Genotype differences in average gene expression

Introduction to R and Differential Expression Analysis

Harvard Chan Bioinformatics Core

https://tinyurl.com/PQG-schedule

Workshop Scope (1/2)
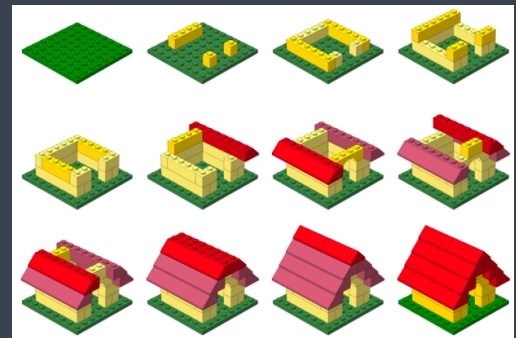
R basics

- ✓ 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)
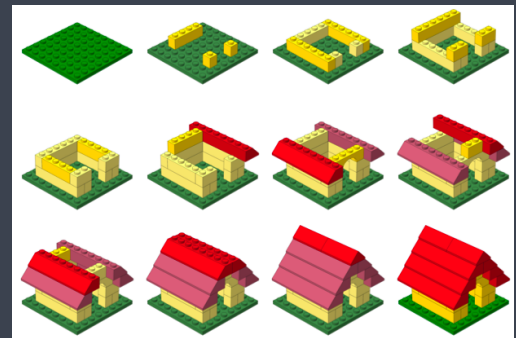
Differential Gene Expression analysis

✓ 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

✓ Functional analysis of gene lists (getting to the biology)

Resources

Resources for RNA-Seq, R, general bioinformatics

Asking for help with R

ggplot2 cheatsheet

Exit survey

https://tinyurl.com/PQG-ExitSurvey

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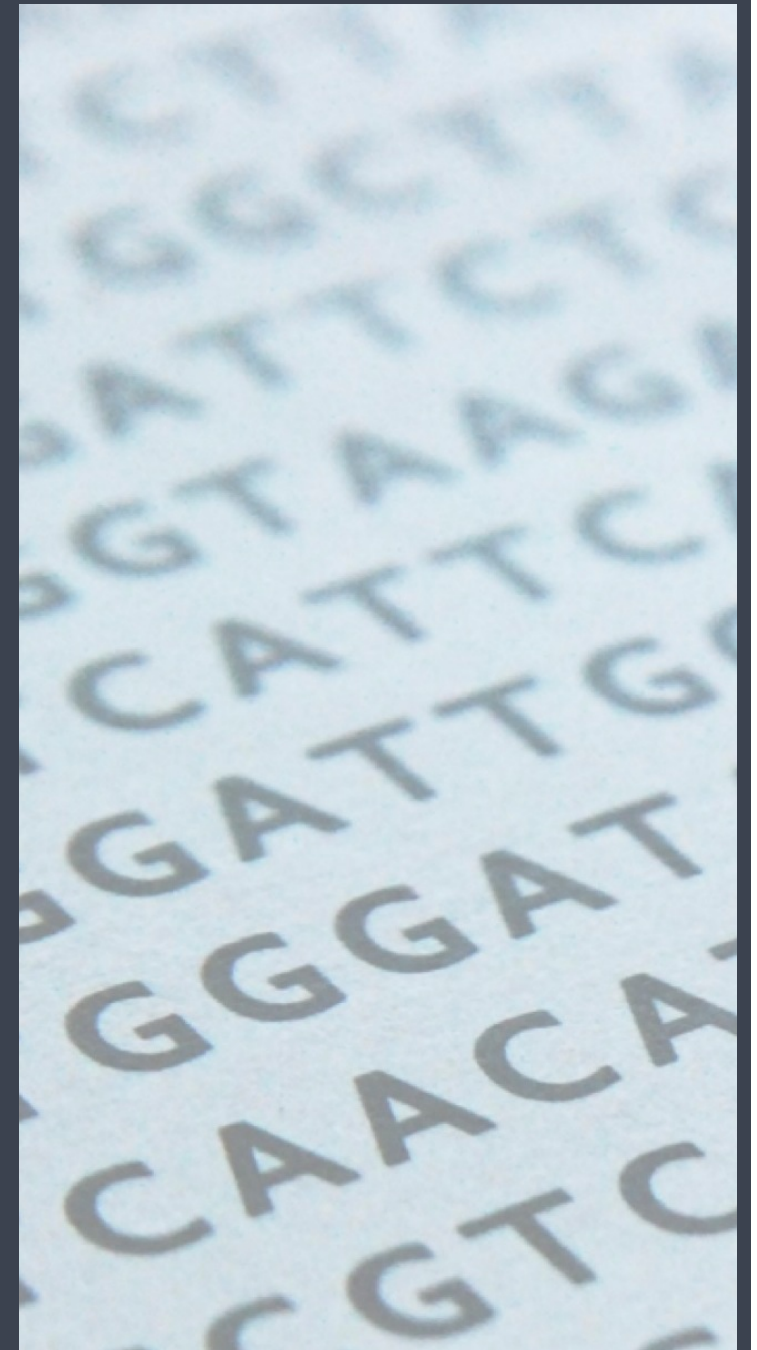
HBC training materials: http://hbctraining.github.io/main

Training email: hbctraining@hsph.harvard.edu

Consulting email: bioinformatics@hsph.harvard.edu

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