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!

This **basic** workshop is a prerequisite for some HBC advanced workshops (ie. **Intro to Variant calling**, etc)

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 the HMS-RC cluster for high-performance computing (HPC)

No prior programming experience required!
Please check link below for eligibility requirements.

May 17th, 21st, and 24th 2024
(9:30am - 12pm each day)

More information & registration link at https://tinyurl.com/HBC-Shell-Intro
Registration fee: $50

Workshop Location: **In-person (Longwood Medical Area)**