

# 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 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*

**November 3rd, 6th & 10th 2020  
(9:30 AM - 12 PM all days)**

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

**Registration fee: \$25**

Workshop Location: **Online**

*Sponsored by Harvard Medical School Foundry, Dana-Farber/Harvard Cancer Center  
& the Harvard Stem Cell Institute (HSCI)*