



# Introduction to ChIP-seq using High-Performance Computing (HPC)

Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

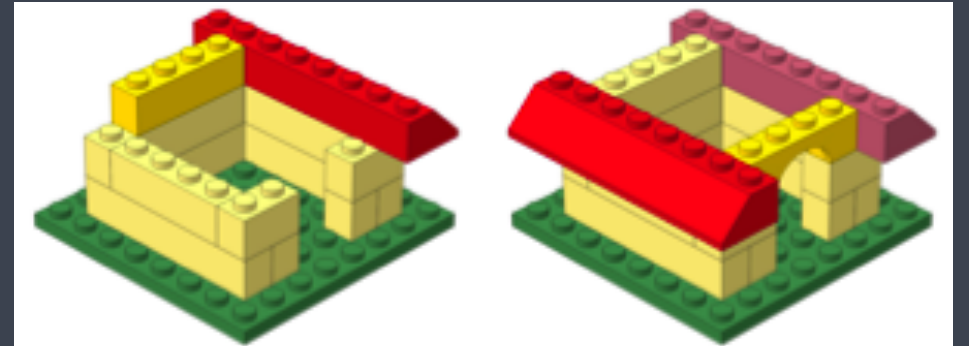
<https://tinyurl.com/hbc-intro-to-chipseq>

# Learning Objectives



- ✓ Learn what a “shell” is and become comfortable with the command line interface
  - Find your way around a filesystem using the command line
  - Work with small and large data files
  - Become more efficient when performing repetitive tasks
- ✓ Understand what a computational cluster is and why we need it
  - Independently access the O2 cluster
  - Perform analysis using the cluster (run programs, pipelines, etc.)

# Learning Objectives



- ✓ Describe best practices for designing an ChIP-seq experiment
- ✓ Describe steps in a typical ChIP-seq analysis workflow
- ✓ Use HMS-RC's O2 compute cluster to efficiently run the ChIP-seq workflow from sequence reads to peak calls, including QC and visualization.

Some steps in the ChIP-seq workflow require a working knowledge of R, and we won't be covering these in much detail.

Survey...

<https://tinyurl.com/chipseq-survey>

# Thanks!

- Shannan Ho Sui (HBC)
- Andy Bergman (HMS-RC)
- Kristina Holton (HMS-RC)
- [Data Carpentry](#)

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# Talk to us early

Involvement in study design to optimize experiments





# Questions?

HBC training team: [hbctraining@hsph.harvard.edu](mailto:hbctraining@hsph.harvard.edu)

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O2 (HMS-RC): [rhelp@hms.harvard.edu](mailto:rhelp@hms.harvard.edu)



# More Information..

HBC training materials: <https://hbctraining.github.io/main>

HBC website: <http://bioinformatics.sph.harvard.edu>

O2 Wiki (HMS-RC): <https://wiki.rc.hms.harvard.edu/display/O2>

## Twitter

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