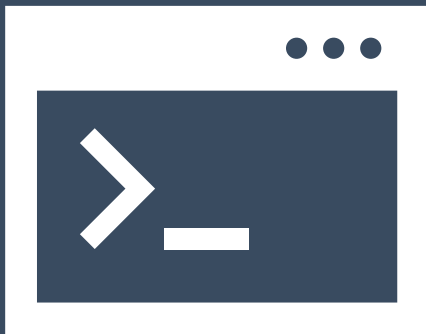


Introduction to the command-line interface (shell)

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



Harvard Chan Bioinformatics Core
in collaboration with
HMS Research Computing



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

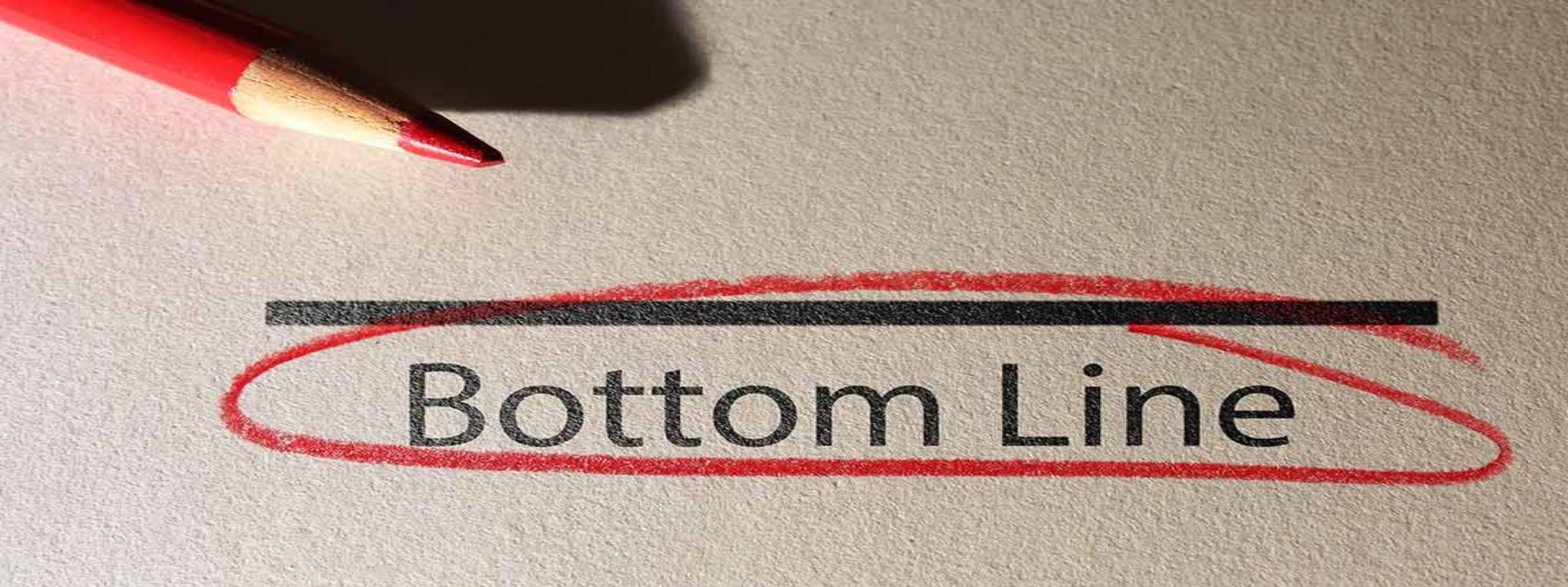


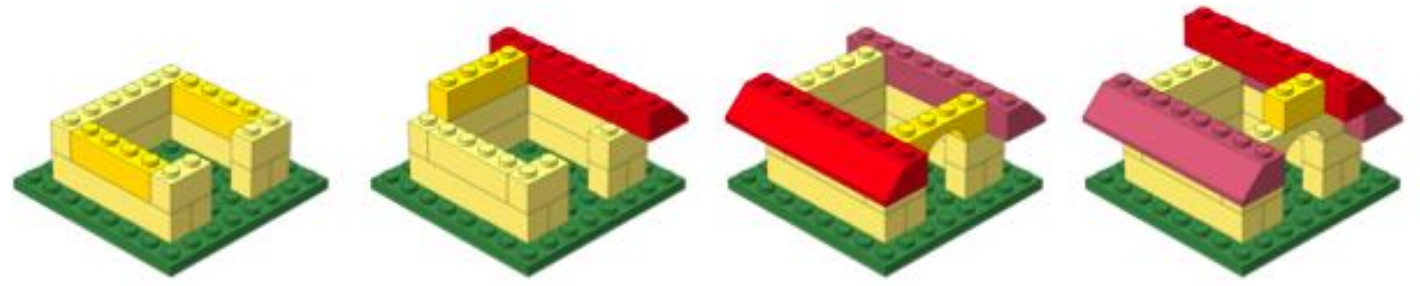
Image source: Balboa Capital Blog

If you plan to process raw high throughput sequencing data yourself, you will need to learn shell.

Exit survey

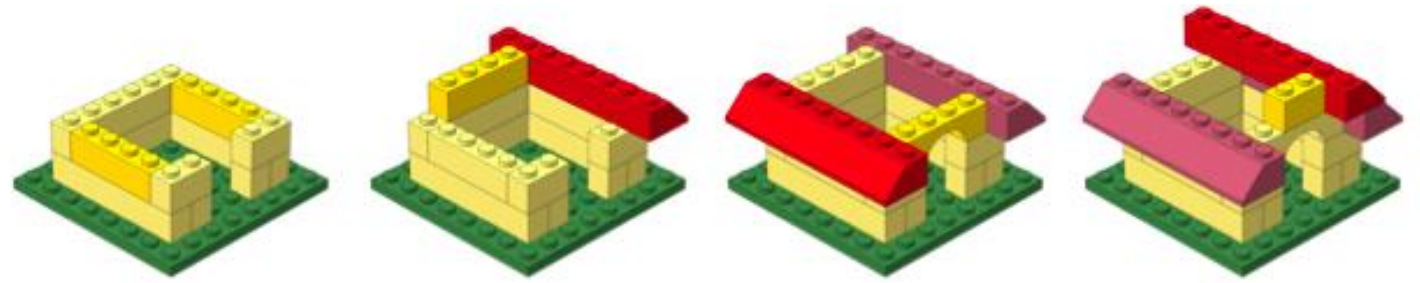
<https://tinyurl.com/hbc-shell-exit>

Keep building!



- ❖ Upcoming HBC advanced shell-based workshops:
 - ❖ Introduction to Variant Calling
 - ❖ September 17th , 20th, 24th and 27th (in-person)
 - ❖ Using paired tumor-normal samples to analyze variants
 - ❖ Introduction to R
 - ❖ October 8th, 11th, 15th and 18th
 - ❖ Basics of programming and figure creation in R

Keep building!



Topic	Pre-requisites	Date/Time	Time	Registration
RShiny	R basics	9/18/24	1 – 4pm	Register!

<https://bioinformatics.sph.harvard.edu/current-bioinformatics-topics-workshops>

Get an O2 account!

[Home](#) > [Service Catalog](#)

Search IT services and kn

O2 Cluster Account

Description

What does it do?

Get an account on O2, the HMS High Performance Compute cluster

Available To

Who is eligible?

Any HMS or HMS-affiliated researcher who has an HMS eCommons account.

Cost

What does it cost?

There is no cost to labs whose PI has a primary or secondary faculty appointment in an HMS Quad department.

If the PI of your lab does not have a primary or secondary faculty appointment in an HMS Quad department, cluster usage will be charged for beginning later in 2021. Please see the following page for current details about rates: <https://it.hms.harvard.edu/rc/core/rates>.

Support

Please fill out the [online help request form](#), or email rchelp@hms.harvard.edu.

How to Access

How do I get it?

Two-factor authentication is required to request an account on O2, as well as for O2 logins once your account is created. Harvard University uses a mobile app called Duo that makes the process quick and easy. Even if you already use Duo for HarvardKey, you will still need to setup a Duo profile for HMS.

- [Setup HMS two-factor Authentication \(HMS Duo Mobile\)](#)
- [Reactivate or Reconnect HMS two-factor Authentication \(HMS Duo Mobile\)](#)

Once you have Duo set up, Click the "Get Service" link to login and complete the request form.

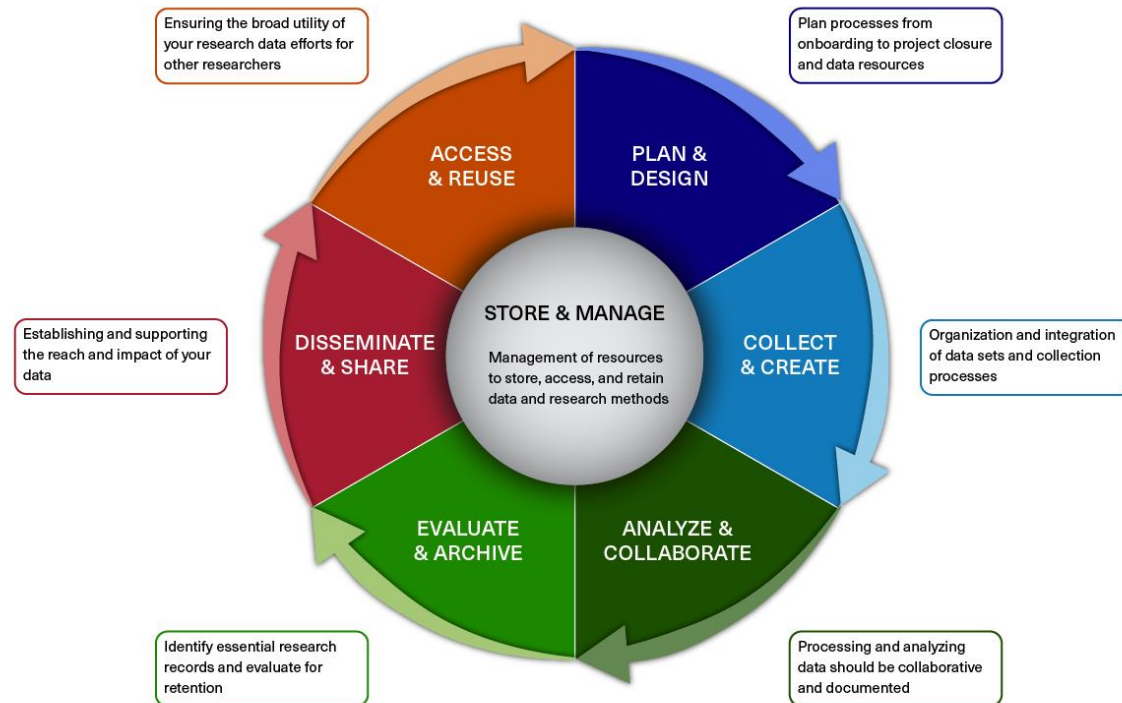
Get this service

Learn more

Don't see what you're looking for?

Research Data Management (RDM)

BIOMEDICAL RESEARCH DATA LIFECYCLE



Date	Time	Event	Location
Sep 11	11am	<u>Preparing for Qualitative Data Analysis</u>	Zoom
Sep 12	12:30pm	Zotero Vs. EndNote Smackdown	Countway Library Classroom L2-025
Sep 13	9am	HKS Data Carpentry: OpenRefine and R	HKS Library, Wexner 434 Ab
Sep 18	12pm	Data Discussions: Let's Make Research Data FAIR	Zoom
Sep 24	1pm	Better Research I: Managing Research Data Efficiently	Countway Library Classroom 102 & 103
Sep 26	10am	Research Management: Project and Lab Onboarding	Zoom

Better RDM practice benefits you

- ❖ **HMS Data Management LMA**

- ❖ **Webpage:** <https://datamanagement.hms.harvard.edu>

- ❖ [Sign up](#) for quarterly email updates

- ❖ **Harvard-wide Research data Management**

- ❖ <https://researchdatamanagement.harvard.edu/>

Join us for HBC Community Breakfast!

- ❖ An opportunity to get to know others in the community
- ❖ Free food and beverages
- ❖ Great conversations



More Info:

<http://bioinformatics.sph.harvard.edu/breakfast/>

Thanks!

- ❖ Kathleen Chappell 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.

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