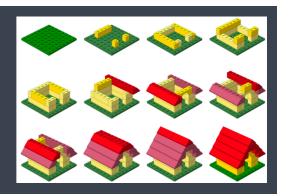# Introduction to Differential Gene Expression Analysis

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

Free RMarkdown workshop tomorrow!

https://hbctraining.github.io/Training-modules/Rmarkdown/

Reproducible research is as important for computational analysis as it is at the bench. Integrating your R data analyses into a report format allows for easy retrieval of the packages/versions and code used to generate your results and figures. It allows for efficient communication of your results with your collaborators. The **knitr** R package allows for the easy generation of professional reports for any R analysis, while allowing for customization and easy revision. In this 3-hour workshop, we will cover the simple RMarkdown syntax and explore options for customizing your reports.

Learning Objectives

- **Understand Rmarkdown syntax and available features:** Exploring the syntax of the Rmarkdown language and different available features.
- **Utilize `knitr` for report generation:** Practicing with `knitr` and different `knitr` options for customizing reports.

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4/3/2019

1 PM - 3:30 PM

Kresge G3 (HSPH)

Exit survey

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

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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