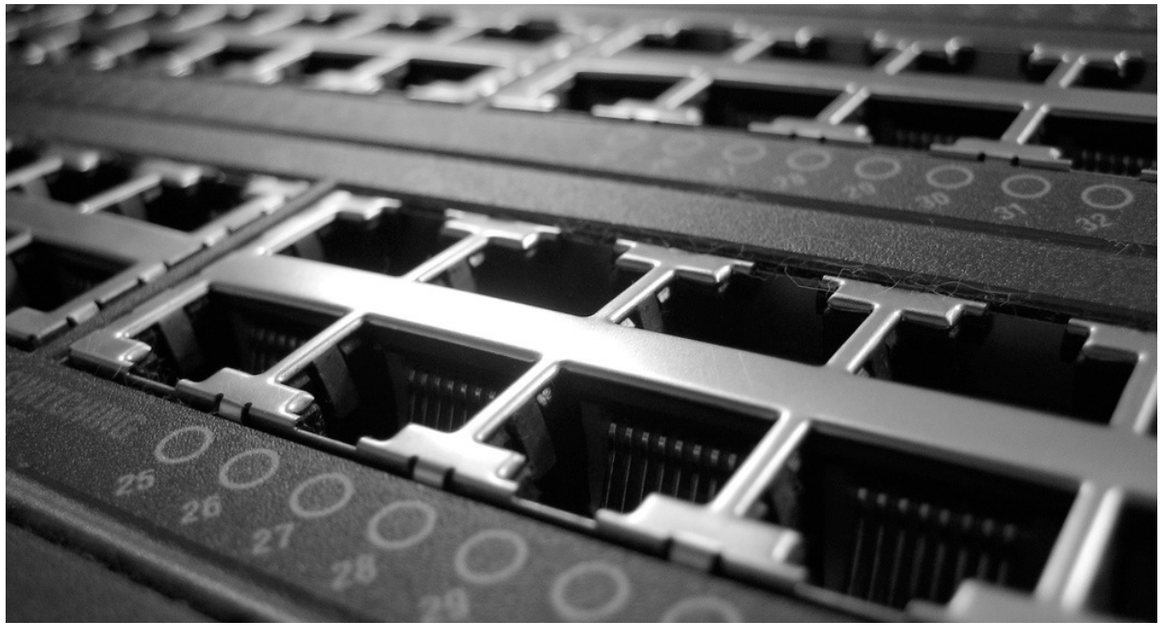


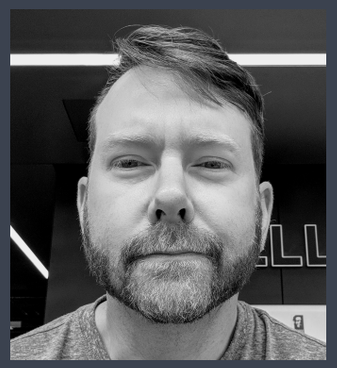
Introduction to Single-cell RNA-seq analysis

Harvard Chan Bioinformatics Core

HBC
Harvard Chan Bioinformatics Core

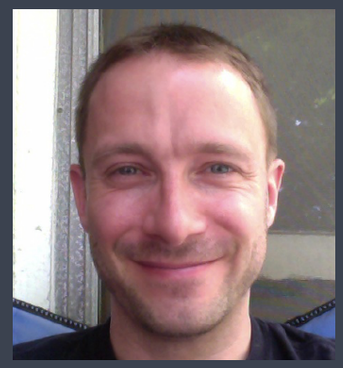
https://tinyurl.com/hbc-intro-to-scrnaseq

Shannan Ho Sui
Director



John Hutchinson
Associate Director

Victor Barrera



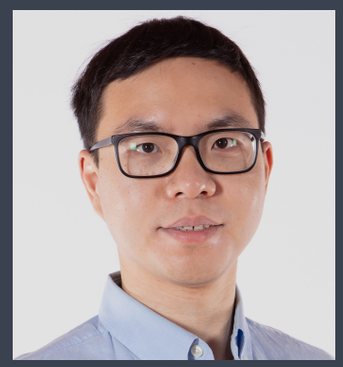
Rory Kirchner

Zhu Zhuo

Preetida Bhetariya

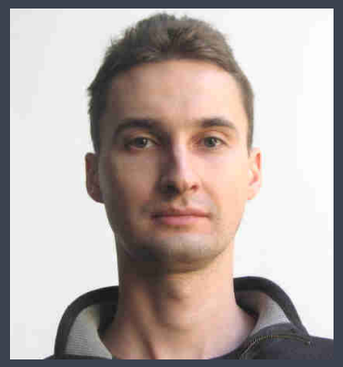
Meeta Mistry

Mary Piper



Jihe Liu

Radhika Khetani
Training Director



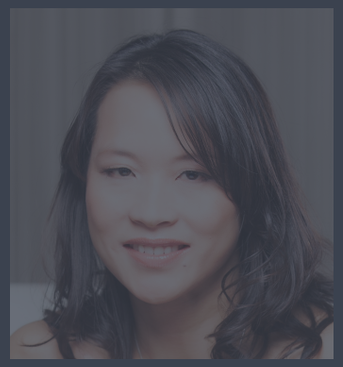
Ilya Sytchev

James Billingsley

Sergey Naumenko

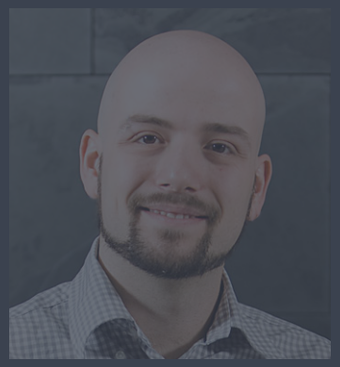
Joon Yoon

Peter Kraft
Faculty Advisor



Shannan Ho Sui
Director

John Hutchinson
Associate Director



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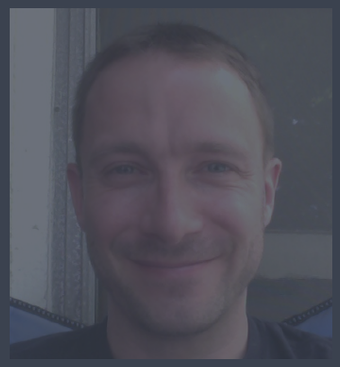

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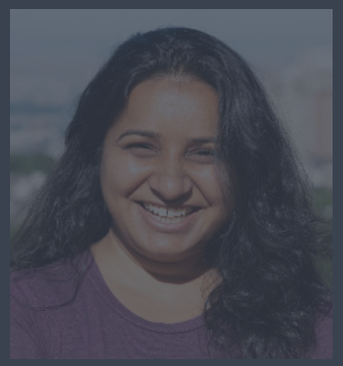

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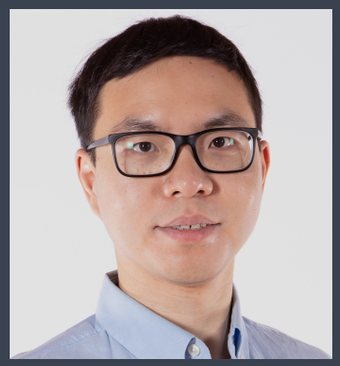

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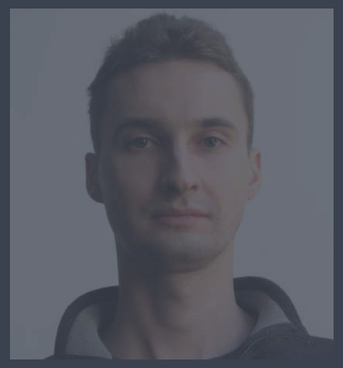

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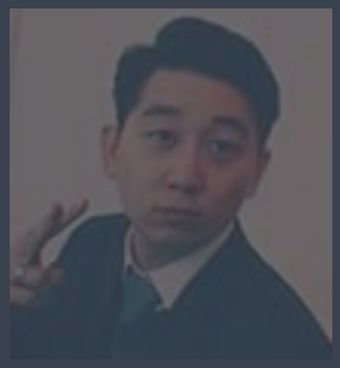
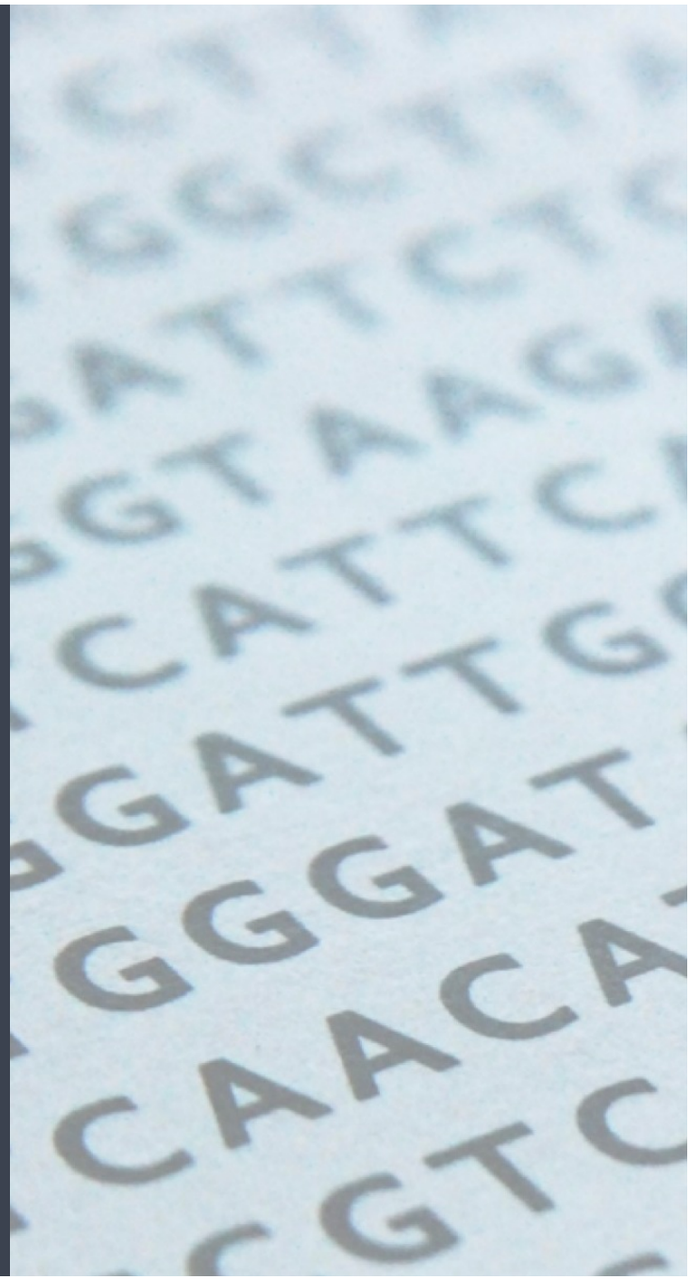


Joon Yoon

Peter Kraft
Faculty Advisor

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



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

Training

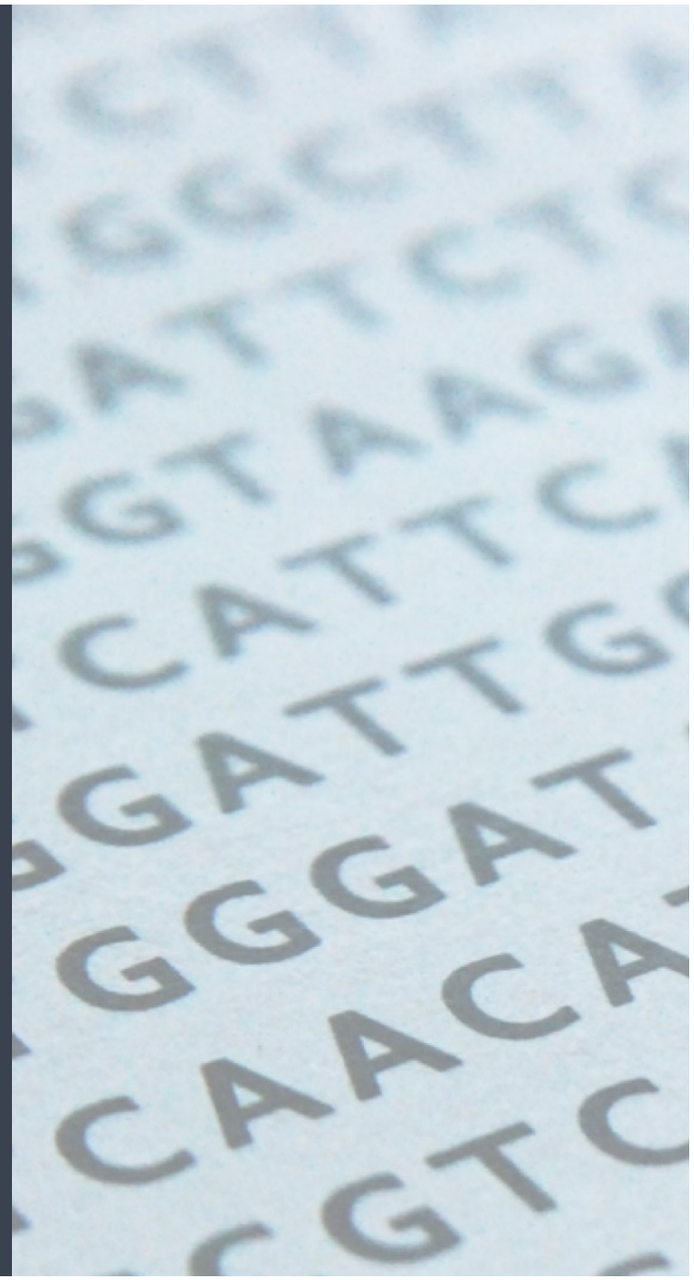
We have divided our short workshops into 2 categories:

1. **Basic Data Skills** - No prior programming knowledge needed (no prerequisites)
2. **Advanced Topics: Analysis of high-throughput sequencing (NGS) data** - Certain “Basic” workshops required as prerequisites.

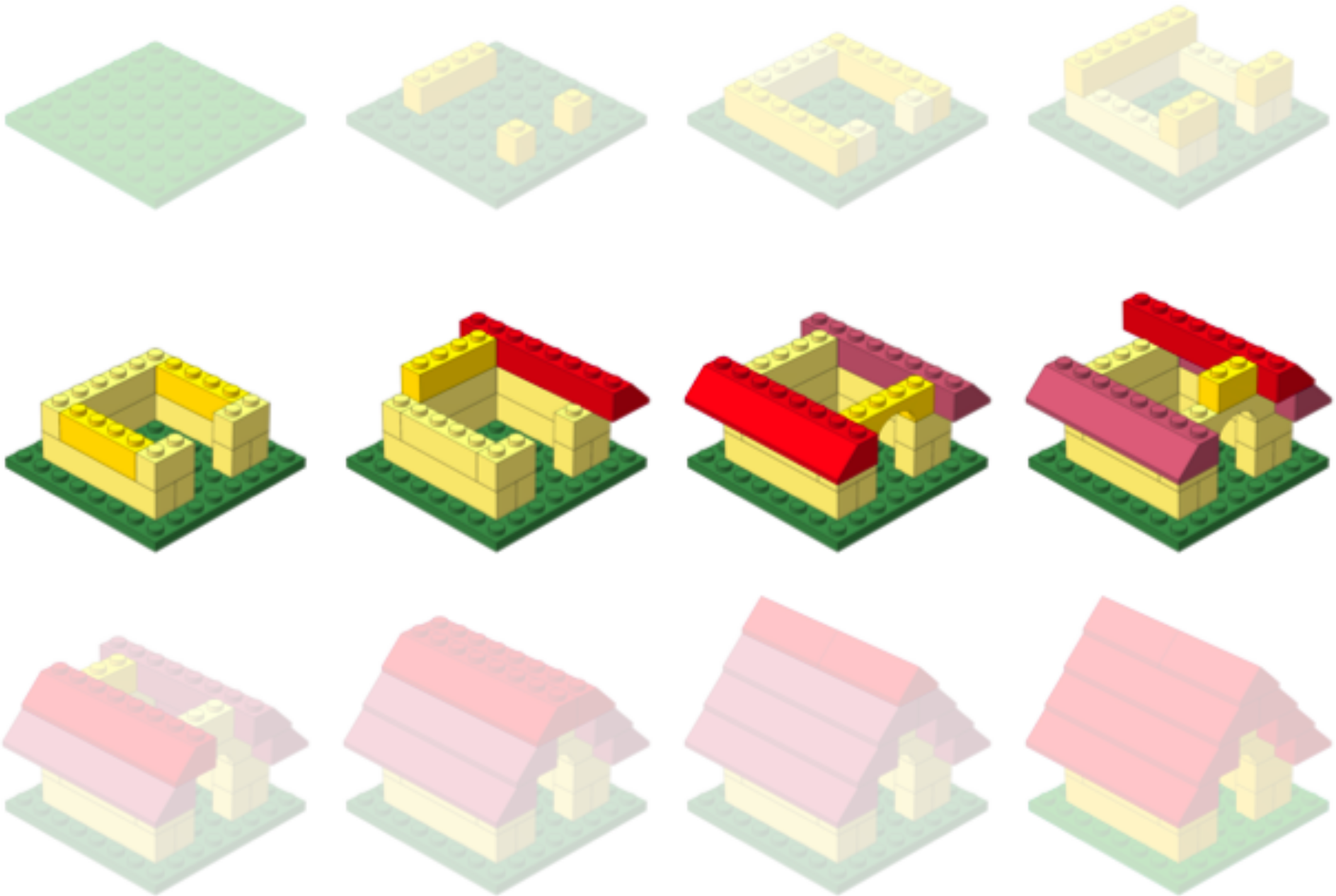
Any participants wanting to take an advanced workshop will have to have taken the appropriate basic workshop(s) within the past 6 months.

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

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



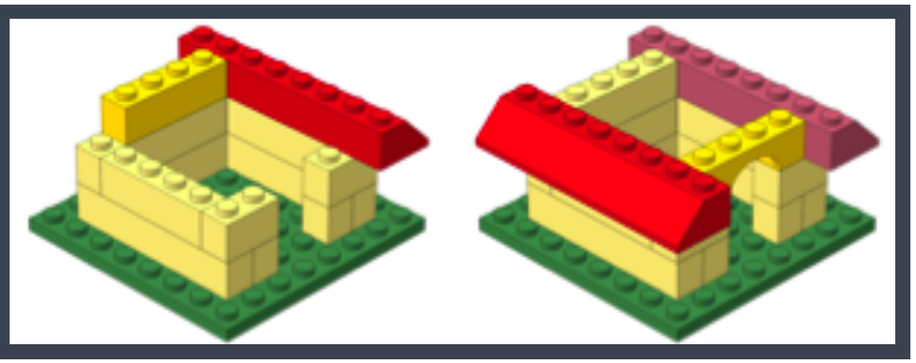
Workshop scope



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

Bioinformatics data analysis

Learning Objectives



- ✓ Describe best practices for designing a Single-cell RNA-seq experiment
- ✓ Describe steps in a Single-cell RNA-seq analysis workflow.
- ✓ Use Seurat and associated tools to perform analysis of single-cell expression data, including data filtering, QC, integration, clustering, and marker identification

Logistics

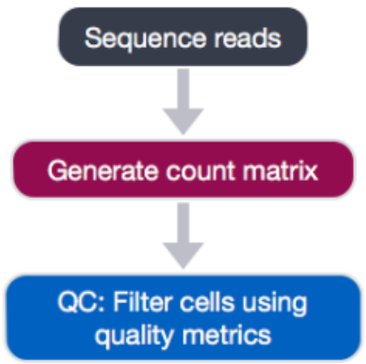
https://tinyurl.com/hbc-intro-to-scrnaseq

Approximate time: 90 minutes

Learning Objectives:

- Understand how to bring in data from single-cell RNA-seq experiments
- Construct QC metrics and associated plots to visually explore the quality of the data
- Evaluate the QC metrics and set filters to remove low quality cells

Single-cell RNA-seq: Quality control



Odds and Ends

- Name tags: Tent Cards
- Post-its
- Phones on vibrate/silent!

Contact us!

Training team : hbctraining@hsph.harvard.edu

Consulting : bioinformatics@hsph.harvard.edu

@bioinfocore