

Introduction to R

Harvard Chan Bioinformatics Core

<https://tinyurl.com/intro-to-r-1-5>

Sponsored by HMS (TnT) and HSCI



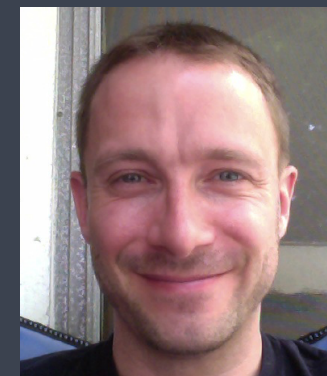
Shannan Ho Sui



John Hutchinson



Brad Chapman



Rory Kirchner



Meeta Mistry



Radhika Khetani



Mary Piper



Lorena Pantano



Victor Barrera



Kayleigh Rutherford

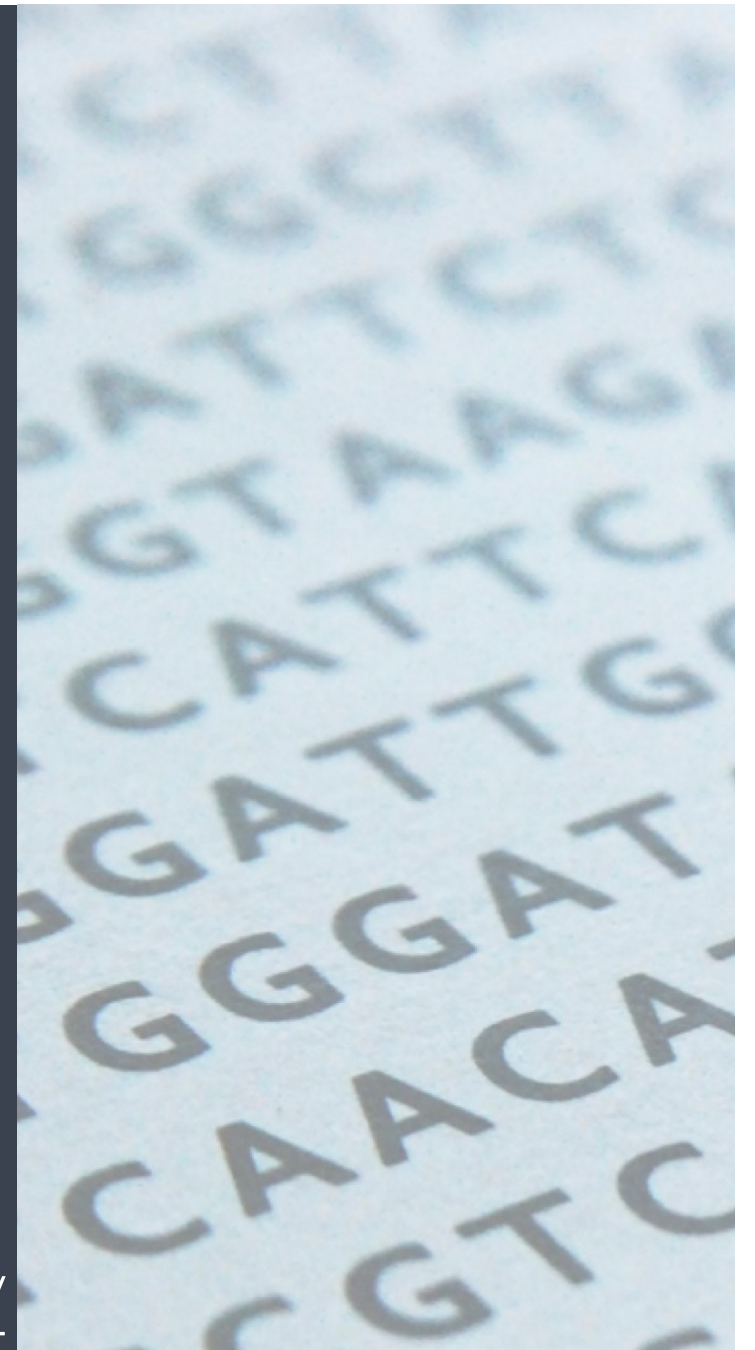


Peter Kraft

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

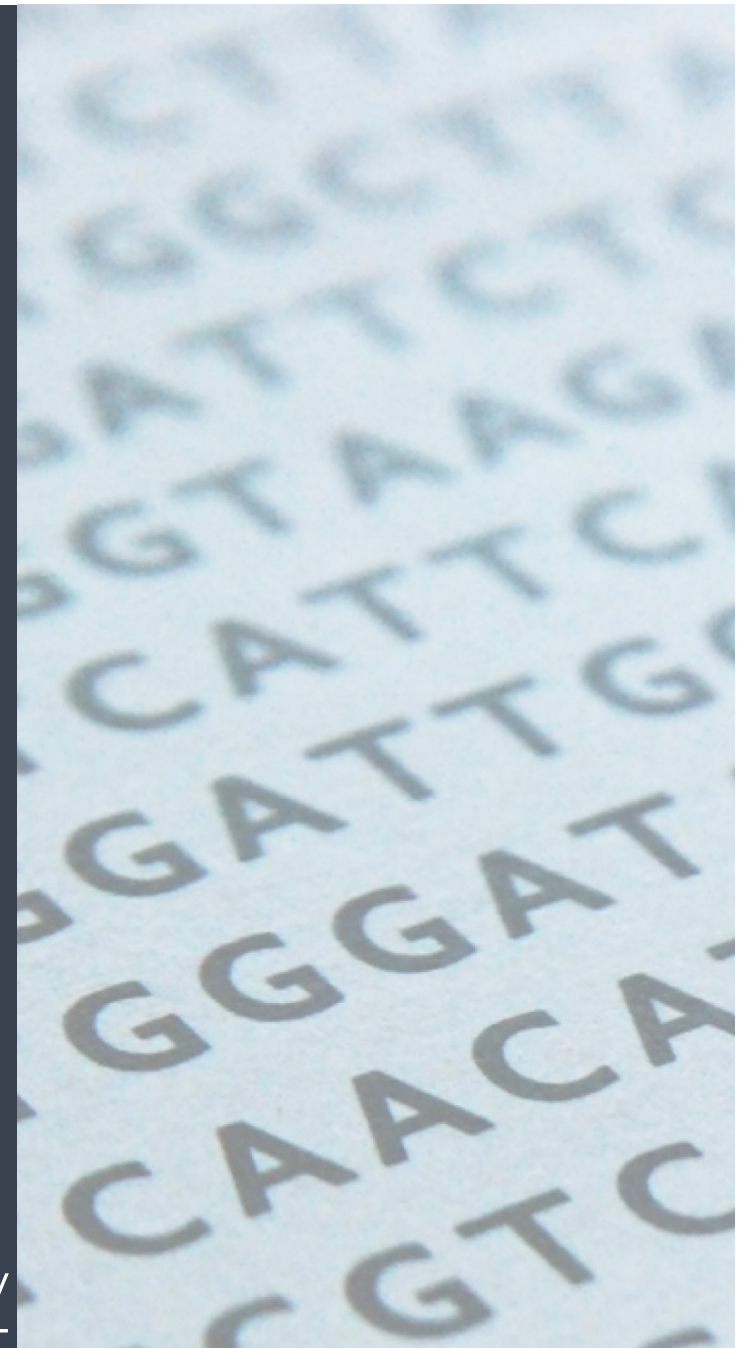
<http://bioinformatics.sph.harvard.edu/>



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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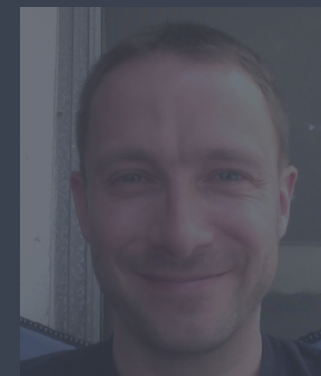
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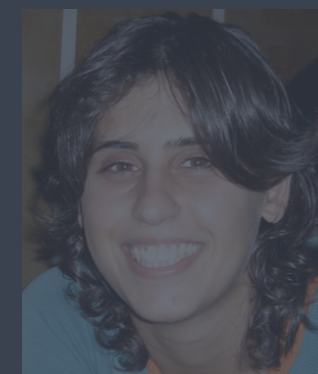
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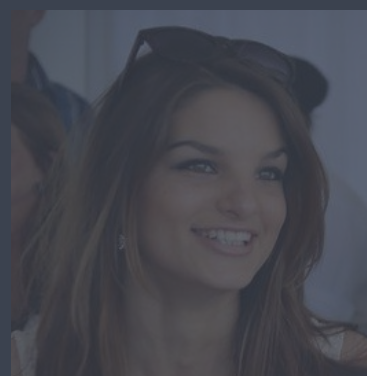
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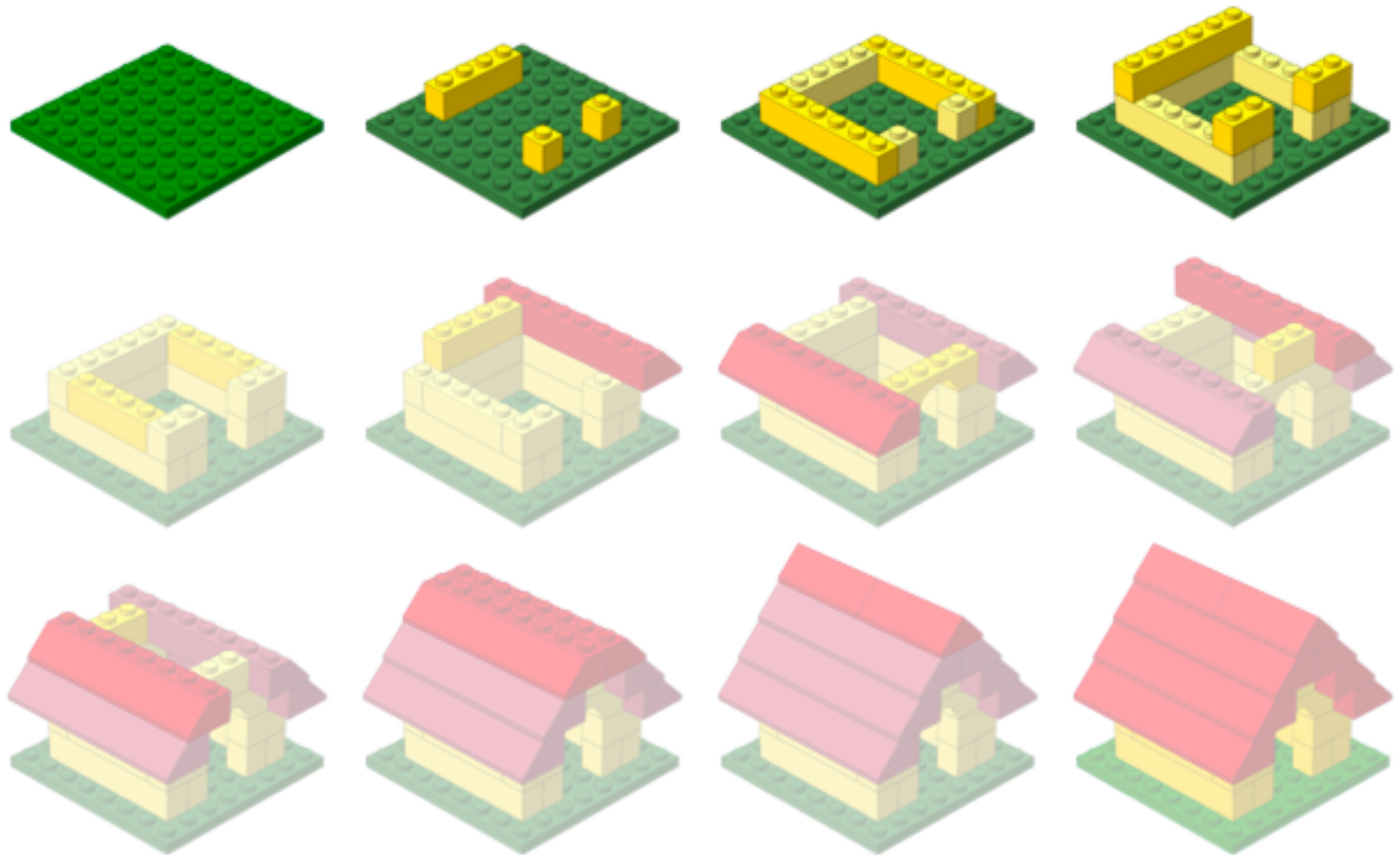


Peter Kraft

Harvard Chan Bioinformatics Core

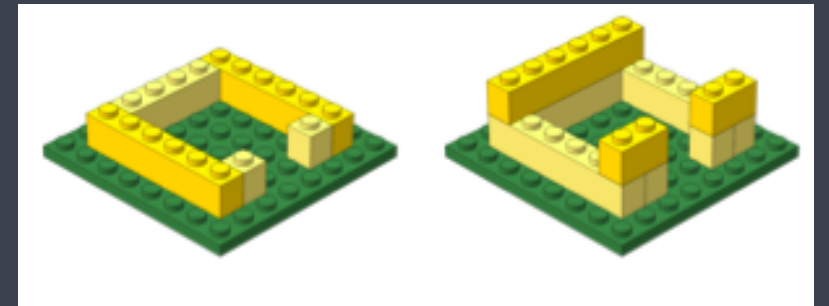
Class Introductions!

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

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