

# Introduction to the command-line interface (shell)

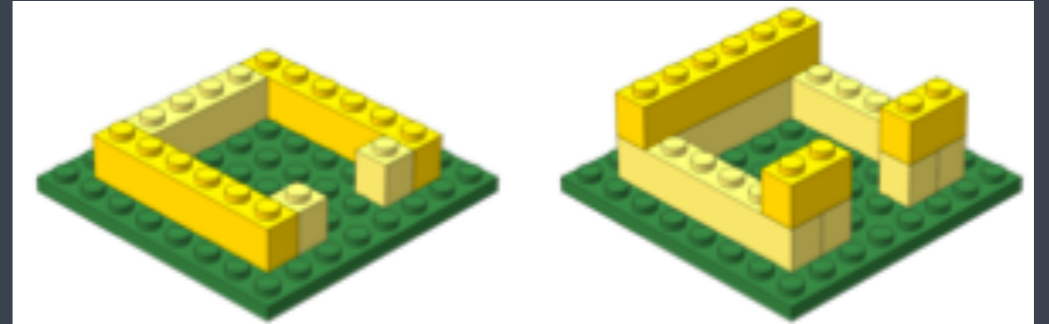
Harvard Chan Bioinformatics Core

in collaboration with

FAS Research Computing

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

# 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

# Exit survey

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

# 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/>

# Thanks!

- FAS-RC crew
  - Daniel Caunt
  - Maggie McFee
  - Raminder Singh
  - Muneeba Syed

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# 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)

*FAS-RC:* [create a ticket](#)

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