

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

Harvard Chan Bioinformatics Core



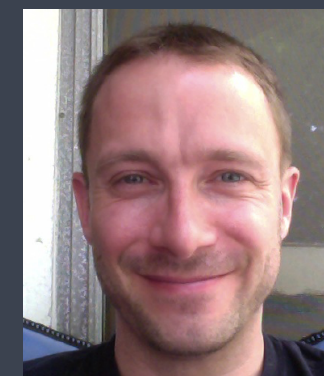
Shannan Ho Sui



John Hutchinson



Brad Chapman



Rory Kirchner



Meeta Mistry



Radhika Khetani



Mary Piper



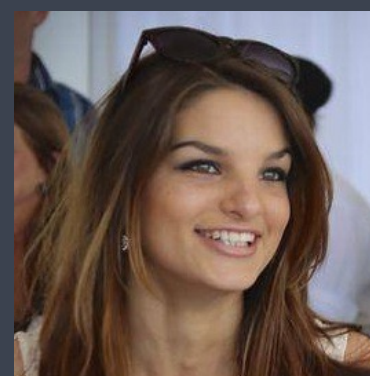
Lorena Pantano



Michael Steinbaugh



Victor Barrera



Kayleigh Rutherford

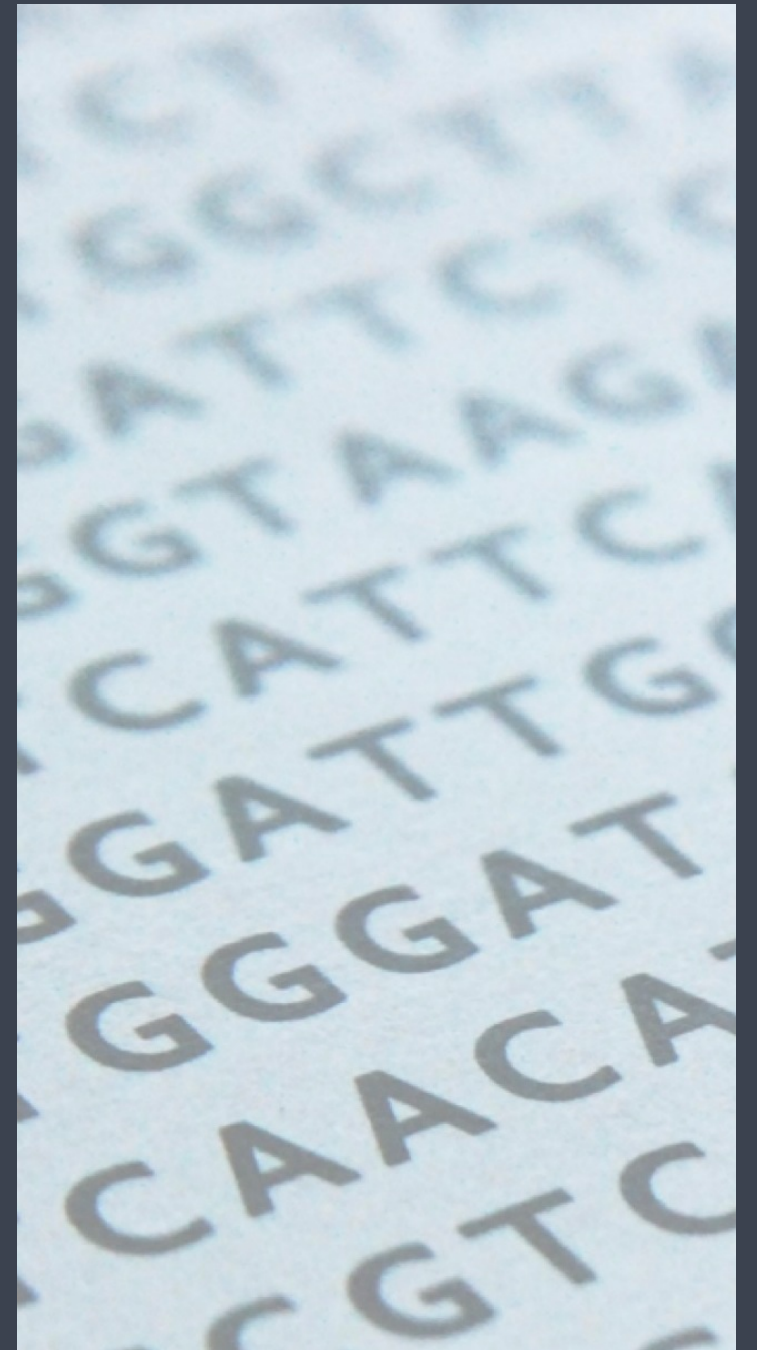


Peter Kraft

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

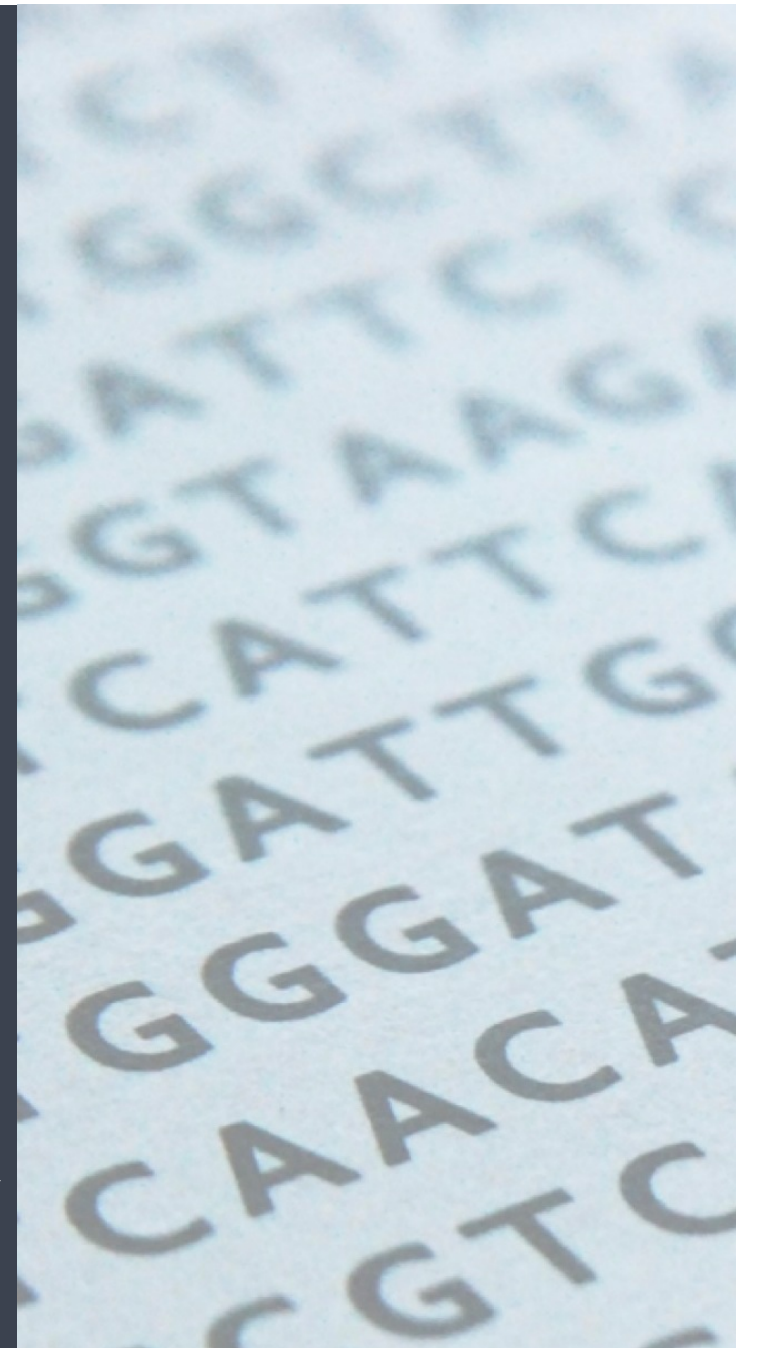
HBC consulting: bioinformatics@hsph.harvard.edu



Training

- Short workshops on introductory, intermediate and advanced topics related to NGS data analysis
- Monthly, 2-3 hour, hands-on and free workshops on “Current Topics in Bioinformatics”
- In-depth courses (8- or 12-day formats)

[http://bioinformatics.sph.harvard.edu/training/
#upcoming-workshopscourses](http://bioinformatics.sph.harvard.edu/training/#upcoming-workshopscourses)





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Introductions!



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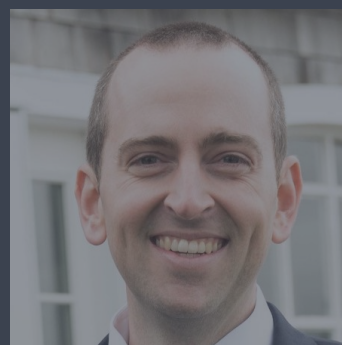
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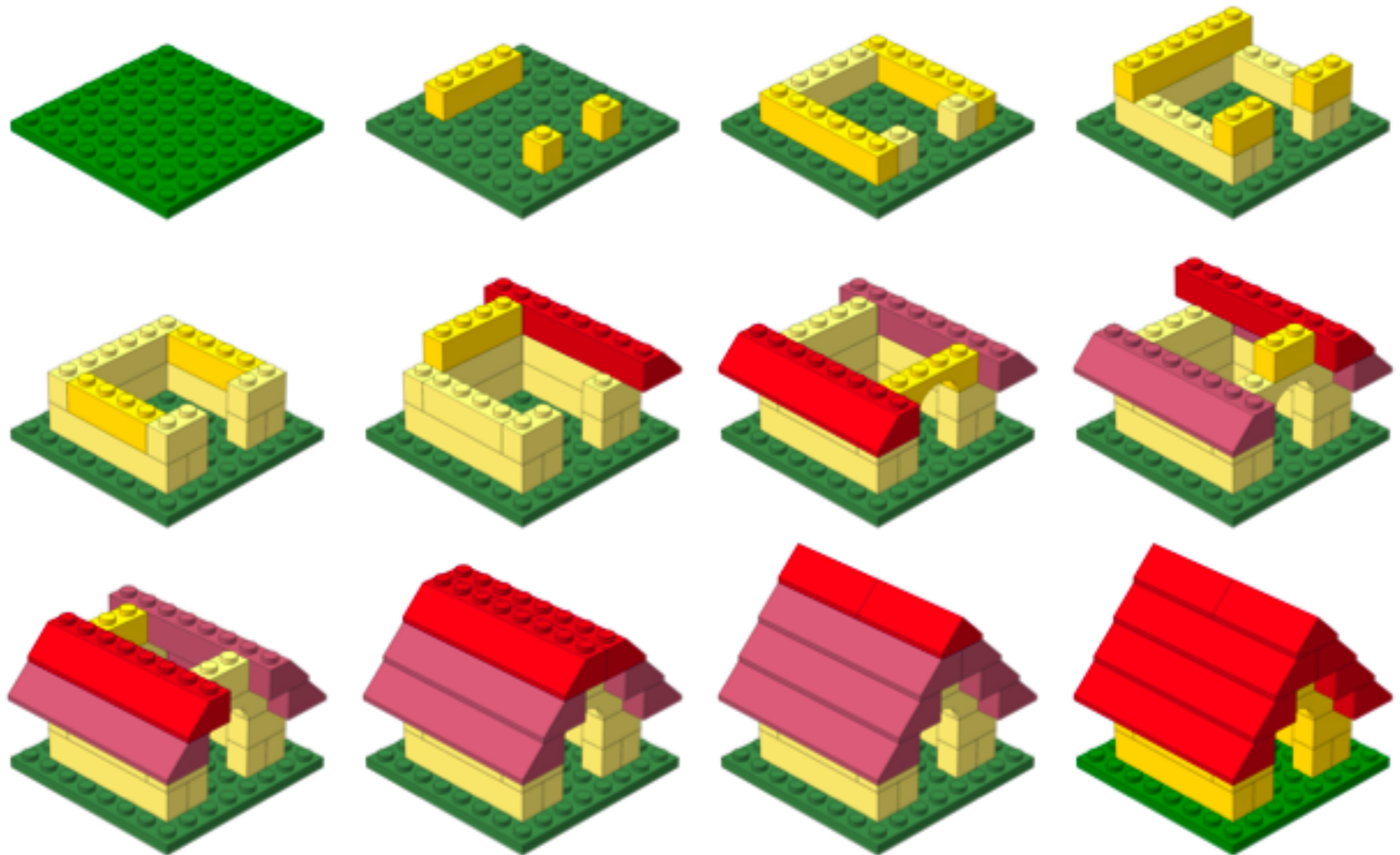


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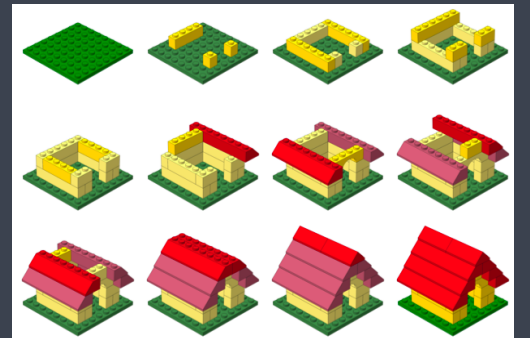
Class Introductions!

Workshop Scope...



Learning R

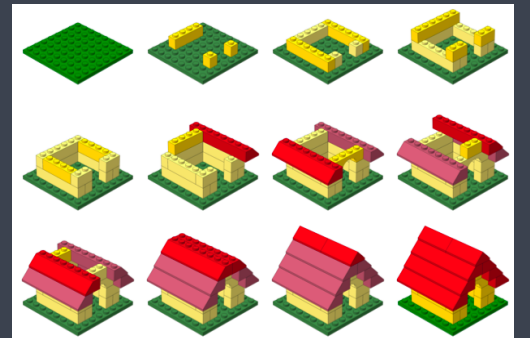
Workshop Scope (1/2)



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 ggplot2

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
- ✓ Use Sleuth to obtain lists of differentially expressed splice isoforms

Contact us!

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