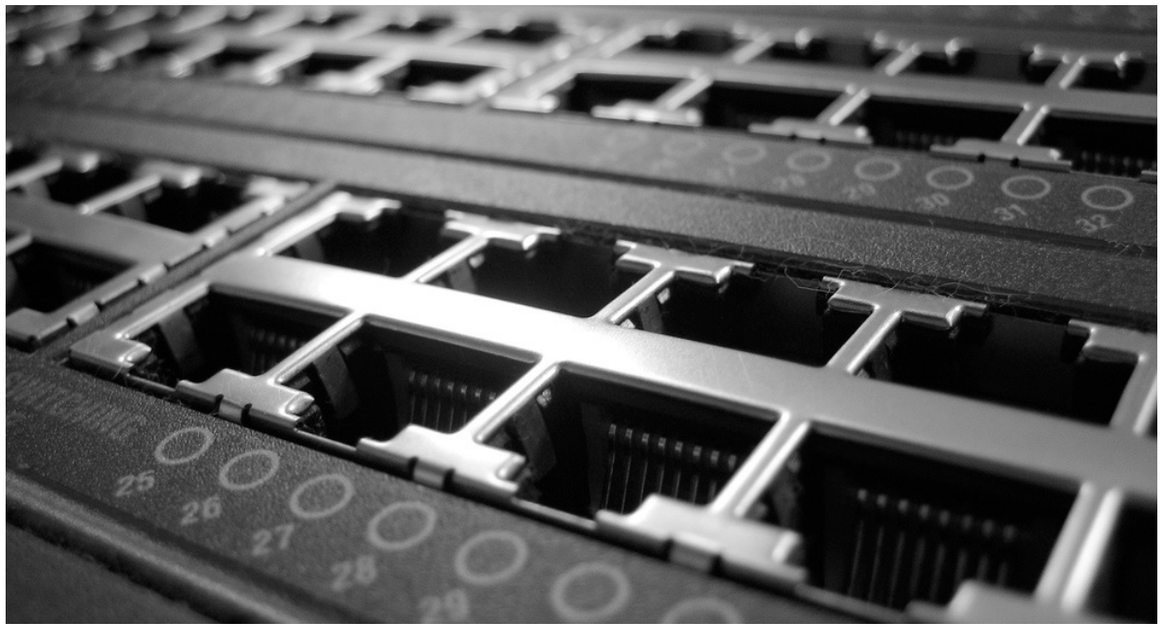


Setting up for success:

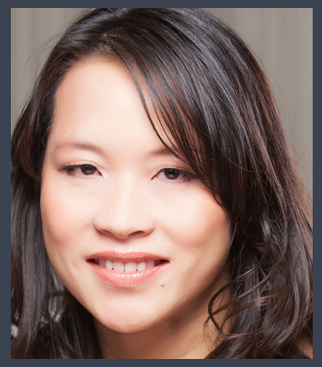
Everything you need to know when planning an RNA-seq experiment

Harvard Chan Bioinformatics Core

Harvard T.H. Chan School of Public Health

Boston, MA

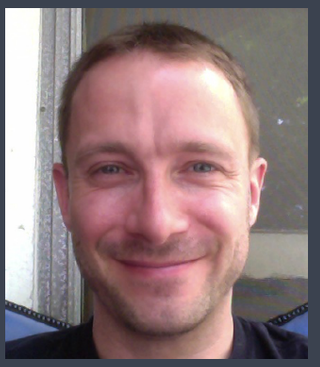
https://hbctraining.github.io/GCC-BOSC-2018/



Shannan Ho Sui

John Hutchinson

Brad Chapman



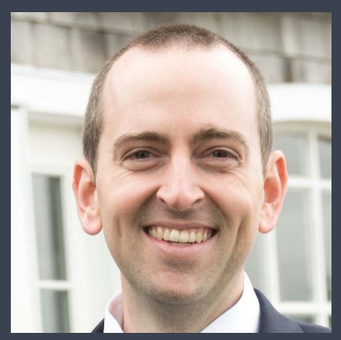
Rory Kirchner

Meeta Mistry

Radhika Khetani

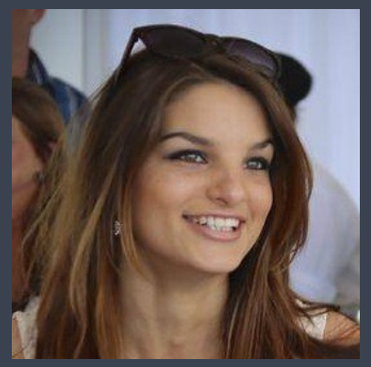
Mary Piper

Lorena Pantano



Michael Steinbaugh

Victor Barrera



Kayleigh Rutherford

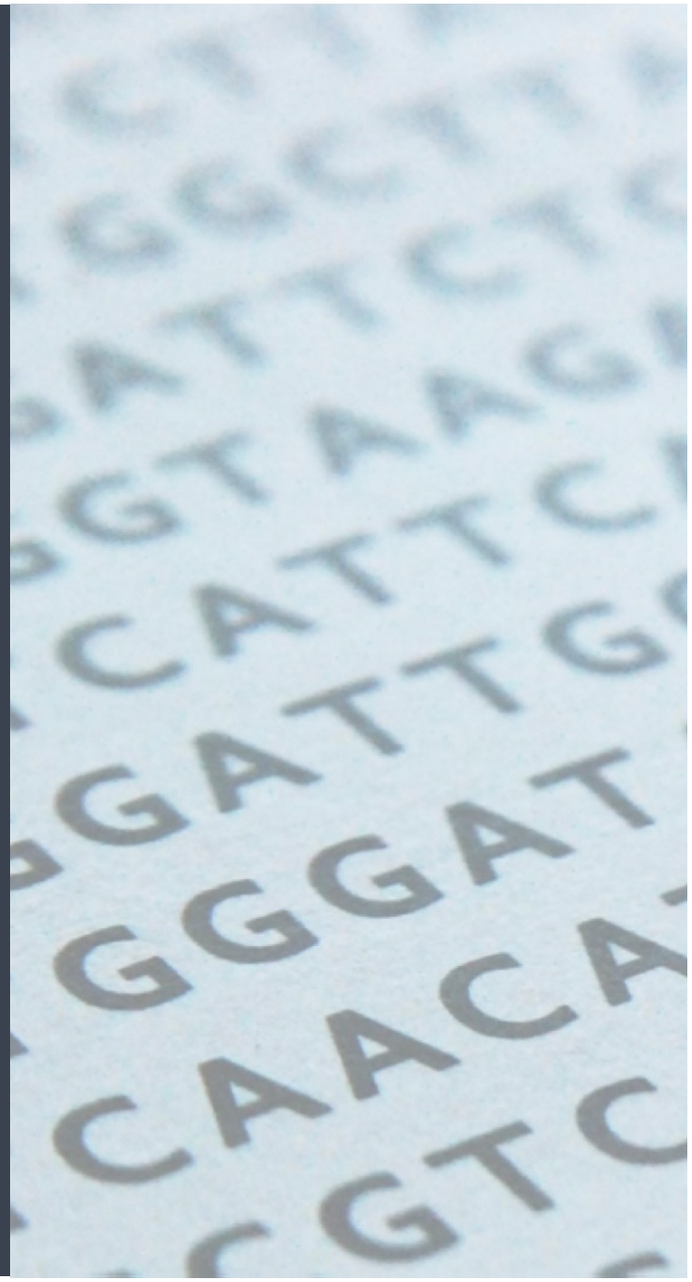
Peter Kraft

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

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

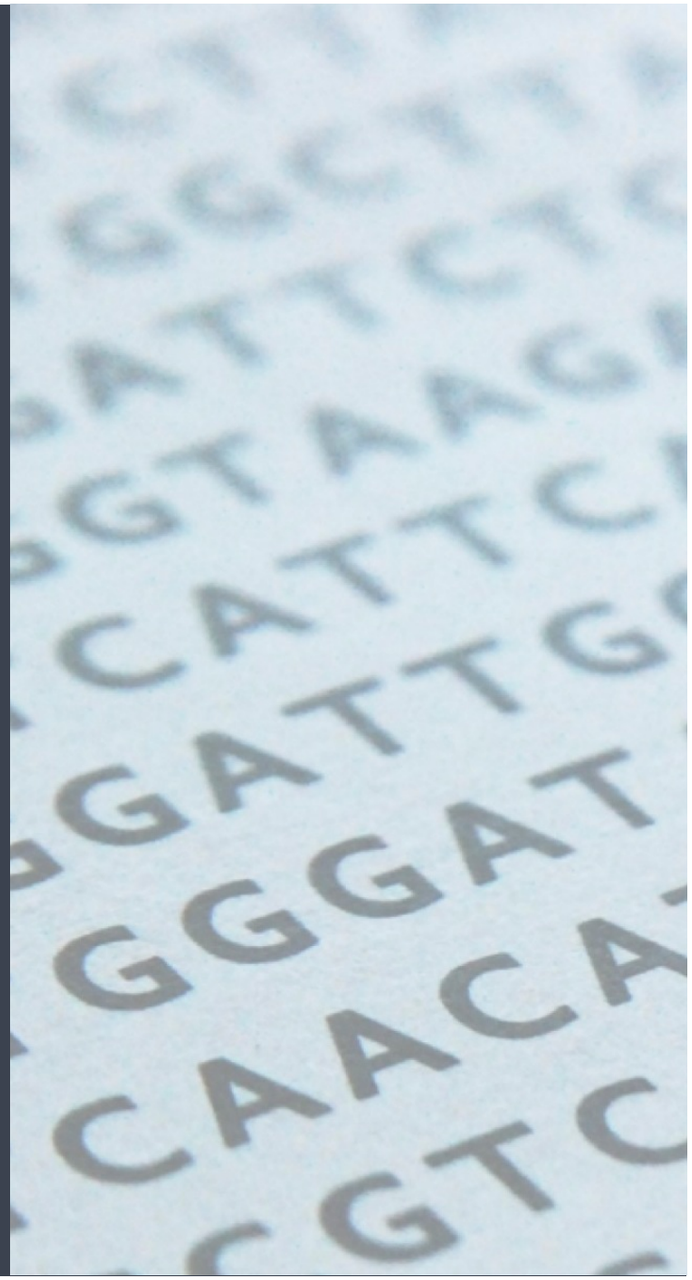
http://bioinformatics.sph.harvard.edu/

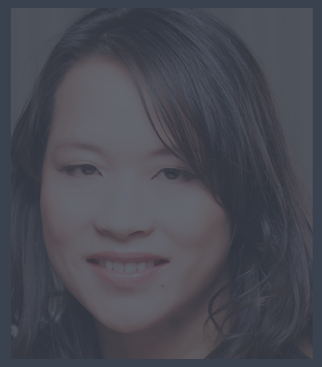


Training

https://hbctraining.github.io/main/

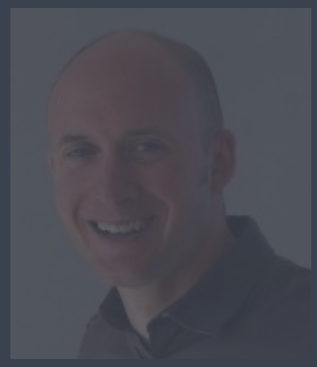
- Short workshops on introductory, intermediate and advanced topics related to NGS data analysis
- Monthly, 2-3 hour, hands-on and free workshops on “Current Topics in Bioinformatics”
- In-depth courses (8- or 12-day formats)



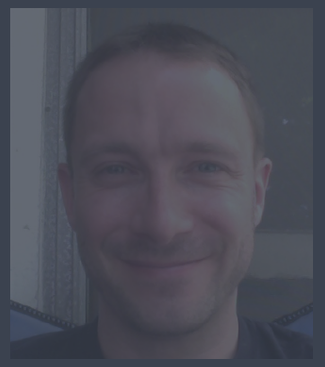


Shannan Ho Sui

John Hutchinson



Brad Chapman

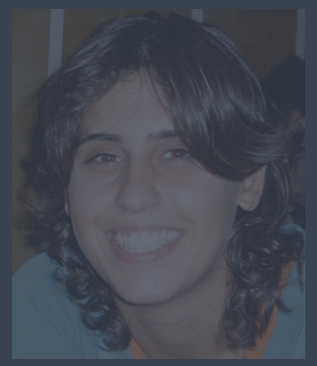


Rory Kirchner

Meeta Mistry

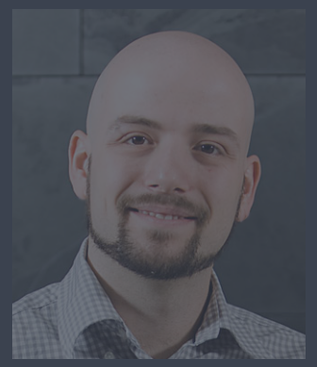
Radhika Khetani

Mary Piper

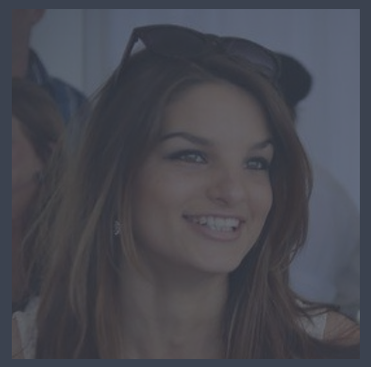


Lorena Pantano

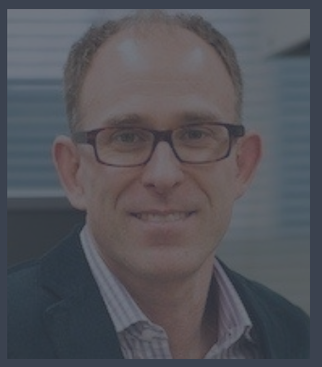
Michael Steinbaugh



Victor Barrera



Kayleigh Rutherford



Peter Kraft

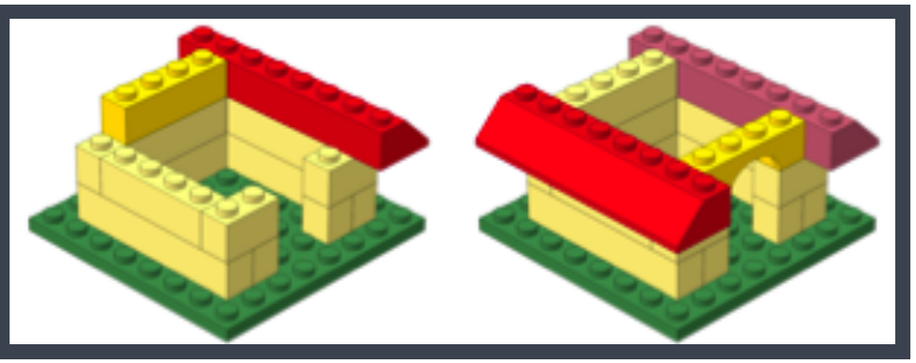
Tell us about yourself…

- Are you doing an RNA-seq experiment right now?
- If so, what stage of the experiment are you at?
- What is your current position, e.g. PI, postdoc, staff?

https://pollev.com/hbctraining945

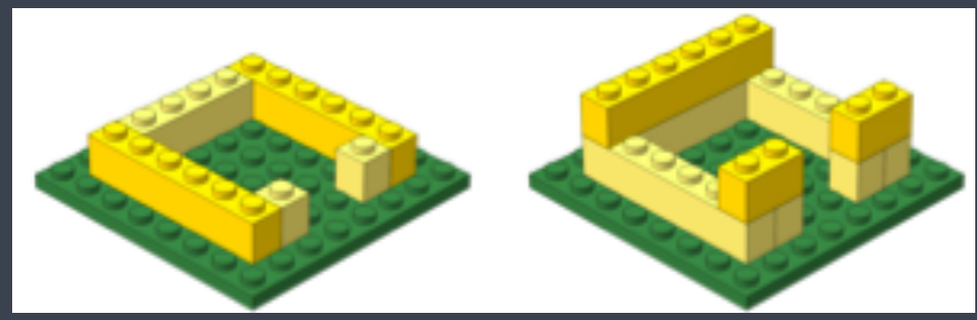
Workshop scope

Learning Objectives



- ✓ Describe the resources needed to perform an experiment to **identify differentially expressed genes using RNA sequencing**, including in the laboratory and computationally.
- ✓ Describe key experimental design considerations.
- ✓ Explain the analysis workflow (including QC) starting with raw data and finishing with a list of differentially expressed genes.
- ✓ List tools and computational skills necessary to implement the various steps in the above-mentioned workflow.

Base components



- ✓ Unix/Linux shell
  - Dealing with large data files (e.g. FASTQ, BAM)
  - Using bioinformatics tools (e.g. STAR, Trinity)
  - Accessing and using high-performance compute clusters
- ✓ R
  - Parsing and working with smaller results files
  - Statistical analysis, e.g. differential expression analysis (DESeq2)
  - Generating publication-quality figures from complex data (ggplot2)

Workshop webpage

https://hbctraining.github.io/GCC-BOSC-2018/

Contact us!

HBC training: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

HBC: @bioinfocore

These materials have been developed by members of the teaching team at the Harvard Chan Bioinformatics Core (HBC). These are open access materials distributed under the terms of the Creative Commons Attribution license (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.