

Harvard Chan Bioinformatics Core

presents:

Introduction to the command-line interface (Unix/Linux/shell/bash)

Are you planning to analyze high-throughput sequencing data?

Are you looking to perform computational tasks more efficiently?

*Do you want to use local clusters/high-performance computing environments
for your data analysis?*

If so, this 1-day workshop is for you!

During this hands-on workshop, participants will learn:

- basic shell commands (file system navigation, moving/copying/searching files, etc.)
- 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

No prior programming experience required!

Please check link below for eligibility requirements.

*This **basic** workshop is a prerequisite for HBC's upcoming **advanced** workshops on NGS data analysis*

March 6th, 2019
(9am - 5pm)

More information & registration link at <https://tinyurl.com/intro-to-shell>

Registration fee: \$35

Workshop Location: **Longwood Medical Area**

*Sponsored by Harvard Medical School's **Tools and Technology Committee** (TnT) &
the **Harvard Stem Cell Institute** (HSCI)*