**Introduction to Command-Line Interface** *(Shell, Bash, Unix, Linux)*

Next workshop dates:

- **Tuesday, November 3rd**: 9:30 AM - 12 PM
- **Friday, November 6th**: 9:30 AM - 12 PM
- **Tuesday, November 10th**: 9:30 AM - 12 PM

*Note:* Registration will open about 2 weeks prior to the workshop dates, and the dates/times above may be updated at that time.

!!NEW!! The format of this workshop has changed. *Instruction will be mostly learner-centric requiring workshop participants to spend between 2-3 hours on reading and exercises from selected lessons before the workshop sessions. Online classes will be focused on exercises and discussion.* Please make sure you take this into account when you sign up for the workshop!

**Description:**
Access to tools and computational resources for large-scale data analysis often require knowledge of the command-line interface (also referred to as Unix or Linux or bash or shell). In this **3-day hands-on workshop** participants will learn the following:

- basic shell commands for navigating the file system, exploring file contents, performing basic operations, such as moving, copying, and renaming
- how to write shell scripts and use "for" loops for efficiently running the same commands on multiple files
- how to use HMS-RC's O2 cluster for high-performance computing (HPC)

Together, this knowledge is critical for researchers looking to improve efficiency when performing computational tasks and it forms the foundation needed to analyze high-throughput sequencing data.

**Prerequisites?**
This is one of our **basic** workshops, and has **NO prerequisites** and no prior programming experience is required.

This workshop is a prerequisite for **advanced** workshops introducing the analysis of RNA-seq and ChIP-seq data.

**Who should attend?**
Eligible* Harvard researchers who:

1. want to learn how and why to use the command line interface (Unix/Linux Shell) to efficiently manage and analyze data
2. want to use local clusters/high-performance computing environments for analyzing data (e.g. HMS-RC's O2 cluster, or FAS-RC's Odyssey cluster)
3. are interested in taking an advanced workshop on analysis of sequencing data within the next 6 - 8 months

**Cost and Registration:**
There is a **non-refundable and non-transferable** $25 registration fee for this workshop.

We will be accepting 35-40 participants on a first-come, first-served basis:

- If you are one of the first 35-40 **eligible** registrants, you will receive an email within 1 week with a link to pay the (non-refundable & non-transferable) $25 registration fee.
- If you are **not** among the first 35-40 **eligible** registrants, you will be added to the waitlist and notified when we open registration for the next iteration of this workshop.

*Note:* You will not have a reserved seat for this workshop until you pay the registration fee. Please make sure you pay within the time stated in that email, else you will lose your spot to someone on the waitlist.

**Eligibility requirements:**

* To be eligible to attend this workshop you should fulfill **at least one** of the following criteria:

- Harvard Medical School researcher in a lab on the Quad, with grants administered by HMS
- Graduate student at the Harvard Medical School
- Researcher affiliated with the Dana-Farber / Harvard Cancer Center (DF/HCC).
- Harvard researchers whose PIs are associated with the HSCI as Principal or Affiliated faculty

If you are unsure of your eligibility, please register anyway and we will get back to you.
Registration is closed.

(Please check the eligibility requirements prior to registering)

Questions?

Please contact us at hbctraining@hsph.harvard.edu with any questions.