

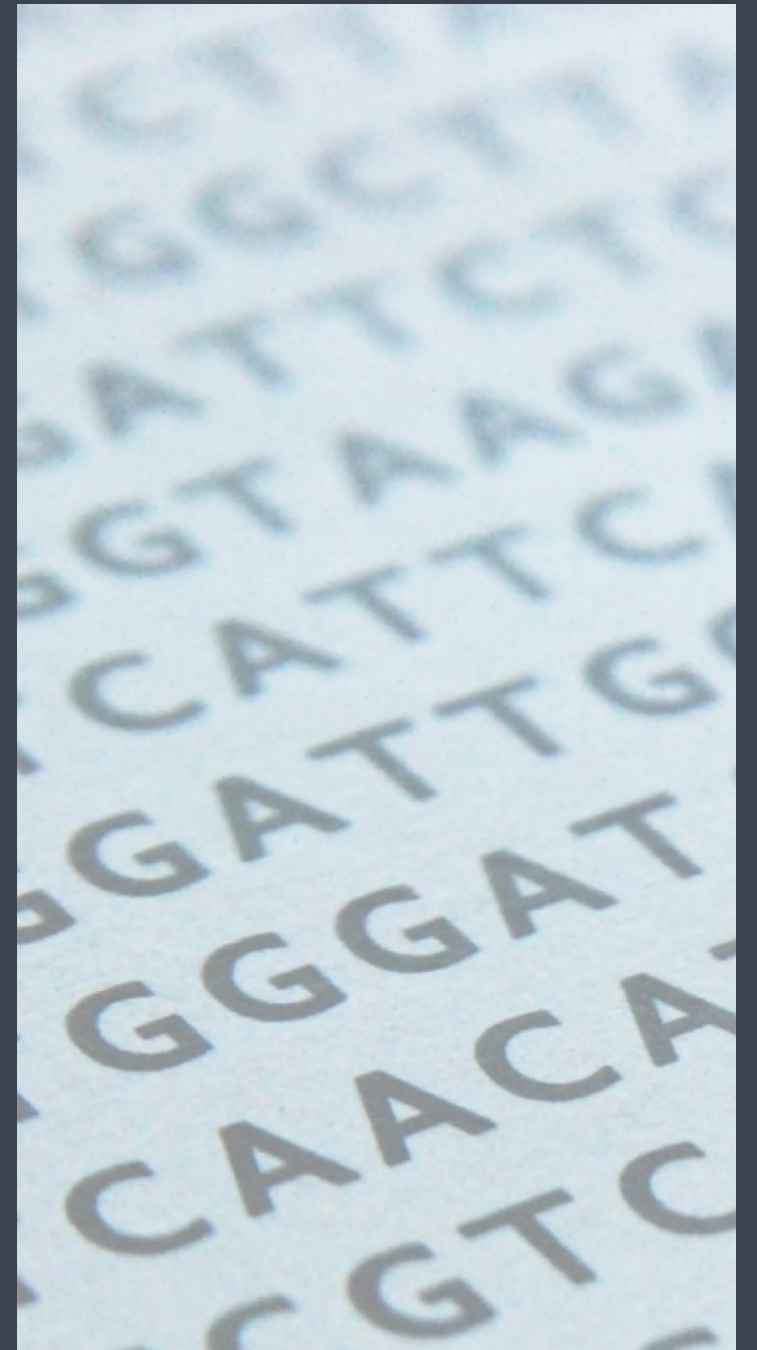
Introduction to R: Basics, Plots, and RNA-seq Differential Expression Analysis

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

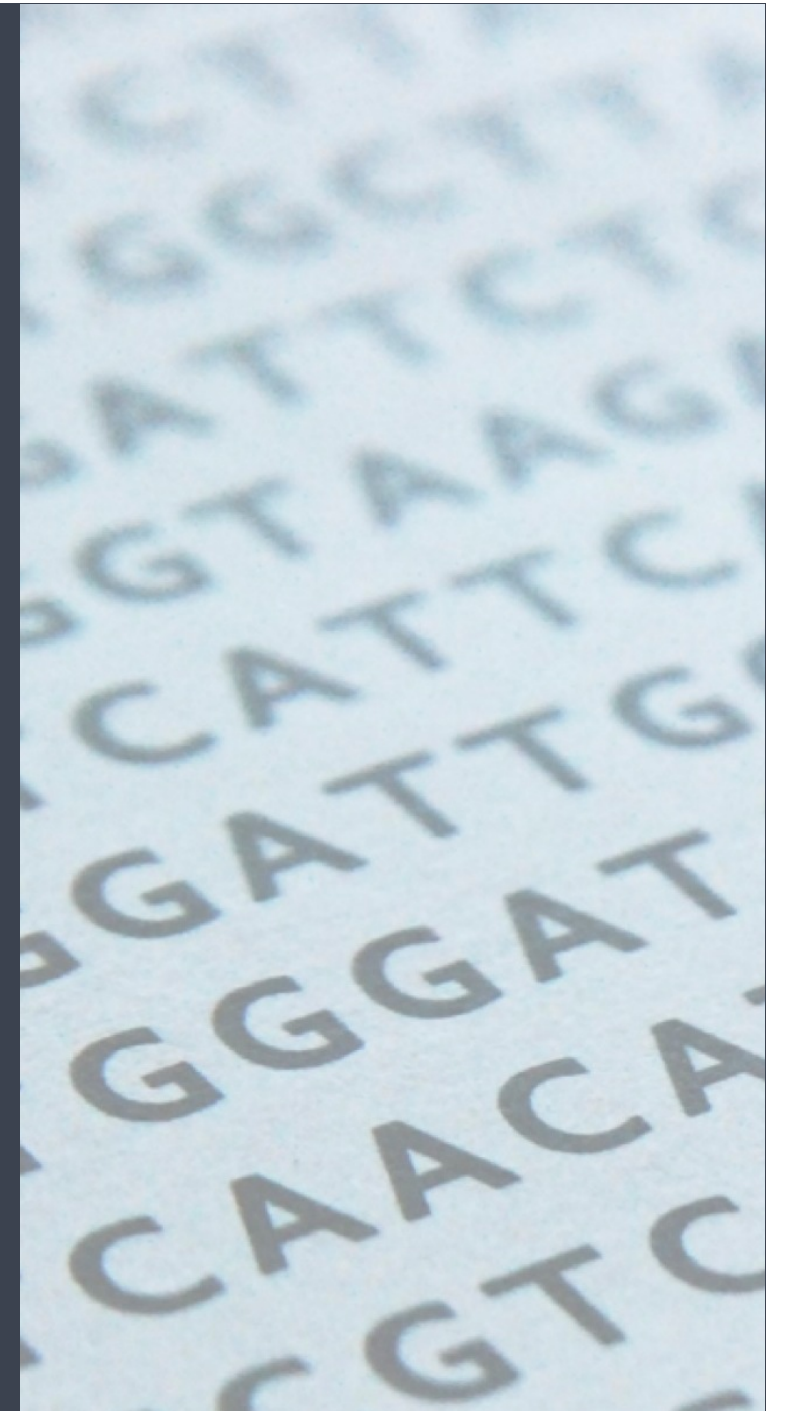
HBC consulting: bioinformatics@hsph.harvard.edu



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





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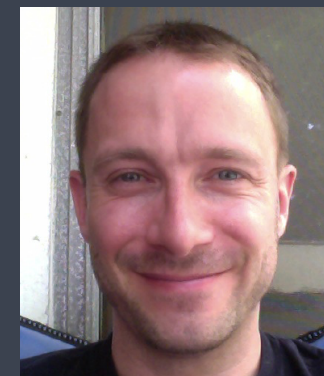
Shannan Ho Sui



John Hutchinson



Brad Chapman



Rory Kirchner



Meeta Mistry



Radhika Khetani



Mary Piper



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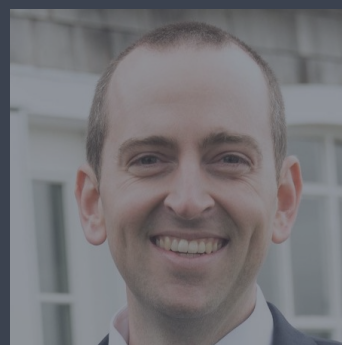
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Victor Barrera

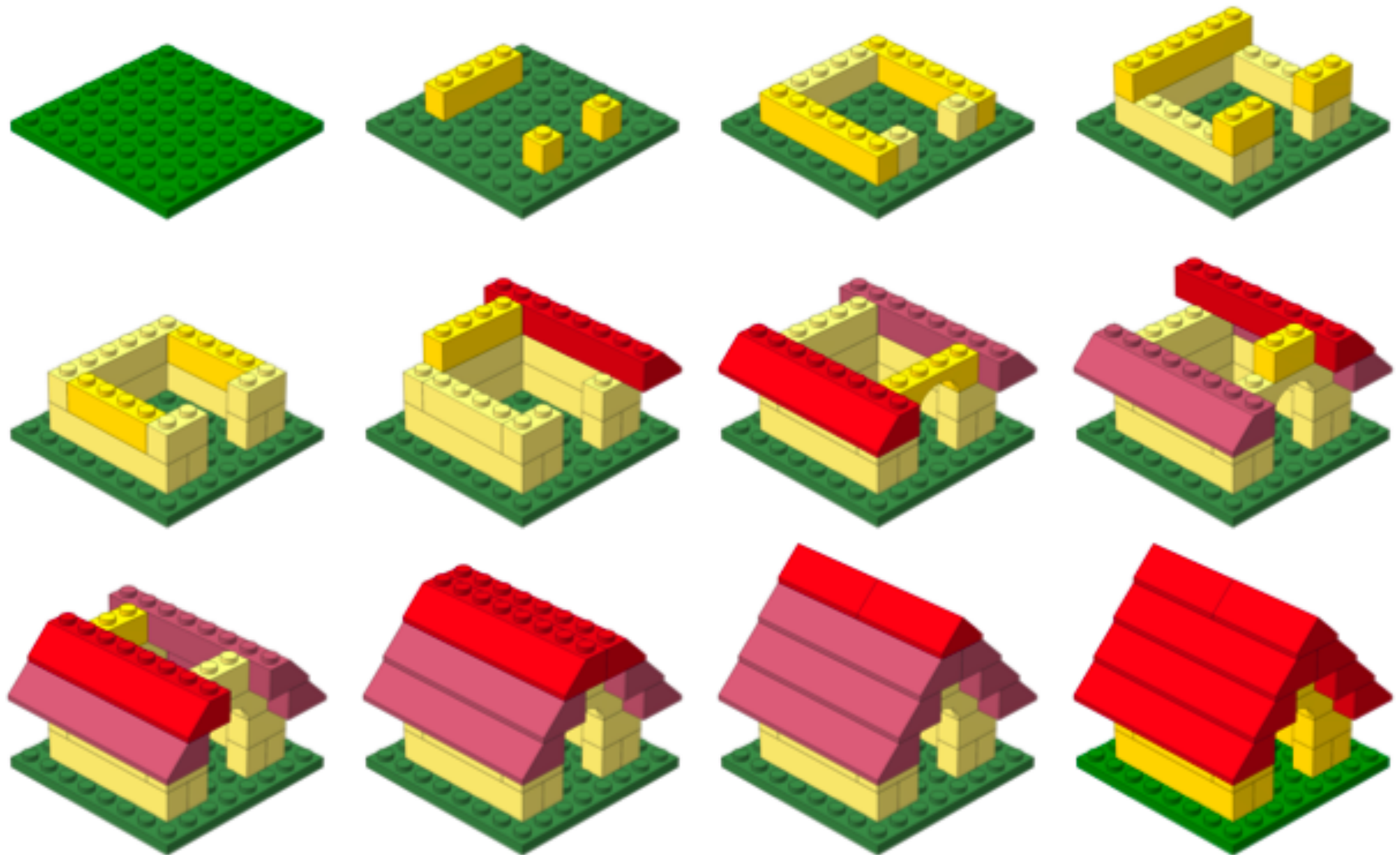


Peter Kraft

Harvard Chan Bioinformatics Core

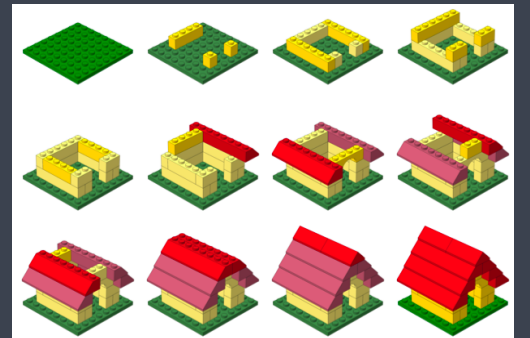
Class Introductions!

Workshop Scope...



Learning R

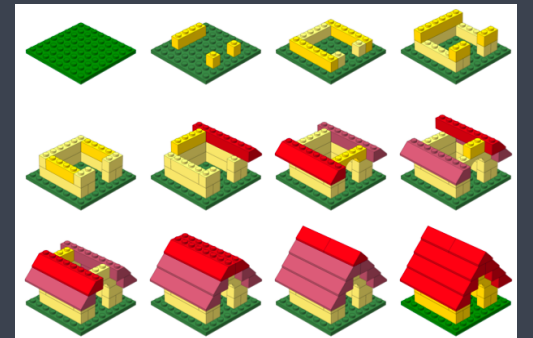
Workshop Scope (1/2)



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!

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

HBC twitter: [@bioinfocore](https://twitter.com/bioinfocore)

Catalyst email: PGE_Bioinformatics@catalyst.harvard.edu

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

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