



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

Harvard Chan Bioinformatics Core

in collaboration with

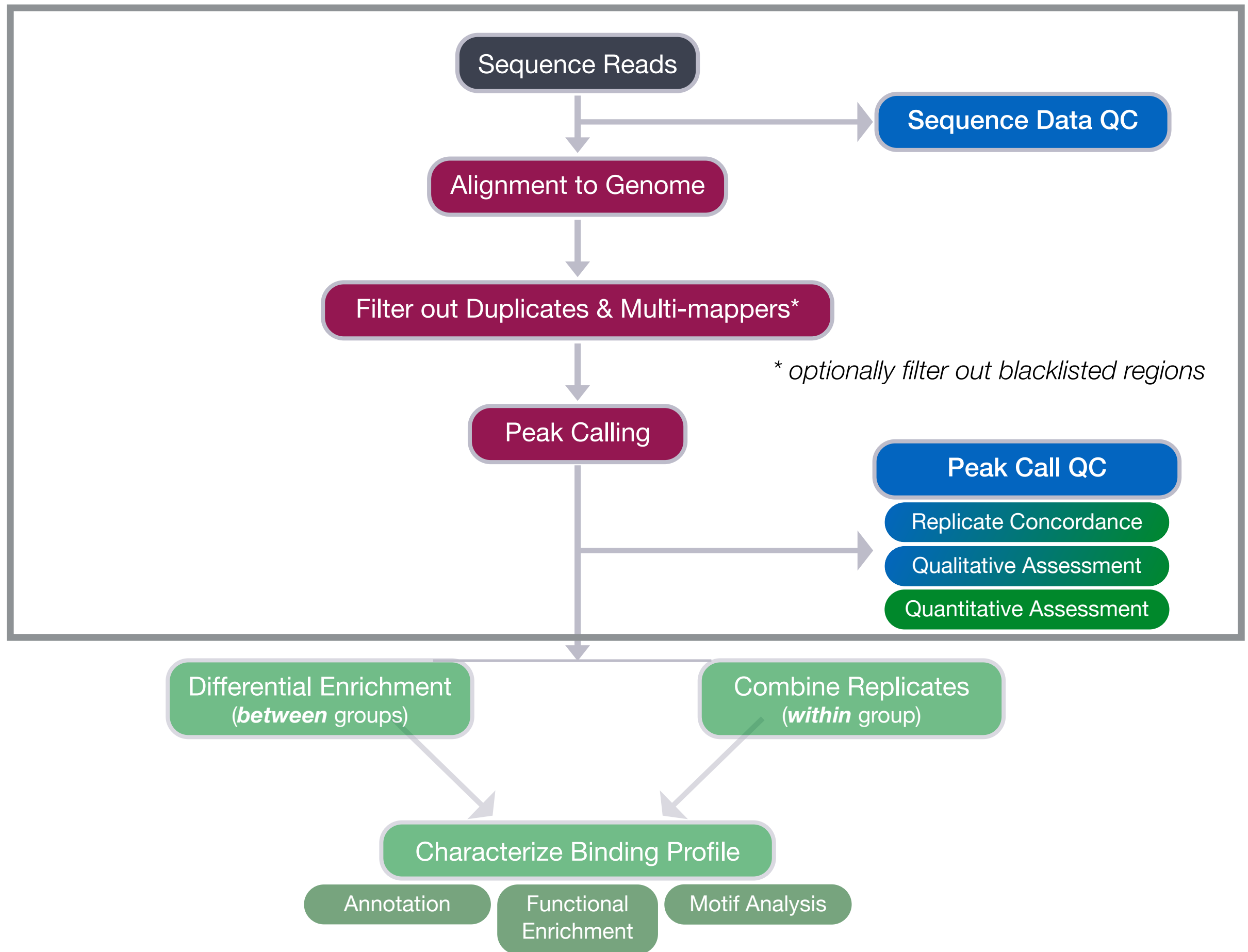
HMS Research Computing

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

# Learning Objectives

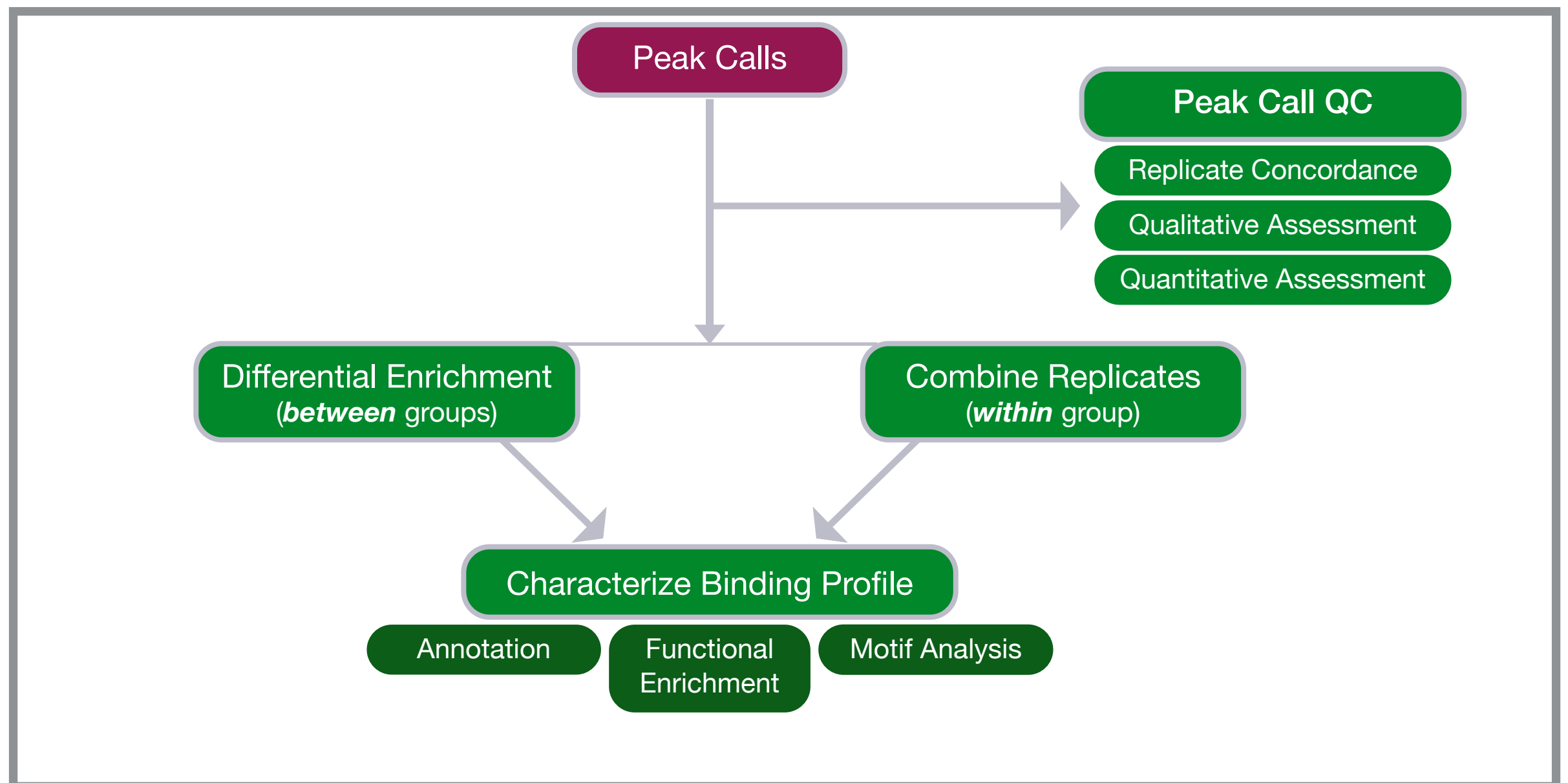


- ✓ Describe best practices for designing a good ChIP-seq experiment
- ✓ Describe steps in an ChIP-seq analysis workflow (from sequence data to peak calls)
- ✓ Learn how to handle various file formats encountered with ChIP-seq analysis
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps



# Introduction to ChIP-seq Part II

## using R



We would love your feedback!

<https://tinyurl.com/chipseq-part1-exitsurvey>

# Thanks!

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

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# Questions?

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

HBC consulting: [bioinformatics@hsph.harvard.edu](mailto:bioinformatics@hsph.harvard.edu)

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





# Talk to us early

Involvement in study design to optimize experiments





# 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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