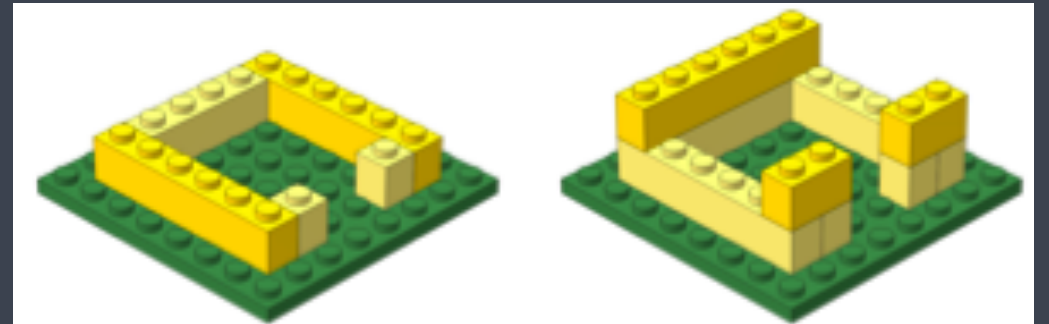
<https://tinyurl.com/hbc-shell>

# 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...



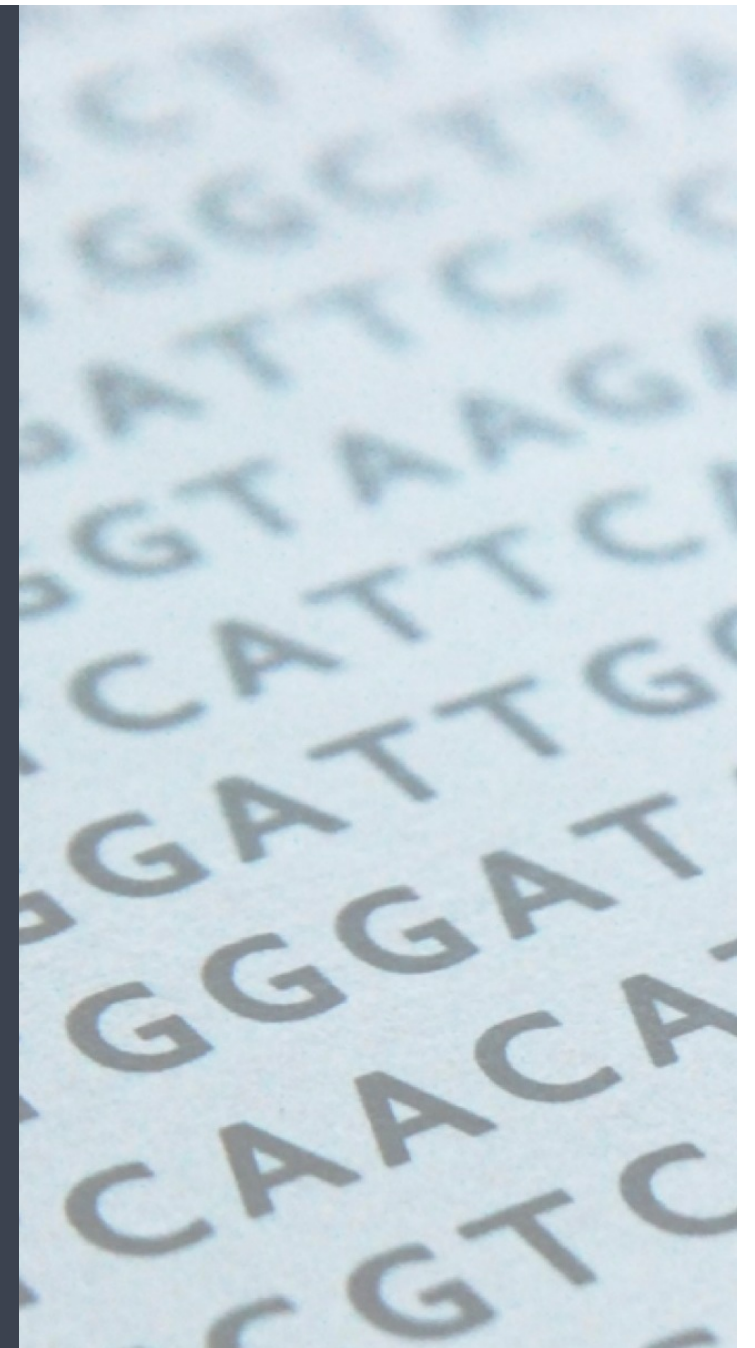
- ✓ Introduction to the command-line interface (shell, Unix, Linux)
  - Dealing with large data files
  - Performing bioinformatics analysis
    - Using tools
    - Accessing and using compute clusters
- ✓ R
  - Parsing and working with smaller results text files
  - Statistical analysis, e.g. differential 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](mailto:hbctraining@hsph.harvard.edu)

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Twitter

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# Thanks!

- Kathleen Keating and Andy Bergman from HMS-RC
- [Data Carpentry](#)

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