

Introduction to R

Harvard Chan Bioinformatics Core

April 30th and May 1st, 2018

<https://tinyurl.com/hbc-intro-R-2day>

Sponsored by HMS (TnT) and HSCI



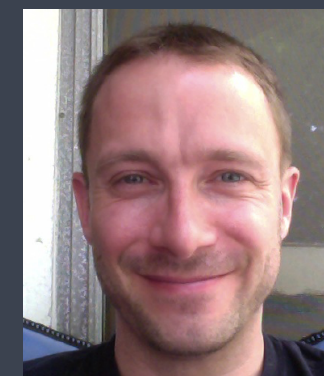
Shannan Ho Sui



John Hutchinson



Brad Chapman



Rory Kirchner



Meeta Mistry



Radhika Khetani



Mary Piper



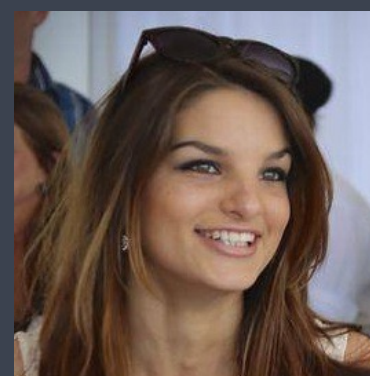
Lorena Pantano



Michael Steinbaugh



Victor Barrera



Kayleigh Rutherford

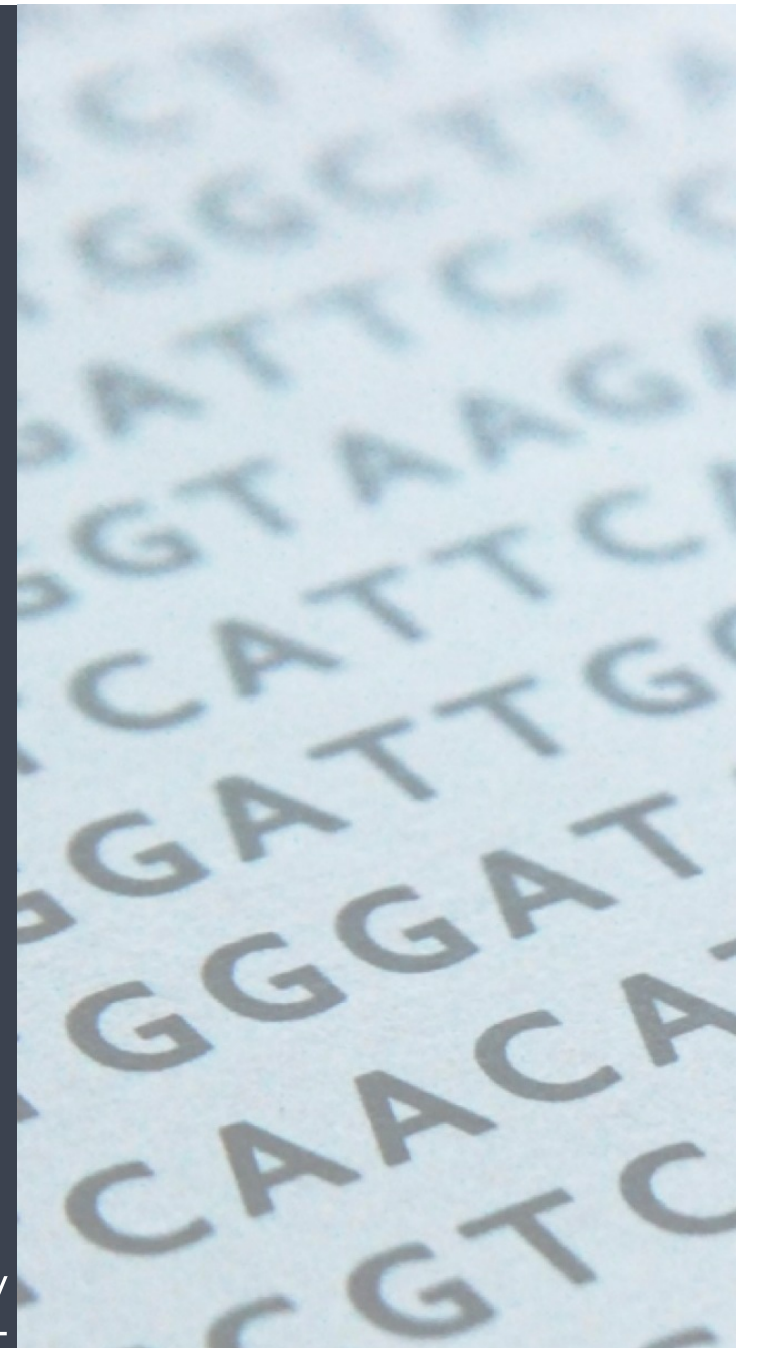


Peter Kraft

Consulting

- RNA-seq analysis: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

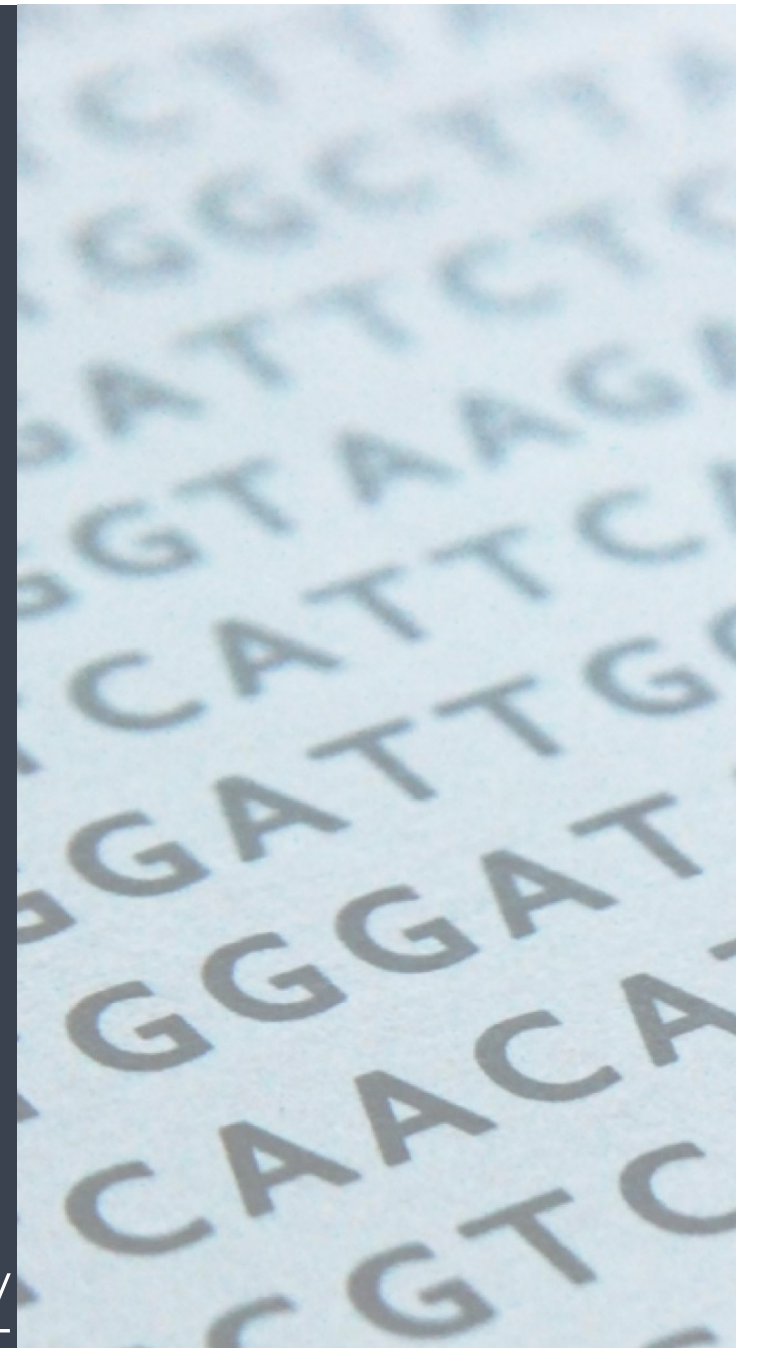
<http://bioinformatics.sph.harvard.edu/>



Training

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

bioinformatics.sph.harvard.edu/training/





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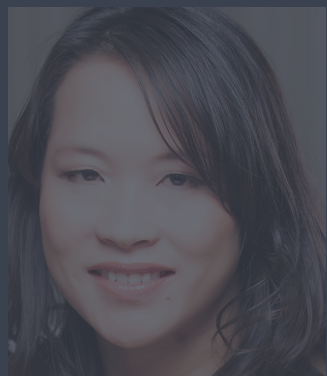
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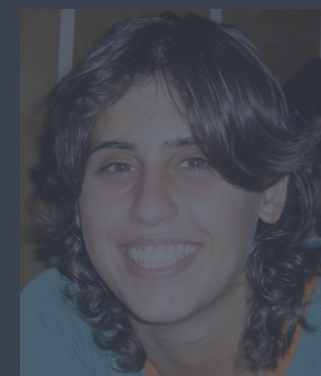
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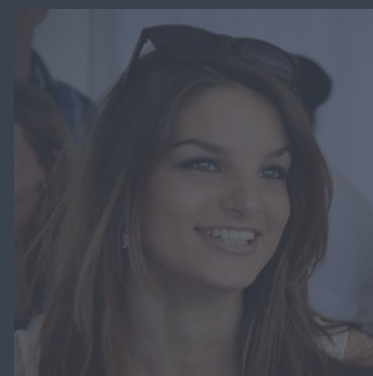
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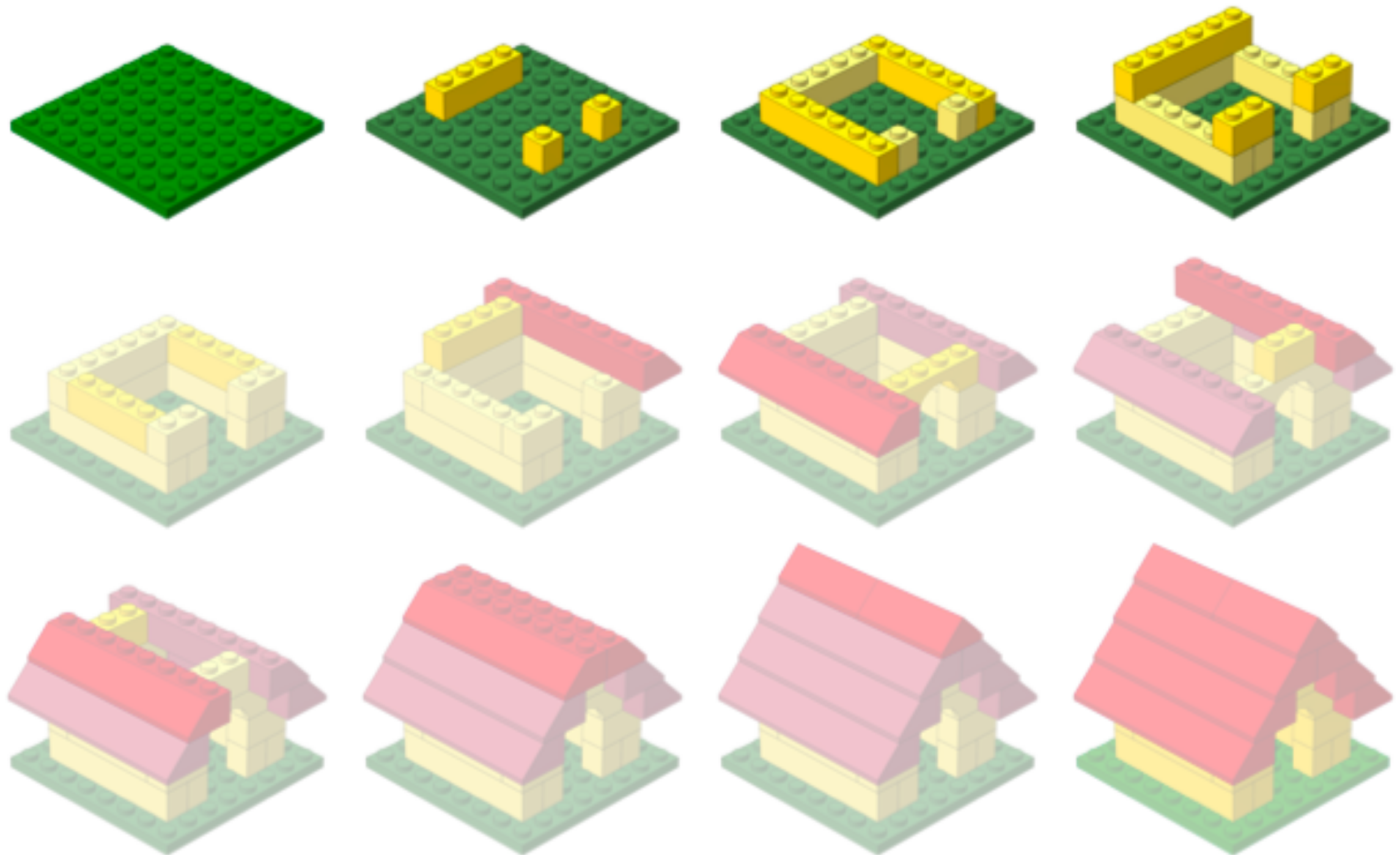


Peter Kraft

Harvard Chan Bioinformatics Core

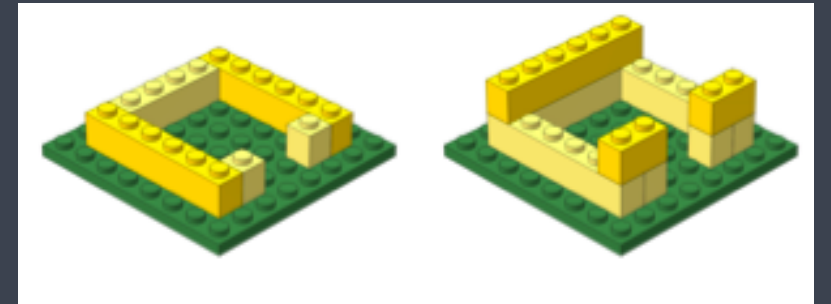
Class Introductions!

Workshop Scope...



Learning R

Workshop Scope



- ✓ Comfortably use 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*

Contact us!

HBC training team: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

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