

Introduction to R and Differential Expression Analysis

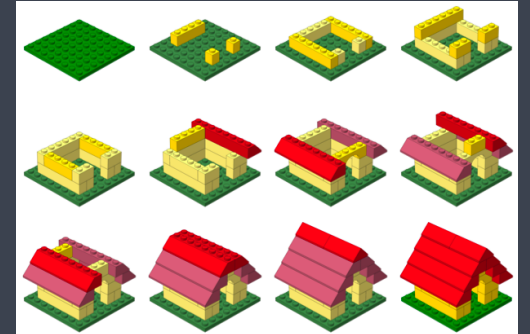
Harvard Chan Bioinformatics Core

February 26th - 28th, 2018

<https://hbctraining.github.io/Intro-to-R-with-DGE/>

Sponsored by HMS (TnT) and HSCI

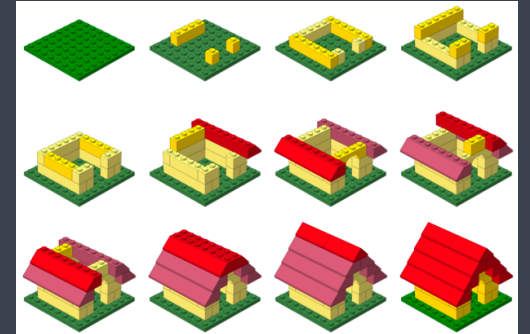
Workshop Scope (1/2)



R basics

- ✓ Become comfortable with 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 simple and complex plotting methods

Workshop Scope (2/2)



Differential Gene Expression analysis

- ✓ Understand the considerations for performing statistical analysis on RNA-seq data
- ✓ Start with gene counts (after alignment and counting)
- ✓ Perform QC on count data
- ✓ Use DESeq2 to perform differential expression analysis on the count data and obtain a list of significantly different genes
- ✓ Visualization of differentially expressed genes

Resources

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

[Asking for help with R](#)

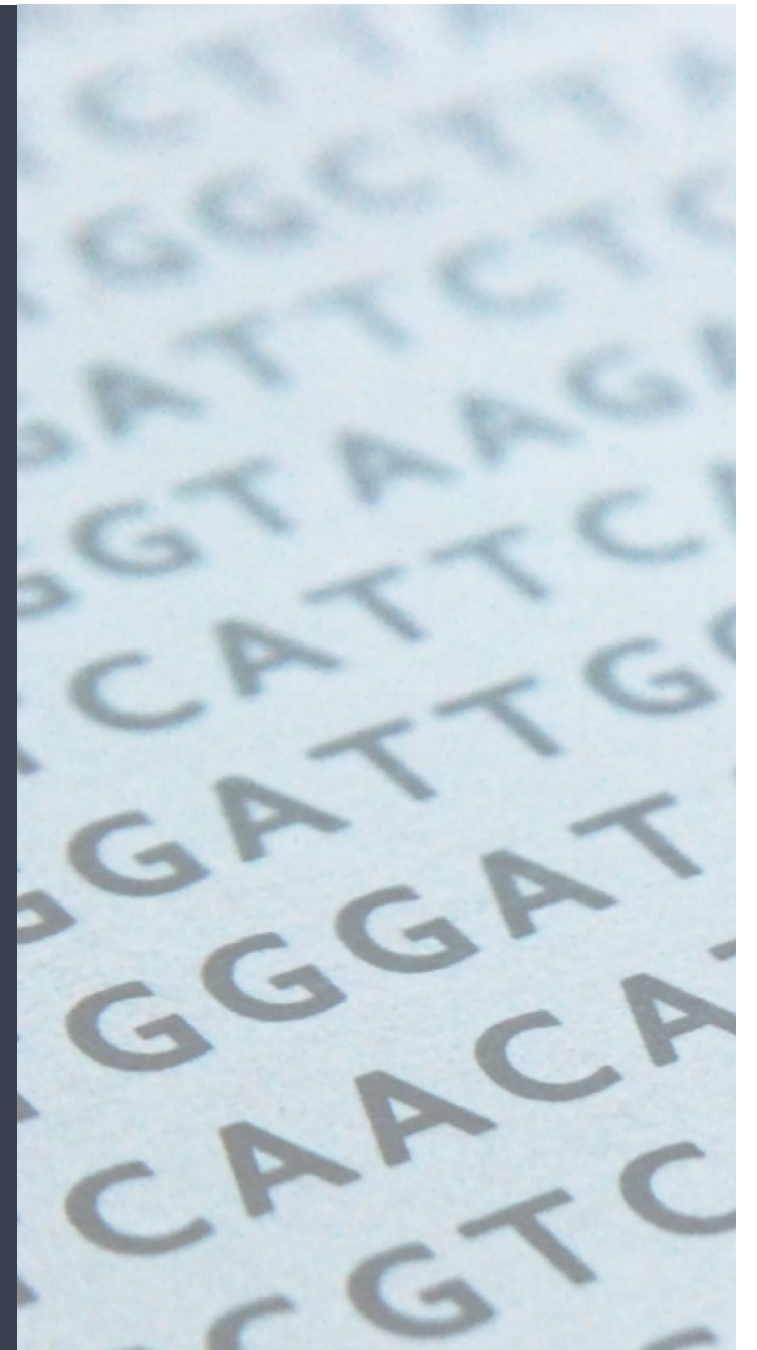
[ggplot2 cheatsheet](#)

Exit survey

<https://tinyurl.com/introR-DGE-exit-survey>

Consulting

- RNA-seq, small RNA-seq and ChIP-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- Quality assurance and 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>

Training email: hbctraining@hsph.harvard.edu

Consulting email: bioinformatics@hsph.harvard.edu

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