

Harvard Chan Bioinformatics Core

presents:

Introduction to ChIP-seq analysis using high-performance computing

For *Harvard* researchers affiliated with
Harvard Medical School labs on the Quad or the *Harvard Stem Cell Institute*

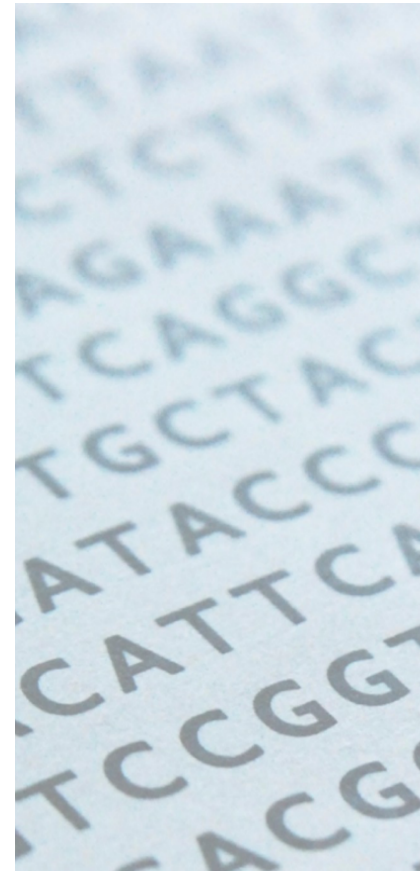
Are you planning to generate and/or analyze ChIP-seq data?

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

This **3-day hands-on** workshop will instruct participants on how to efficiently analyze sequencing data using the command-line interface and high-performance computing (HPC), with a focus on ChIP-seq data analysis. This workshop will introduce:

- UNIX/Linux shell (bash)
- ChIP-seq data analysis workflow (QC, peak calling, visualization)
- O2 compute cluster (HMS-RC)

Prior sequence analysis or command-line experience not required



July 30th - August 1st, 2018
(9am - 5pm)

More information & registration link at <https://tinyurl.com/chipseq-hpc-2018>

Registration fee: \$75

Workshop Location: Longwood Medical Area

Sponsored by: *The Harvard Medical School Tools and Technology Committee (TnT)*
& *The Harvard Stem Cell Institute (HSCI)*