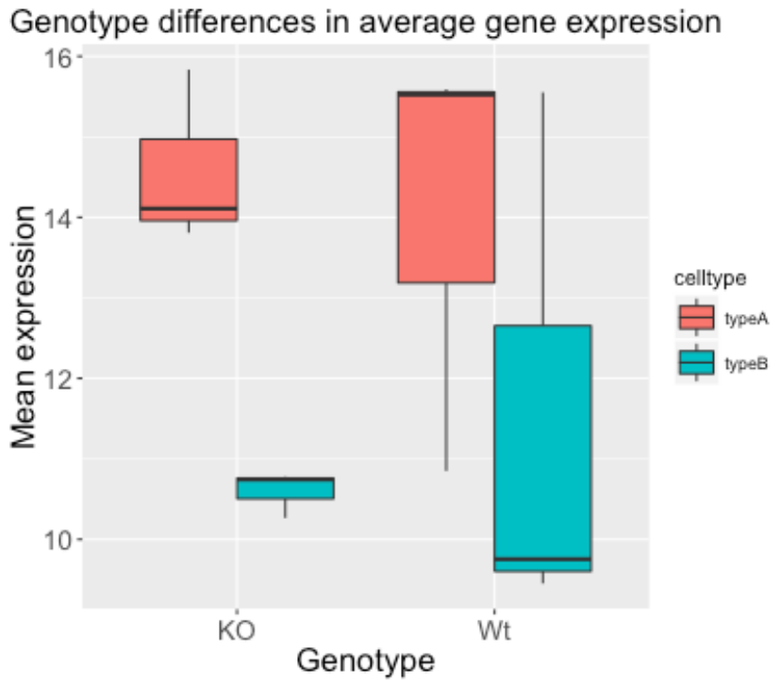


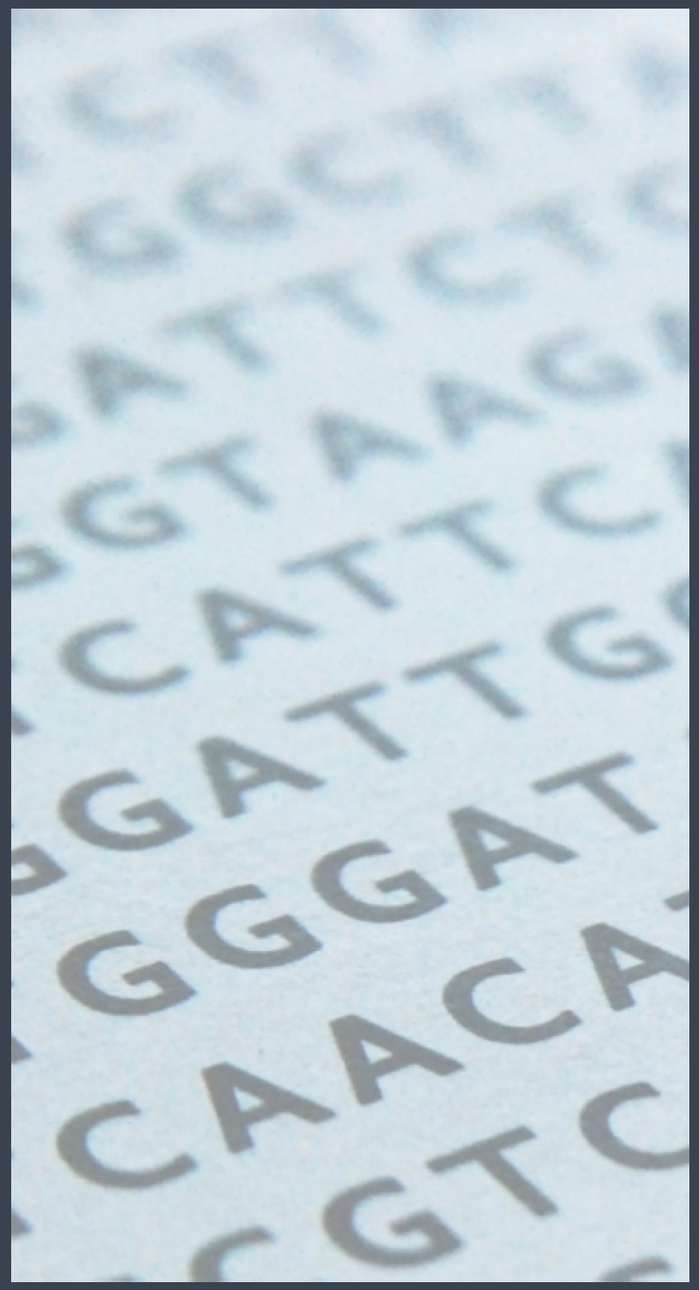
Introduction to R: Basics, Plotting & Differential Expression Analysis

Harvard Chan Bioinformatics Core

Consulting

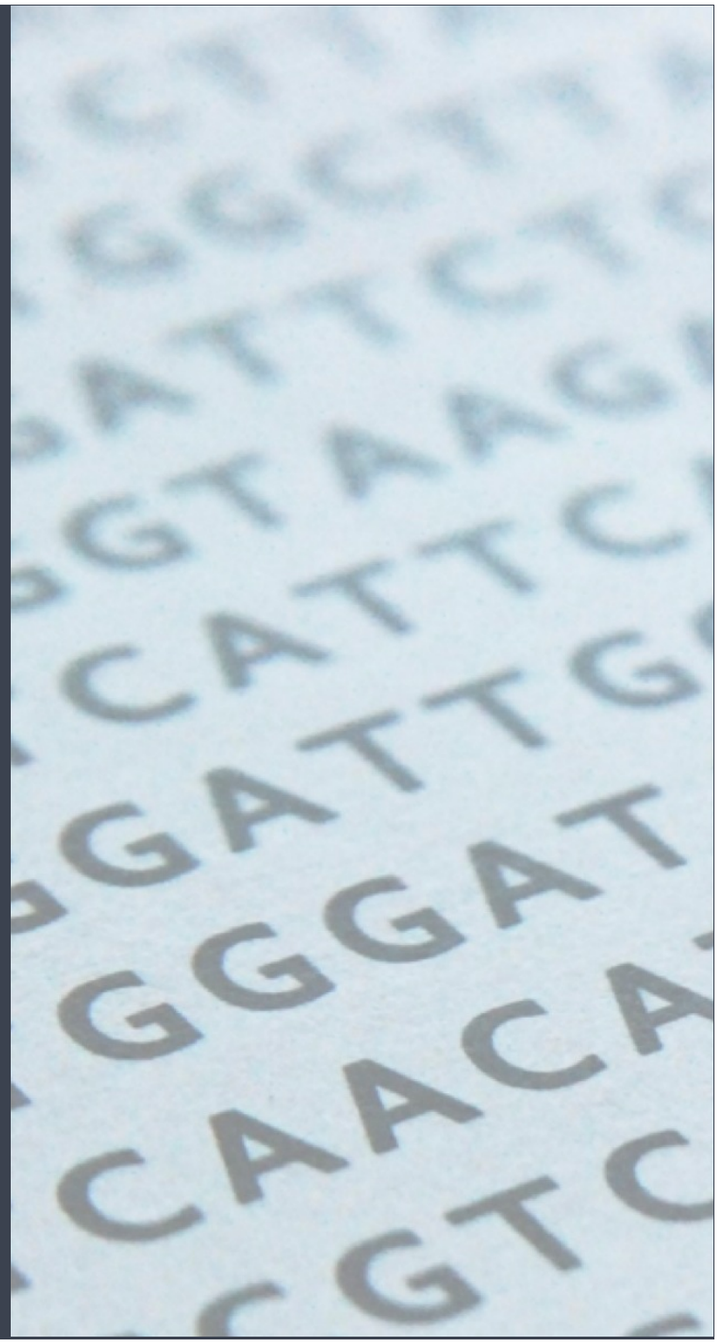
- RNA-seq, small RNA-seq and ChIP-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- Quality assurance and analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

HBC consulting: bioinformatics@hsph.harvard.edu



Training

- Short workshops on introductory, intermediate and advanced topics related to NGS data analysis
- In-depth courses (8- or 12-day formats)



HBC training team: hbctraining@hsph.harvard.edu

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

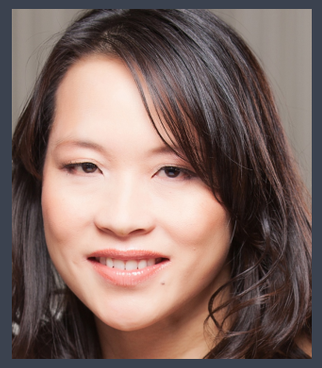
NIEHS / CFAR
Bioinformatics
Core

Center for Stem
Cell
Bioinformatics

Harvard
Catalyst
Bioinformatics
Consulting &
Training

HMS
Tools &
Technology

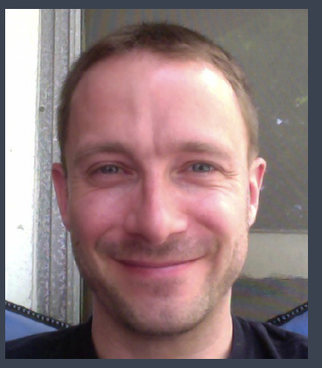
Harvard
NeuroDiscovery
Center



Shannan Ho Sui

John Hutchinson

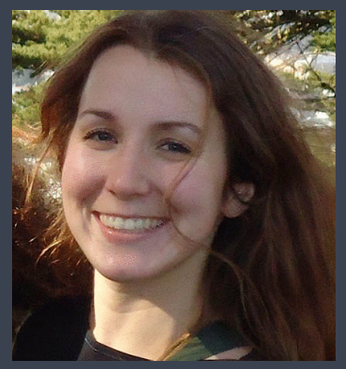
Brad Chapman



Rory Kirchner

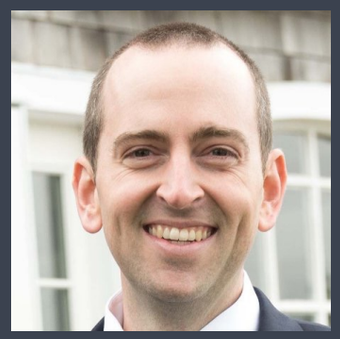
Meeta Mistry

Radhika Khetani



Mary Piper

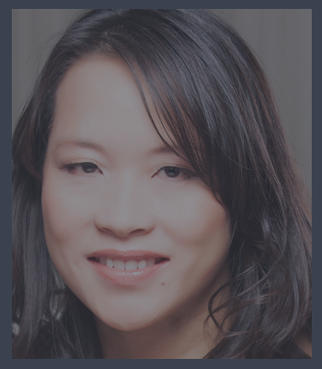
Lorena Pantano



Michael Steinbaugh

Victor Barrera

Peter Kraft



Shannan Ho Sui

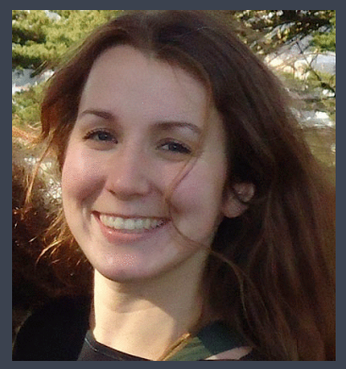
John Hutchinson

Brad Chapman

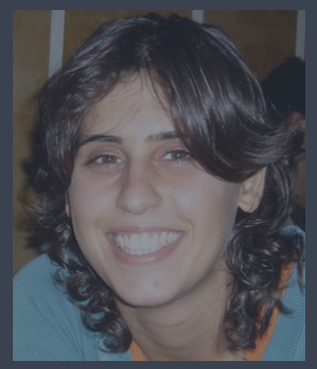
Rory Kirchner

Meeta Mistry

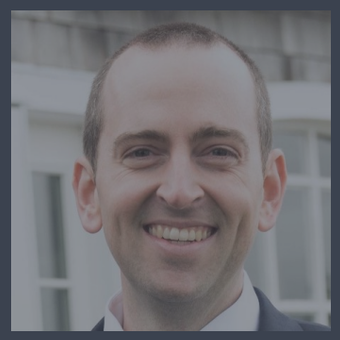
Radhika Khetani



Mary Piper

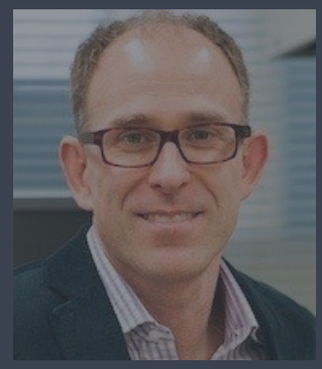


Lorena Pantano



Michael Steinbaugh

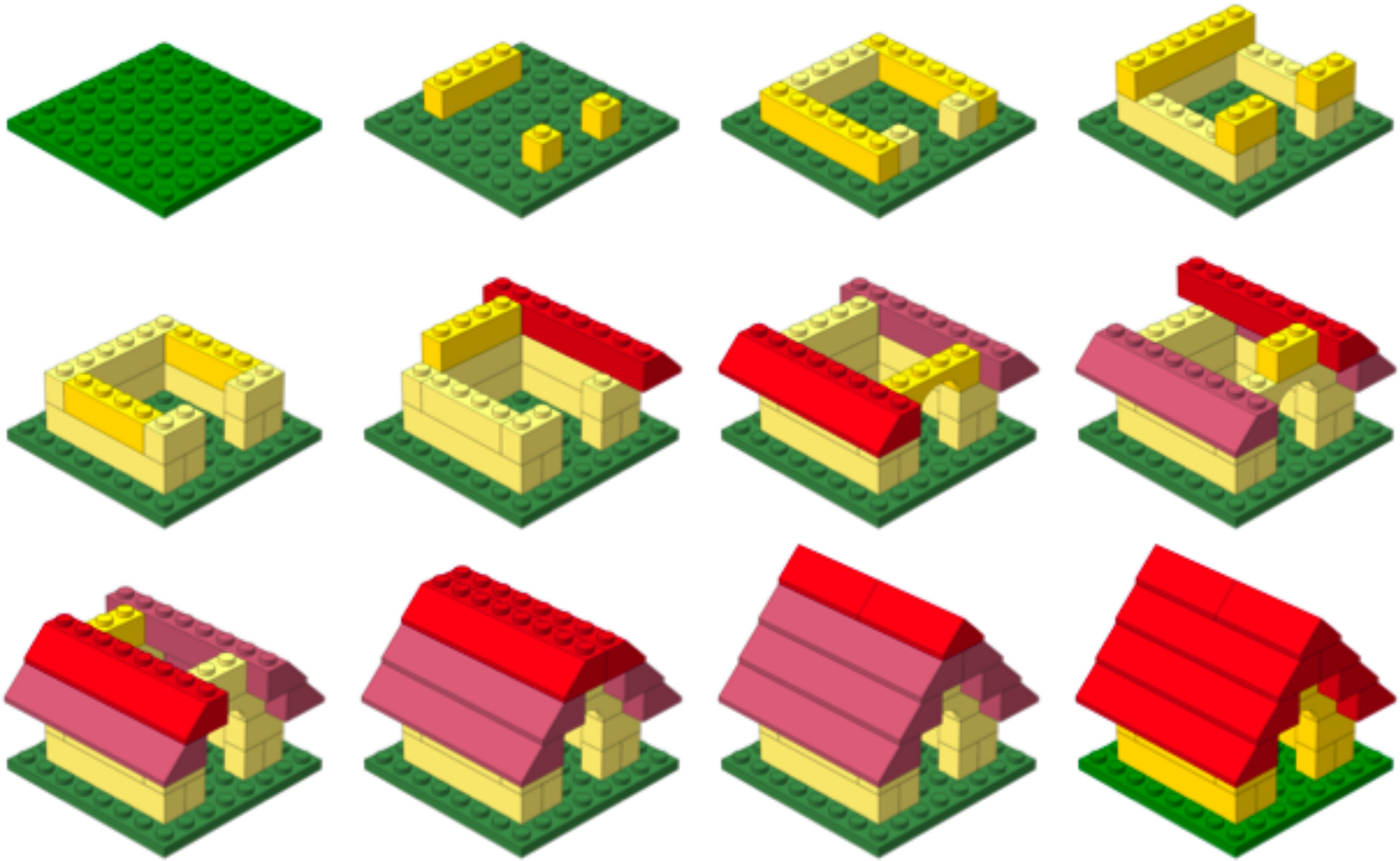
Victor Barrera



Peter Kraft

Class Introductions!

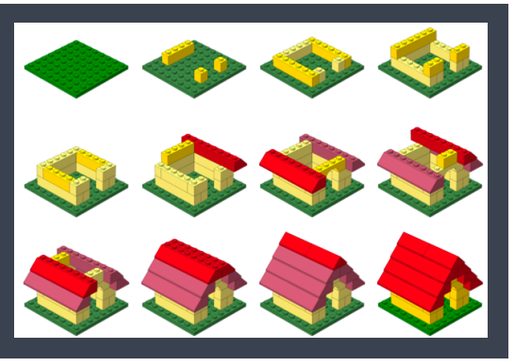
Workshop Scope…



Learning R

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

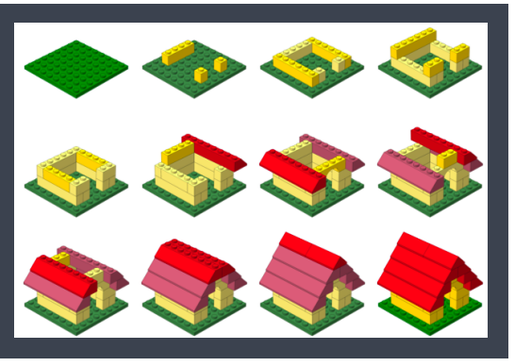
Workshop Scope (1/2)



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

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

HBC twitter: @bioinfocore

Catalyst email: PGE_Bioinformatics@catalyst.harvard.edu

Catalyst website: http://catalyst.harvard.edu/education.html

Catalyst twitter: @HarvardCatalyst