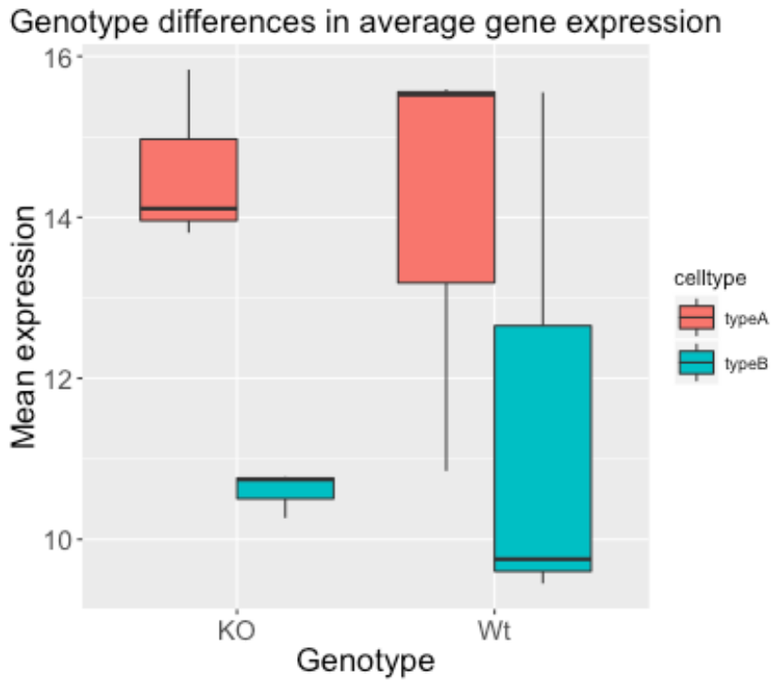
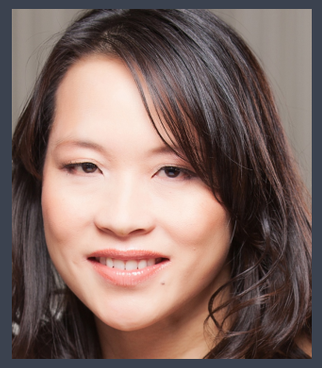


Introduction to R and Differential Expression Analysis

Harvard Chan Bioinformatics Core

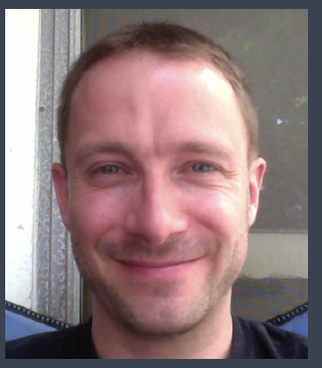
https://hbctraining.github.io/Intro-to-R-with-DGE/



Shannan Ho Sui

John Hutchinson

Brad Chapman



Rory Kirchner

Meeta Mistry

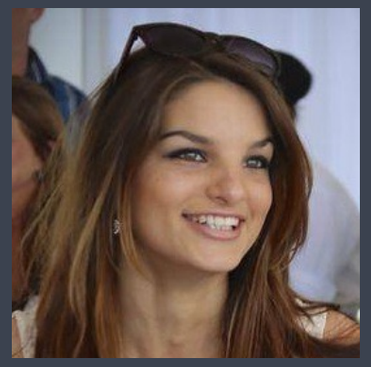
Radhika Khetani

Mary Piper

Lorena Pantano

Michael Steinbaugh

Victor Barrera



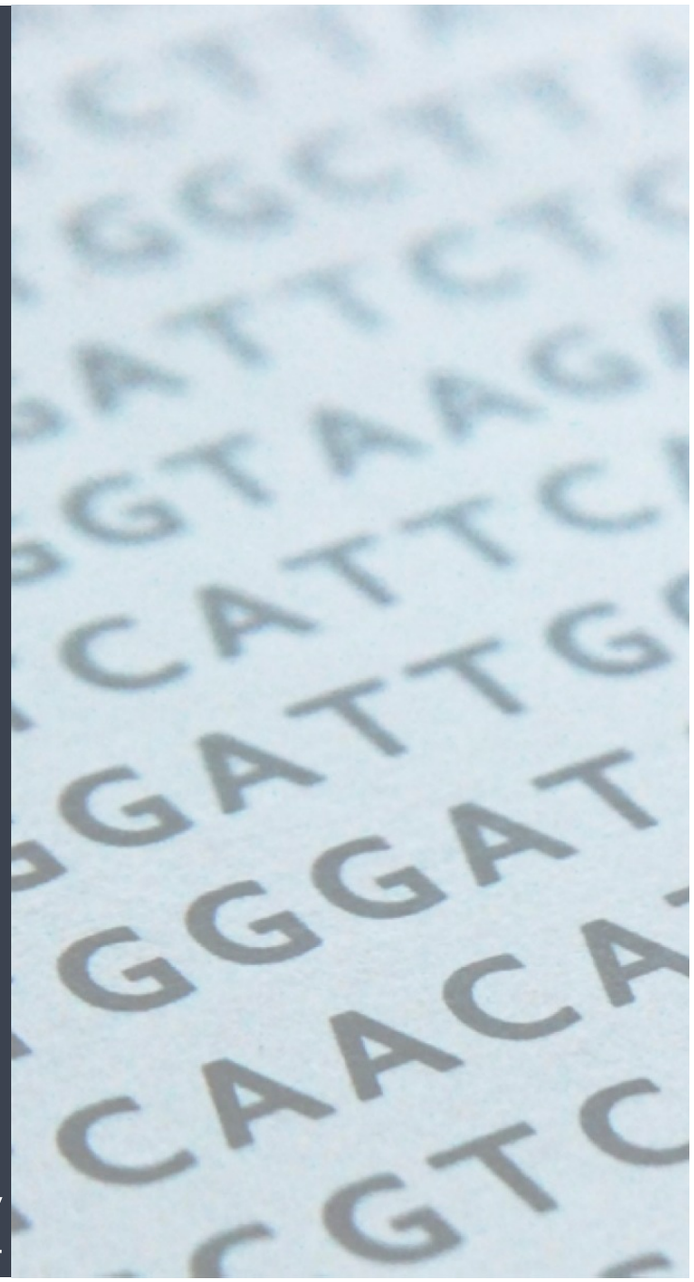
Kayleigh Rutherford

Peter Kraft

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

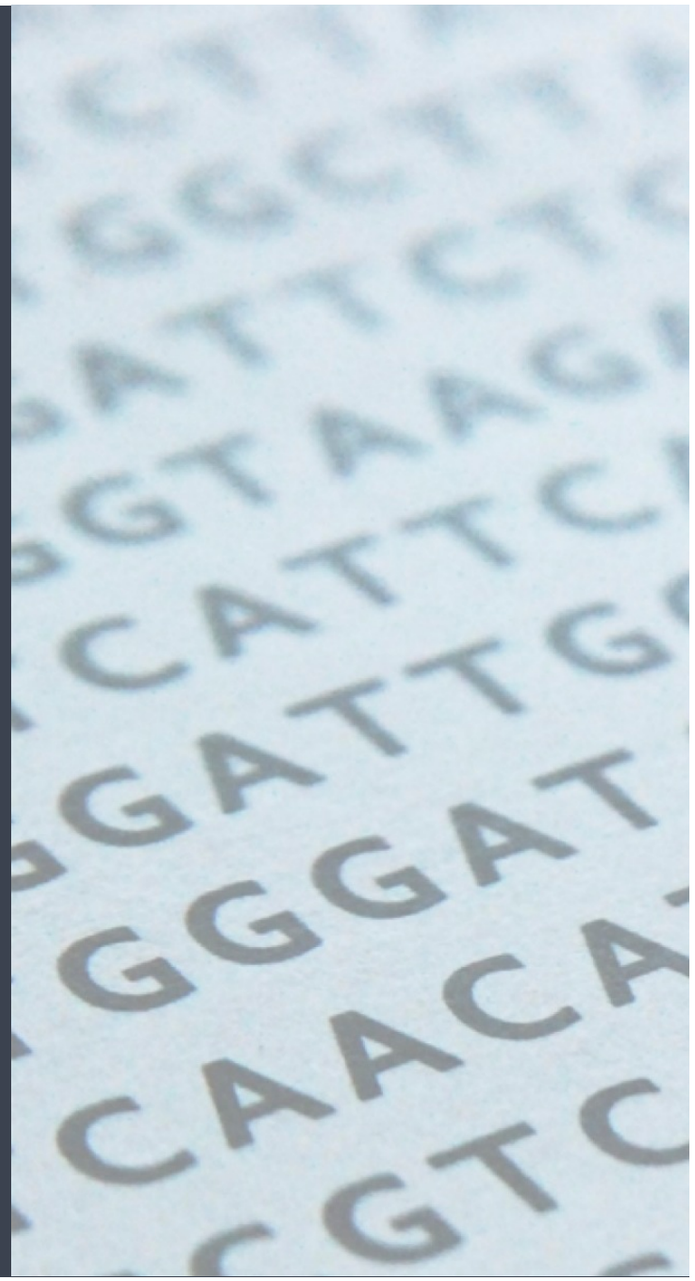
http://bioinformatics.sph.harvard.edu/



Training

- Short workshops on introductory, intermediate and advanced topics related to NGS data analysis
- In-depth course - September 5th -October 11th
  http://tinyurl.com/ngs-course-info-2018
- Monthly, 2-3 hour, hands-on and free workshops on “Current Topics in Bioinformatics”

http://bioinformatics.sph.harvard.edu/training/#upcoming-workshopscourses



HARVARD T.H. CHAN SCHOOL OF PUBLIC HEALTH

HSCI HARVARD STEM CELL INSTITUTE

HARVARD CATALYST
THE HARVARD CLINICAL AND TRANSLATIONAL SCIENCE CENTER

HARVARD MEDICAL SCHOOL

NIEHS / CFAR Bioinformatics Core

Center for Stem Cell Bioinformatics

Harvard Catalyst Bioinformatics Consulting

HMS Tools & Technology

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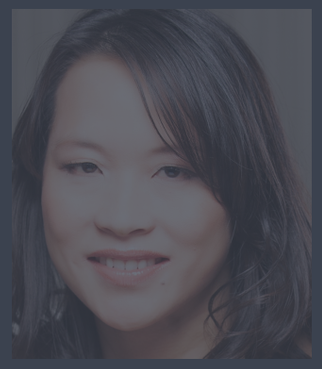
Introductions!



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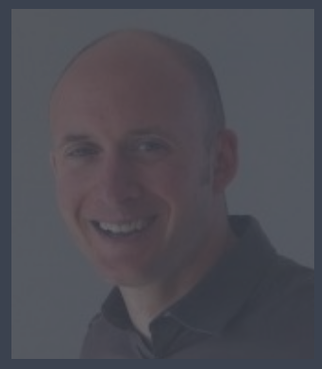
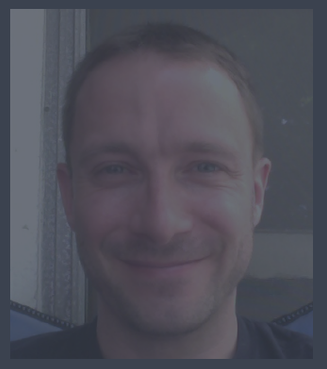


Brad Chapman



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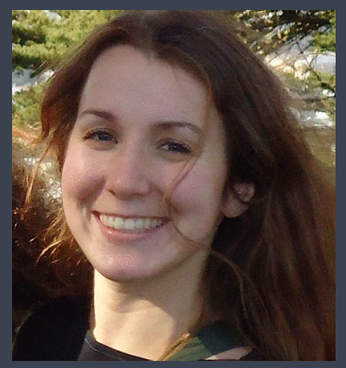
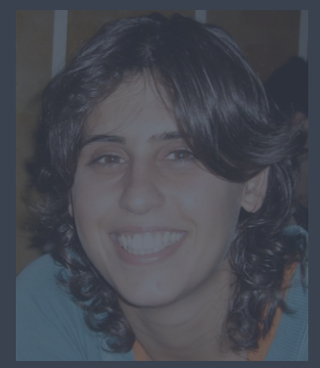


Mary Piper



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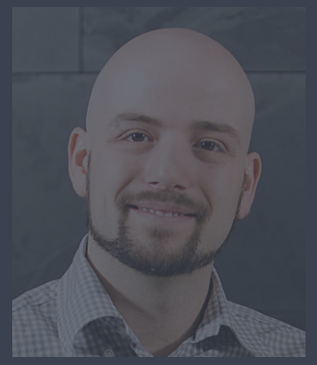
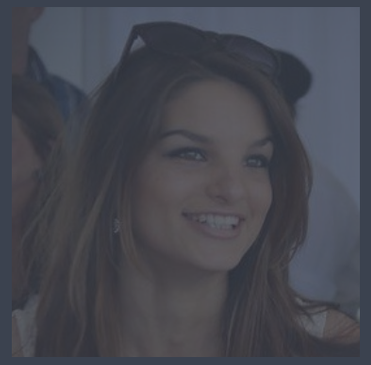
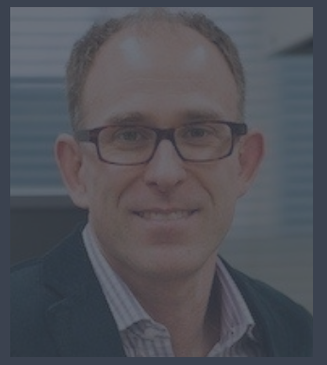


Victor Barrera



Kayleigh Rutherford

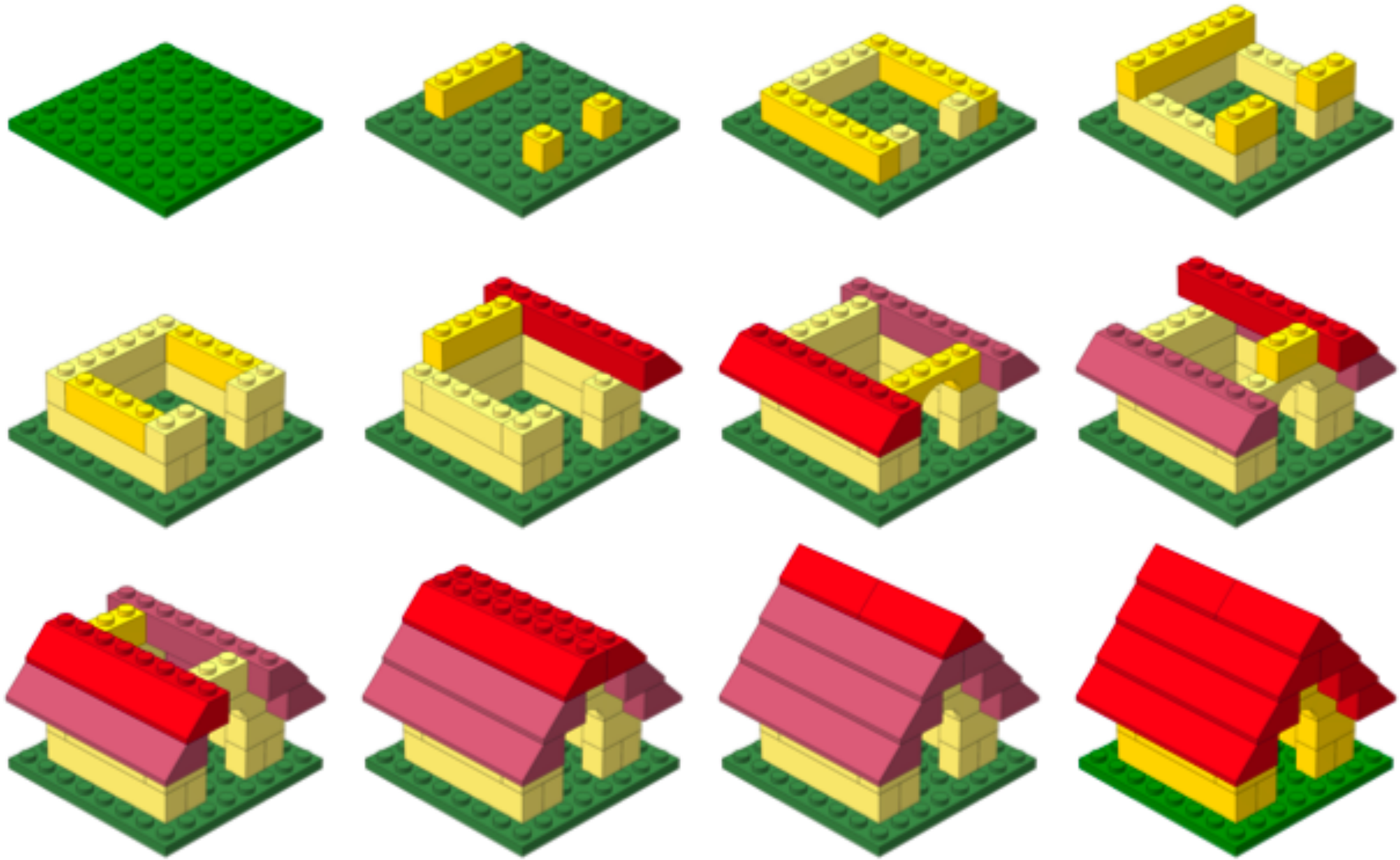


Peter Kraft

Harvard Chan Bioinformatics Core

Class Introductions!

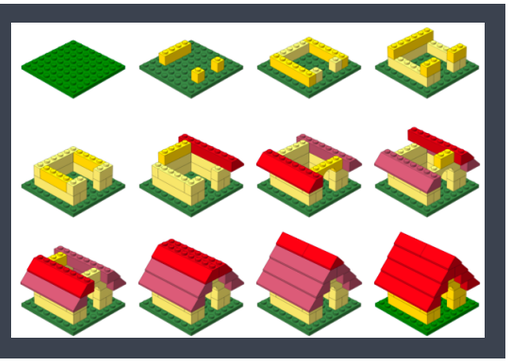
Workshop Scope…



Learning R

http://anoved.net/tag/lego/page/3/

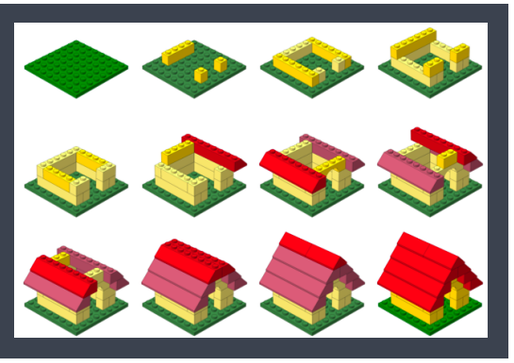
Workshop Scope (1/2)



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

Contact us!

HBC training team: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

@bioinfocore