

Introduction to the command-line interface (shell)

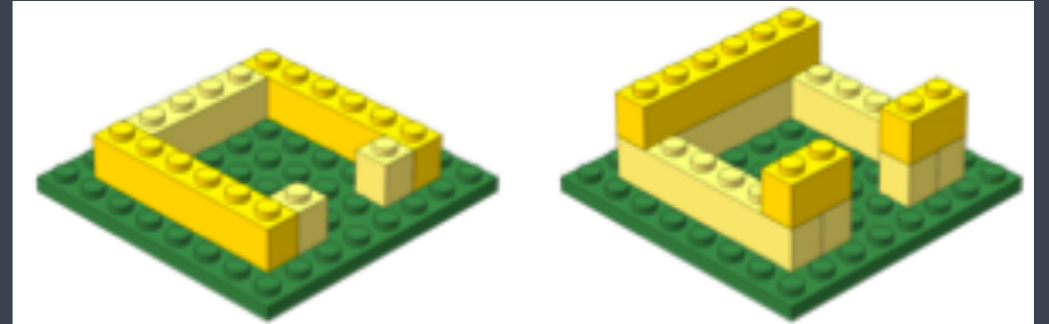
Harvard Chan Bioinformatics Core

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

Exit survey

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

Get an O2 account!

<https://rc.hms.harvard.edu/#cluster>

HPC Cluster Account

NOTE: for after hours emergency support please contact the IT service desk and let them know you have a research computing issue by calling (617) 432-2000 or e-mailing itservicedesk@hms.harvard.edu.

The O2 cluster is a shared high-performance computing environment serving a large research community with diverse research requirements and workflows, including dedicated hardware available for high-memory and GPU-intensive tasks. Tens of thousands of jobs run on the cluster every day, and we are constantly improving the job handling software and configuration to balance throughput between our many users.

Hundreds of HMS-affiliated researchers use RC's high-performance computing environment for big and small projects in next-gen sequencing analysis, molecular dynamics, mathematical modeling, image analysis, proteomics, and other areas. **Click the Account Request button below to get an account for O2.** For more information, please view the [O2 documentation](#).

[Account Request](#)

[O2 Slurm Intro](#)

[O2 Wiki](#)

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/>

Bioinformatics Community Networking Breakfast!

- *Free and open to the LMA community*
- *Food and seats are **first-come-first-served***
- *Last Wednesday of every month*

Date	Location
March 25th	HMS' Jeffrey Modell Center for Immunology, Room 100A
April 29th	HMS' Jeffrey Modell Center for Immunology, Room 100A
May 27th	HMS' Jeffrey Modell Center for Immunology, Room 100A
June 24th	HMS' Jeffrey Modell Center for Immunology, Room 100A

Upcoming short workshops

HBC's monthly short workshops

- Workshops on bioinformatics methods & related skills
- Once a month for 3 hours
- First-come-first-served, no registration required
- Free and open to everyone at Harvard University and its affiliates

Spring 2020 Schedule:

Topic	Date	Time	Location	Pre requisites
Introduction to R	January 15th	1 PM	HSPH Kresge G1	None
Introduction to tidyverse and Data Visualization with ggplot2	February 12th	1 PM	HSPH Kresge G1	Introduction to R
Gene Annotations and Functional Analysis of Gene Lists	March 18th	1 PM	HSPH Kresge G1	Introduction to R
Generating Data Analysis Reports with RMarkdown	April 15th	1 PM	HSPH Kresge G1	Introduction to R

Thanks!

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

These materials have been developed by members of the teaching team at the [Harvard Chan Bioinformatics Core \(HBC\)](#). These are open access materials distributed under the terms of the [Creative Commons Attribution license \(CC BY 4.0\)](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.



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): rhelp@hms.harvard.edu

Twitter

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