

Introduction to R

Harvard Chan Bioinformatics Core

<https://tinyurl.com/introR-feb2018>



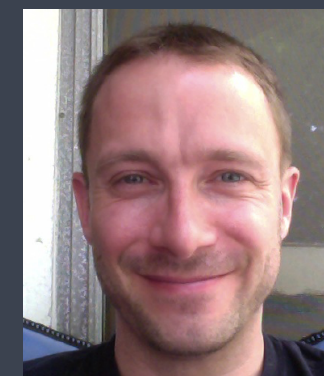
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John Hutchinson
(Associate Director)



Brad Chapman



Rory Kirchner



Meeta Mistry



Radhika Khetani
(Training Director)



Mary Piper



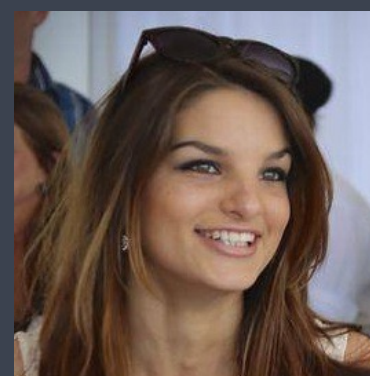
Lorena Pantano



Michael Steinbaugh



Victor Barrera



Kayleigh Rutherford

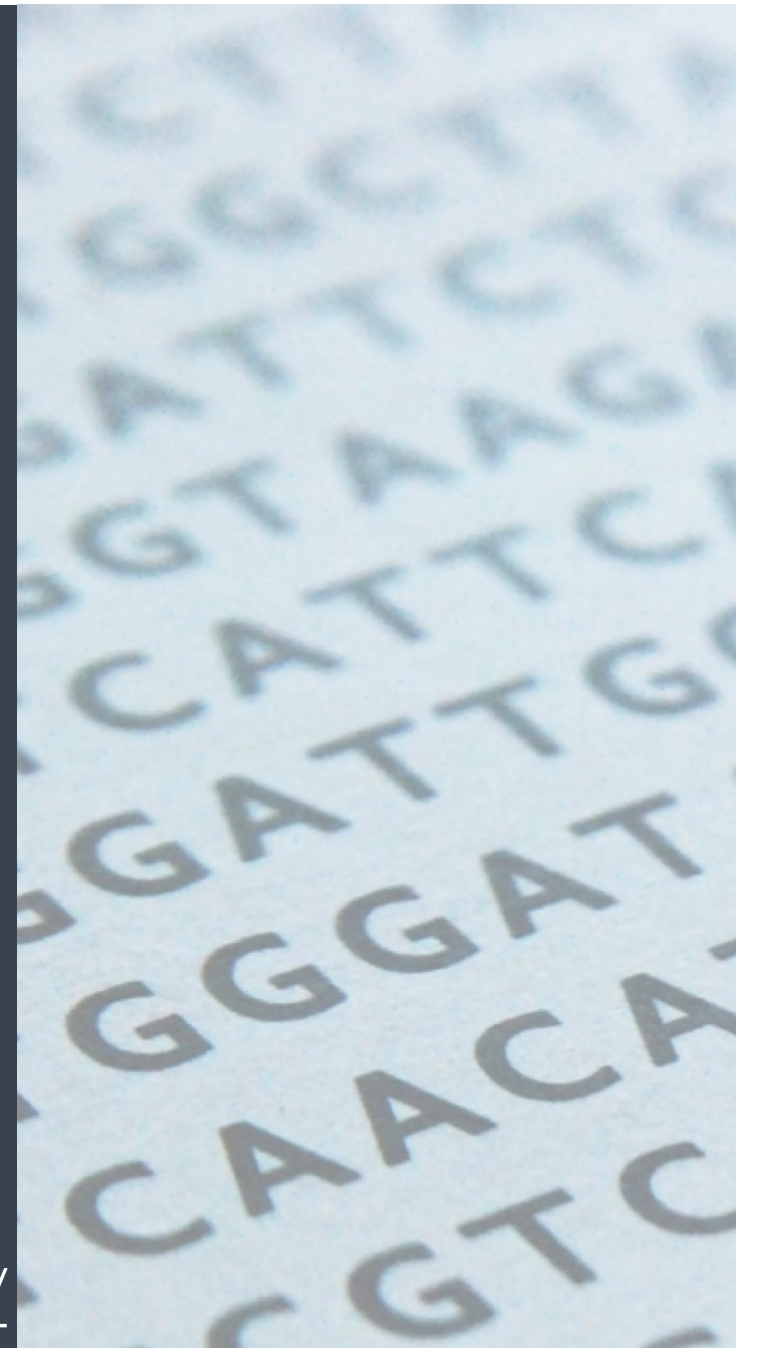


Peter Kraft
(Faculty Director)

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

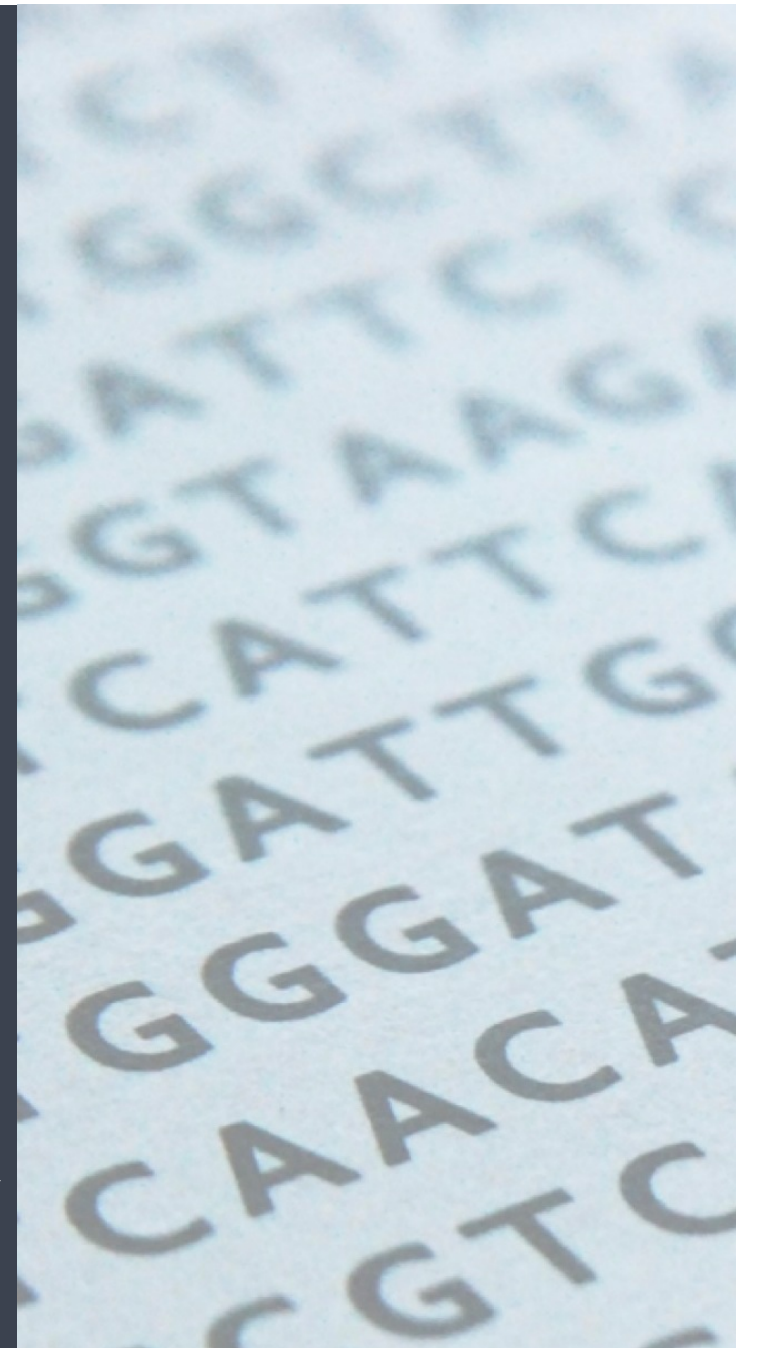
<http://bioinformatics.sph.harvard.edu/>



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)

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





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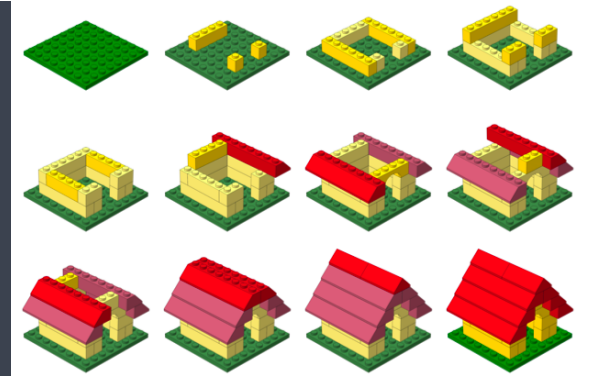
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Technology

Workshop Scope...

Learning Objectives



- ✓ Become comfortable with RStudio (a graphical interface for using 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

Contact us!

Training questions? hbctraining@hsph.harvard.edu

Consulting questions? bioinformatics@hsph.harvard.edu

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