



# Introduction to the command-line interface (shell)

Harvard Chan Bioinformatics Core

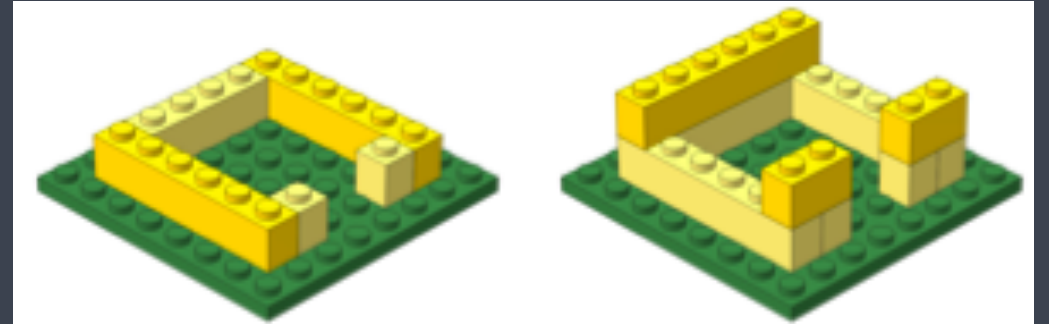
in collaboration with

HMS Research Computing

Jan 17, 2019

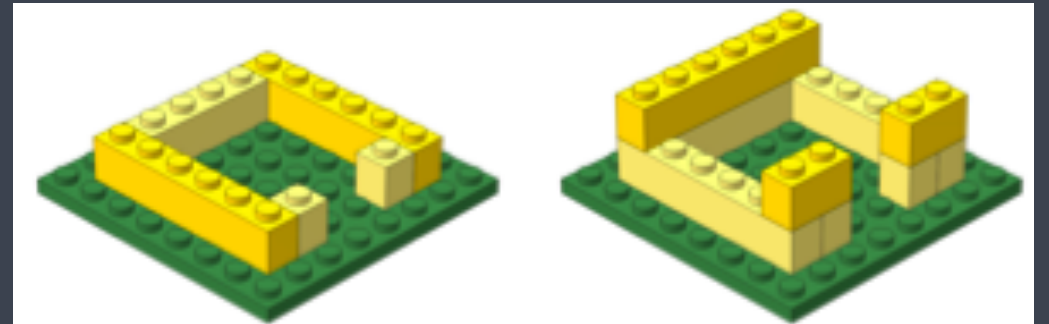
<https://tinyurl.com/hbc-shell>

# 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

## Spring 2019 Schedule

We are structuring the training schedule such that it gives interested researchers several opportunities to take the basic workshops.

Topic	Category	Date	Duration	Prerequisites
Introduction to the command-line interface (shell)	Basic	January 17th	1 day	None
Introduction to R	Basic	January 28th & 29th	1.5 days	None
Introduction to the command-line interface (shell)	Basic	February 13th	1 day	None
Introduction to (bulk) RNA-seq	Advanced	Late February	2 days	Intro to shell
Introduction to R	Basic	Early March	1.5 days	None
Introduction to differential gene expression analysis (bulk RNA-seq)	Advanced	Late March	2 days	Intro to R
Introduction to the command-line interface (shell)	Basic	Early April	1 day	None
Introduction to ChIP-seq analysis	Advanced	Late April	2 days	Intro to R + shell

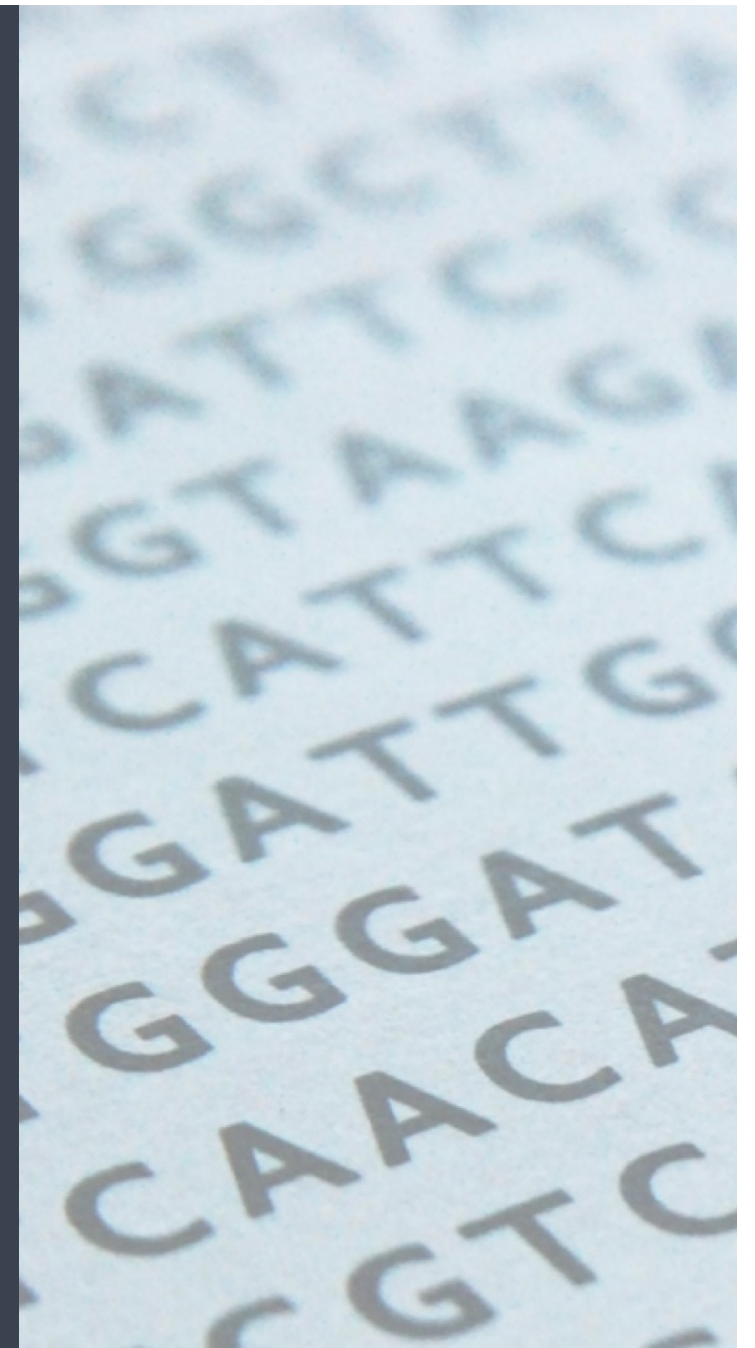
# Exit survey

<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



# 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)

*Consulting email:* [bioinformatics@hsph.harvard.edu](mailto:bioinformatics@hsph.harvard.edu)

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Twitter

[@bioinfocore](https://twitter.com/bioinfocore)

# Thanks!

- Kristina Holton and Andy Bergman from HMS-RC
- [Data Carpentry](#)

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