

Introduction to R

Harvard Chan Bioinformatics Core

<https://tinyurl.com/intro-to-r-1-5>

Sponsored by HMS (TnT) and HSCI

Learning Objectives



- ✓ Comfortably use RStudio (a graphical interface for R)
- ✓ Fluently interact with R using RStudio
- ✓ Become familiar with R syntax
- ✓ Understand data structures in R
- ✓ Inspect and manipulate data structures
- ✓ Install packages and use functions in R
- ✓ Visualize data using *ggplot2*

Resources

[Resources for RNA-Seq, R, general bioinformatics](#)

[Asking for help with R](#)

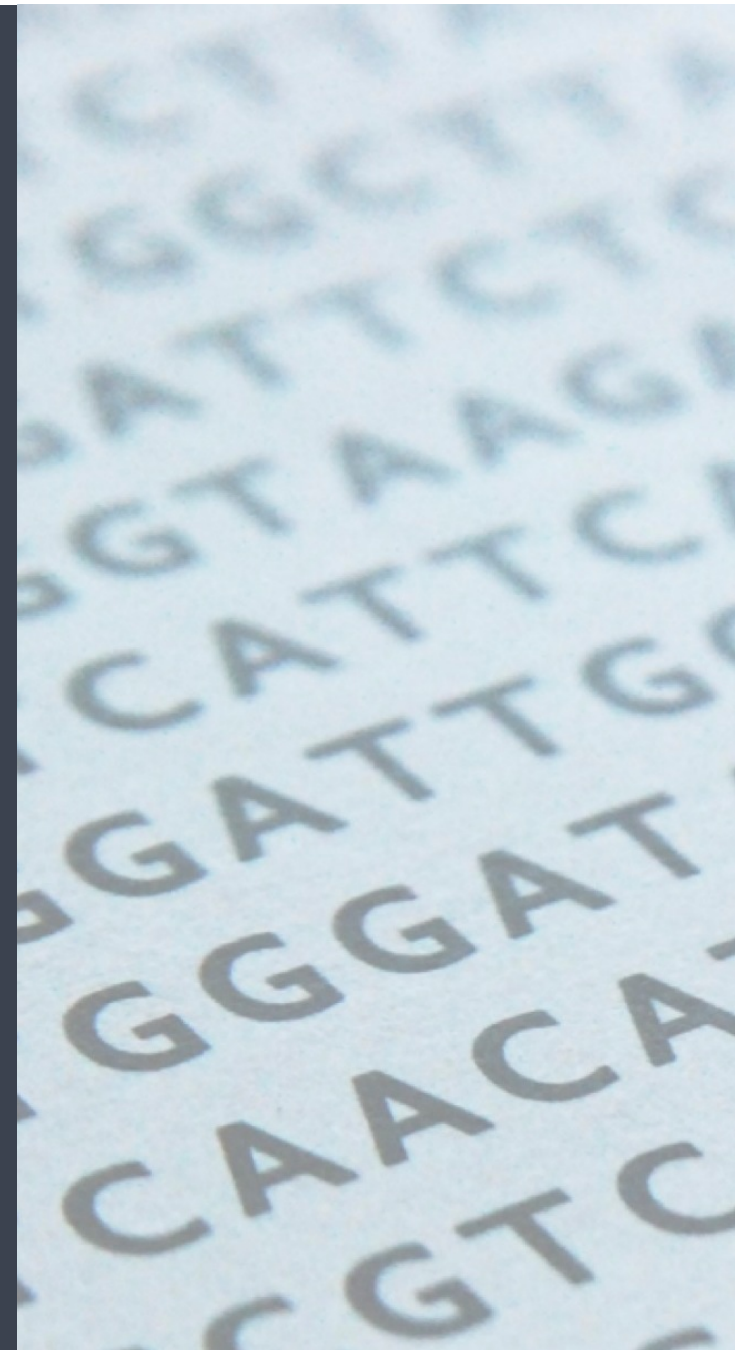
[ggplot2 cheatsheet](#)

Exit survey

<http://tinyurl.com/HMS-HSCI-introR-exit-survey>

Consulting

- RNA-seq: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support



Contact us!

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

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

HBC workshop listserv: <https://tinyurl.com/hbc-mailing-list>

Training email: hbctraining@hsph.harvard.edu

Consulting email: bioinformatics@hsph.harvard.edu

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