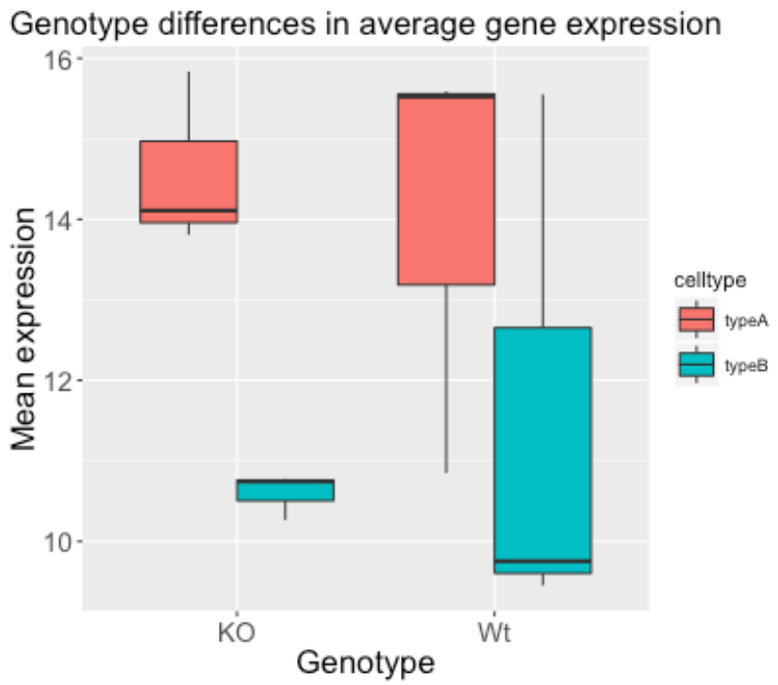
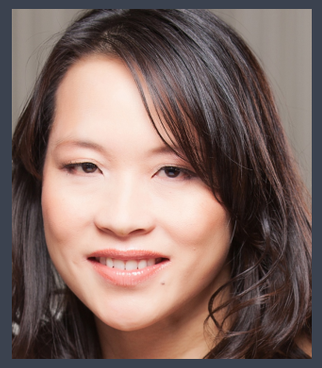


Introduction to R

Harvard Chan Bioinformatics Core

April 30th and May 1st, 2018

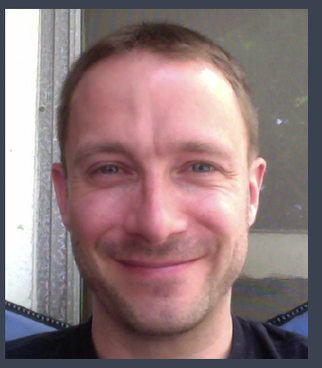
https://tinyurl.com/hbc-intro-R-2day



Shannan Ho Sui

John Hutchinson

Brad Chapman



Rory Kirchner

Meeta Mistry

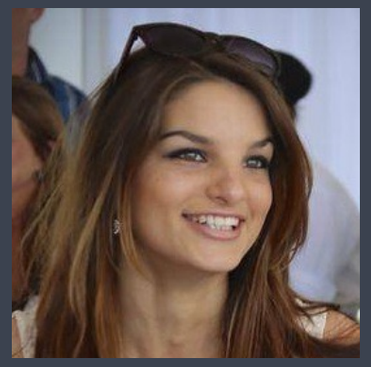
Radhika Khetani

Mary Piper

Lorena Pantano

Michael Steinbaugh

Victor Barrera



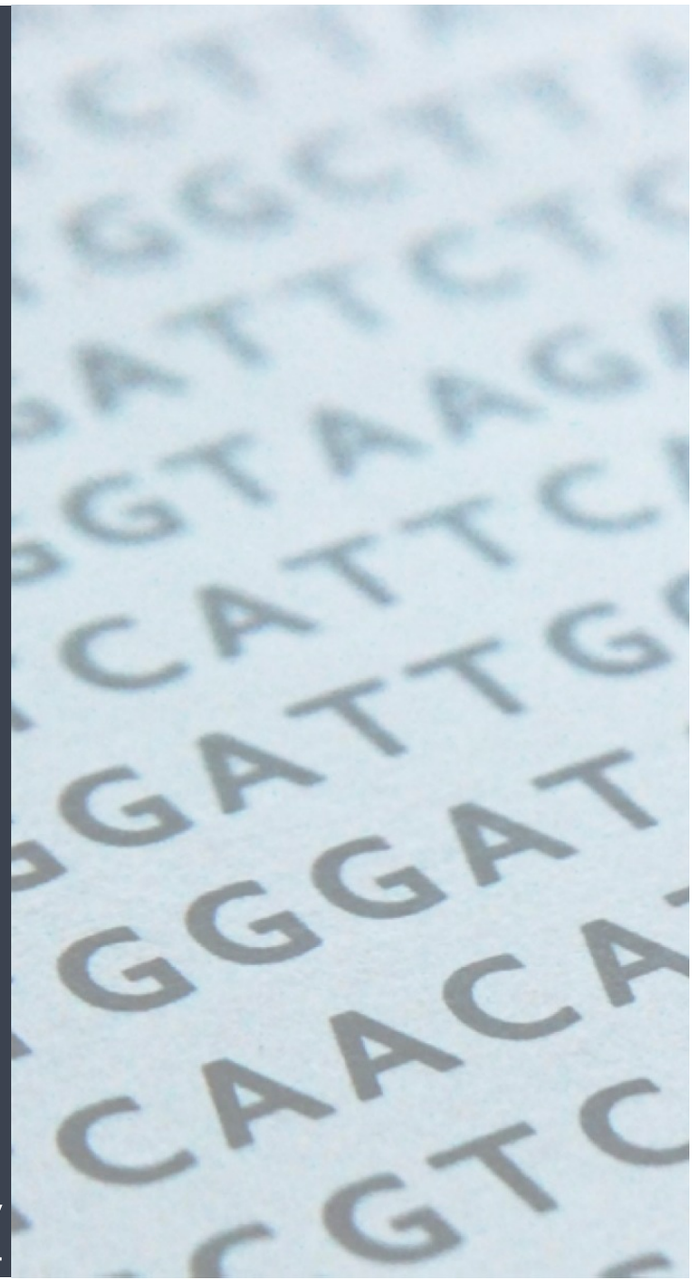
Kayleigh Rutherford

Peter Kraft

Consulting

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

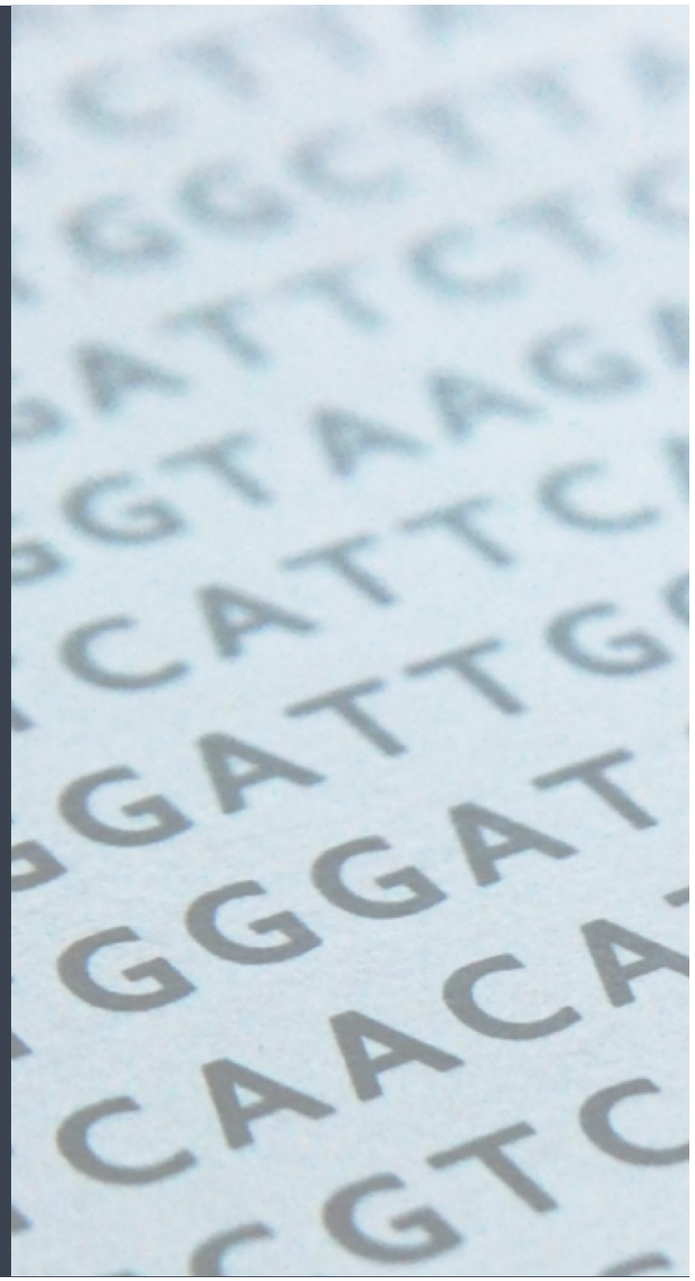
http://bioinformatics.sph.harvard.edu/



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)

http://bioinformatics.sph.harvard.edu/training/#upcoming-workshopscourses



HARVARD T.H. CHAN SCHOOL OF PUBLIC HEALTH

HSCI HARVARD STEM CELL INSTITUTE

HARVARD CATALYST
THE HARVARD CLINICAL AND TRANSLATIONAL SCIENCE CENTER

HARVARD MEDICAL SCHOOL

NIEHS / CFAR Bioinformatics Core

Center for Stem Cell Bioinformatics

Harvard Catalyst Bioinformatics Consulting

HMS Tools & Technology Committee

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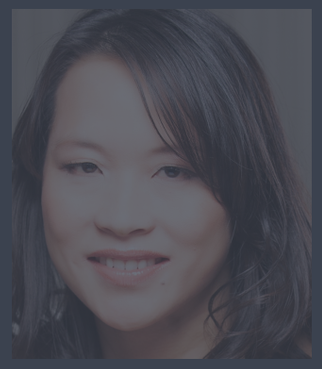

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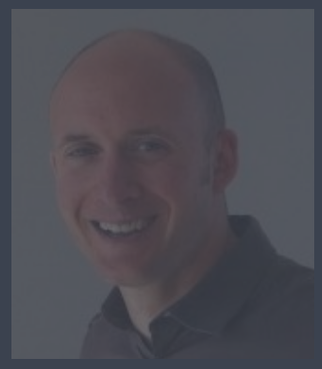
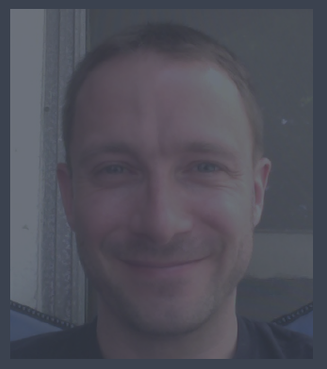


Brad Chapman



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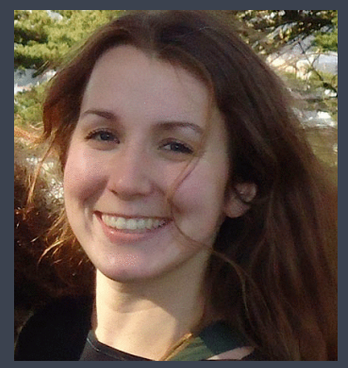
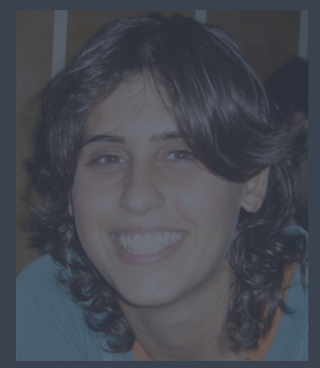


Mary Piper



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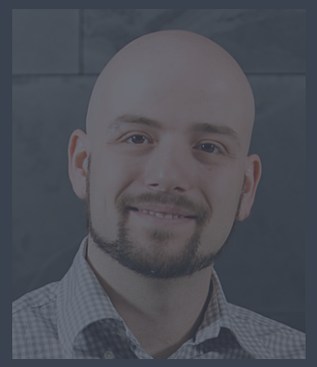
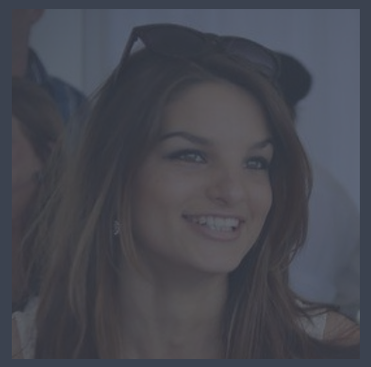
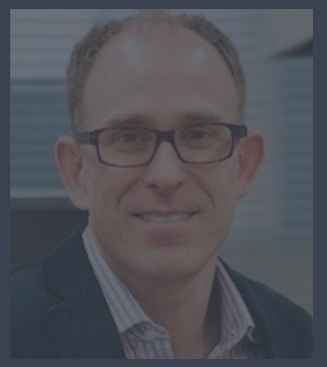


Victor Barrera



Kayleigh Rutherford

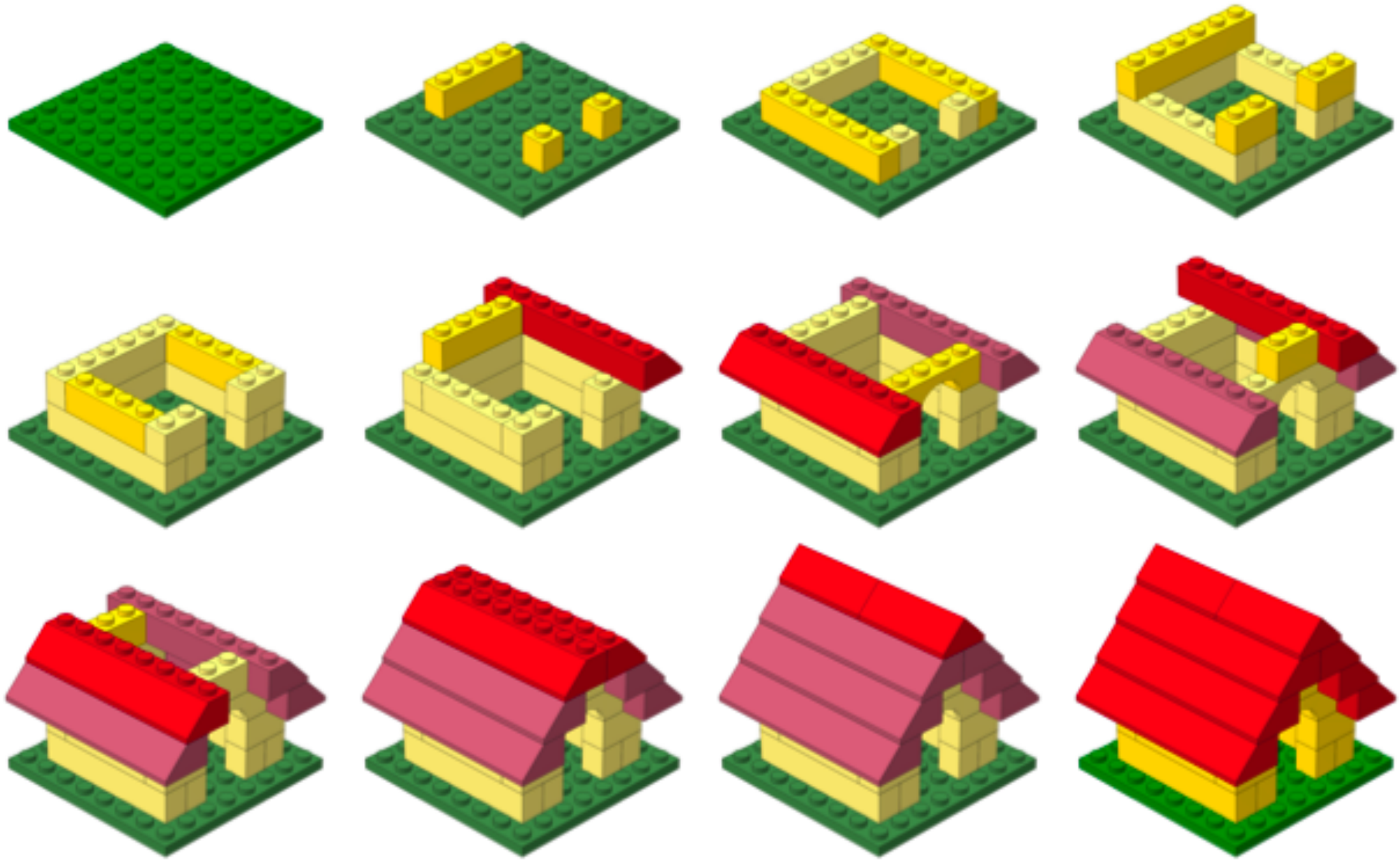


Peter Kraft

Harvard Chan Bioinformatics Core

Class Introductions!

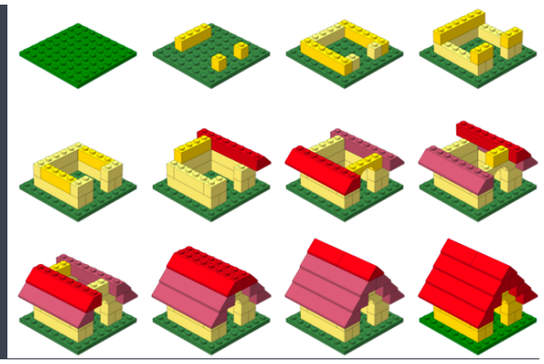
Workshop Scope…



Learning R

http://anoved.net/tag/lego/page/3/

Learning Objectives



- ✓ 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

Contact us!

HBC training team: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

@bioinfocore