

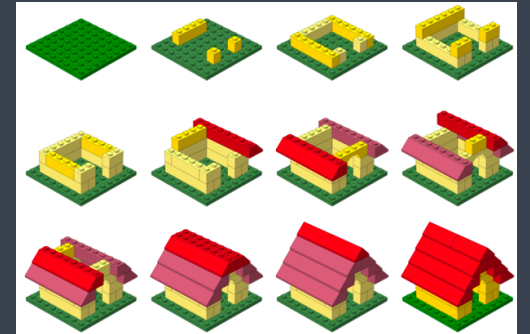


# Introduction to Differential Gene Expression Analysis

Harvard Chan Bioinformatics Core

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

# 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](#)

# 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*

Date: **August 28<sup>th</sup>, 2019**

Time: **9:00 to 10:30 am**

Venue: **Modell 100A (Armenise)**

**Fred S. Rosen Lecture Hall**



# Contact us!

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

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