

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

Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

https://tinyurl.com/hbc-chipseq-schedule

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.



https://tinyurl.com/chipseq-exit-survey

Thanks!

- Shannan Ho Sui (HBC)
- Andy Bergman (HMS-RC)
- Kathleen Keating (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 HBC consulting: bioinformatics@hsph.harvard.edu O2 (HMS-RC): rchelp@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/02

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