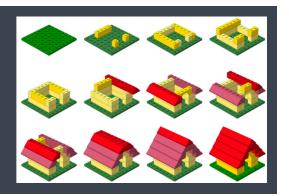# Introduction to Differential Gene Expression Analysis

Harvard Chan Bioinformatics Core

https://tinyurl.com/hbc-intro-to-dge

Sponsored by HMS (TnT) and HSCI

Workshop Scope

✓ 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

✓ Visualize results of the analysis

✓ Perform functional analysis on the lists of differentially expressed genes

Resources

- [All workshop materials](#)

- [2-3 hour workshops](#)

- [DESeq2 vignette](#)

- [More about color palettes in R](#)

- [Multiple plots in a single figure using gridExtra](#)

- [R for Data Science](#)

- Tidyverse lessons from HBC: [here](#) & [here](#)

Exit survey

http://tinyurl.com/intro-to-dge-exit

Bioinformatics Community Networking Breakfast!

- ***Free and open*** *to the LMA community*

- *Food and seats are* ***first-come-first-served***

- ***Last Wednesday*** *of every month*

<u>Date</u>**:** October 30th, 2019

<u>Time</u>**:** 9:00 to 10:30 am

<u>Venue</u>**:** Modell 100A (Armenise)

Fred S. Rosen Lecture Hall

Contact us!

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

Training email: hbctraining@hsph.harvard.edu

Consulting email: bioinformatics@hsph.harvard.edu

Twitter

@bioinfocore