Introduction to Single-cell RNA-seq Analysis

https://tinyurl.com/hbc-scrnaseq-online

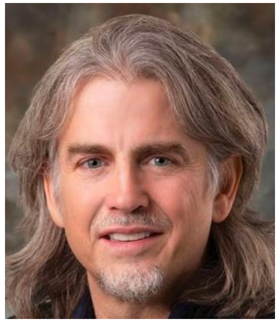
Harvard Chan Bioinformatics Core

Introductions!

Shannan Ho Sui
Director

Meeta Mistry
Associate Director

Lorena Pantano
Director of Bioinformatics Platform



John Quackenbush
Faculty Advisor

Upen Bhattarai

Heather Wick

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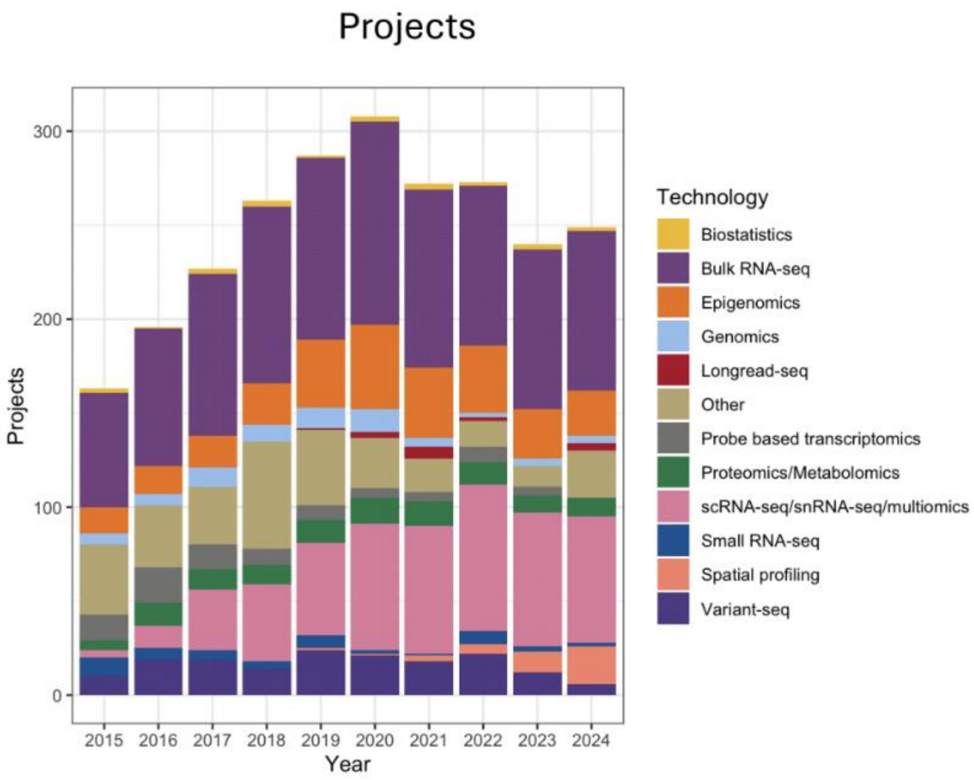
Consulting

- Transcriptomics: Bulk, single cell, small RNA
- Epigenomics: ChIP-seq, CUT&RUN, ATAC-seq, DNA methylation
- Variant discovery: WGS, resequencing, exome-seq and CNV
- Multiomics integration
- Spatial biology
- Experimental design and grant support



https://bioinformatics.sph.harvard.edu/services

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AND TRANSLATIONAL
SCIENCE CENTER

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MEDICAL SCHOOL

Training

- Hands-on workshops design to reflect best practices, reproducibility and an emphasis on experimental design
  - Basic Data Skills
    - Shell
    - R
  - Advanced Topics: Analysis of high-throughput sequencing data
    - Chromatin Biology
    - Bulk RNA-seq
    - Differential Gene Expression
    - scRNA-seq
    - Variant Calling
  - Current Topics in Bioinformatics

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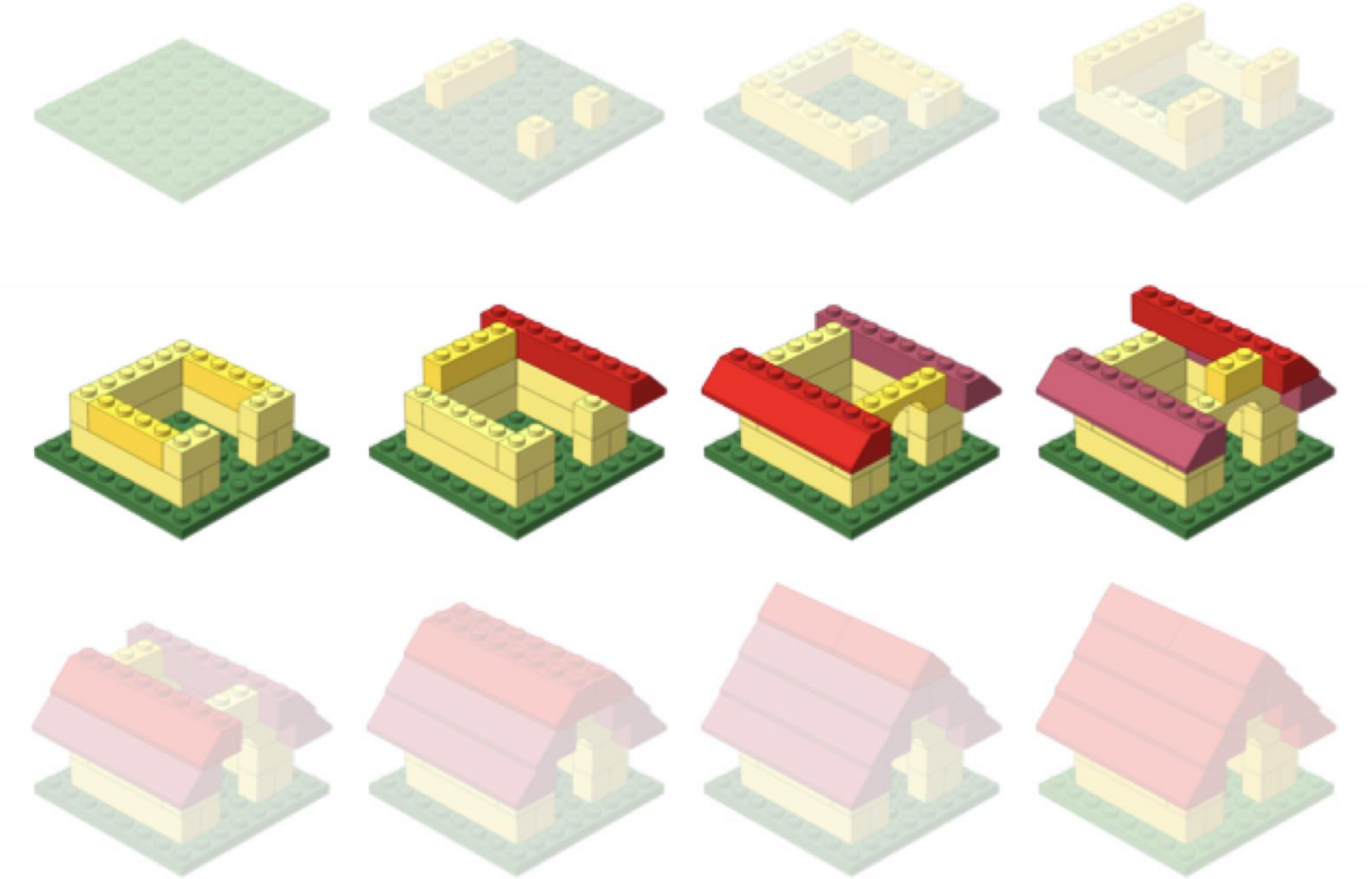
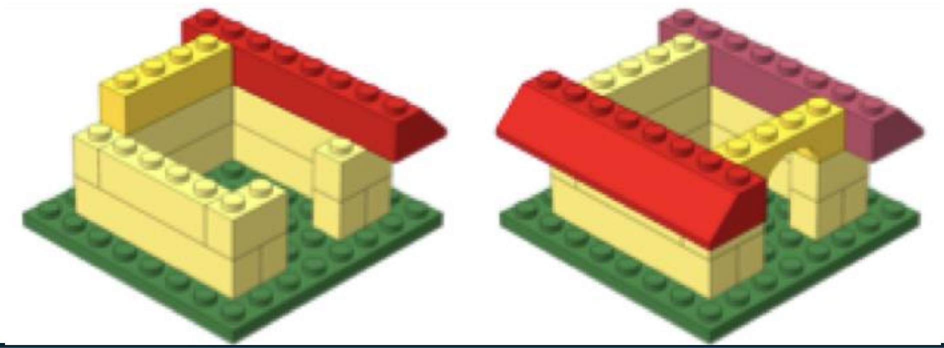
Workshop scope



Bioinformatic Data Analysis

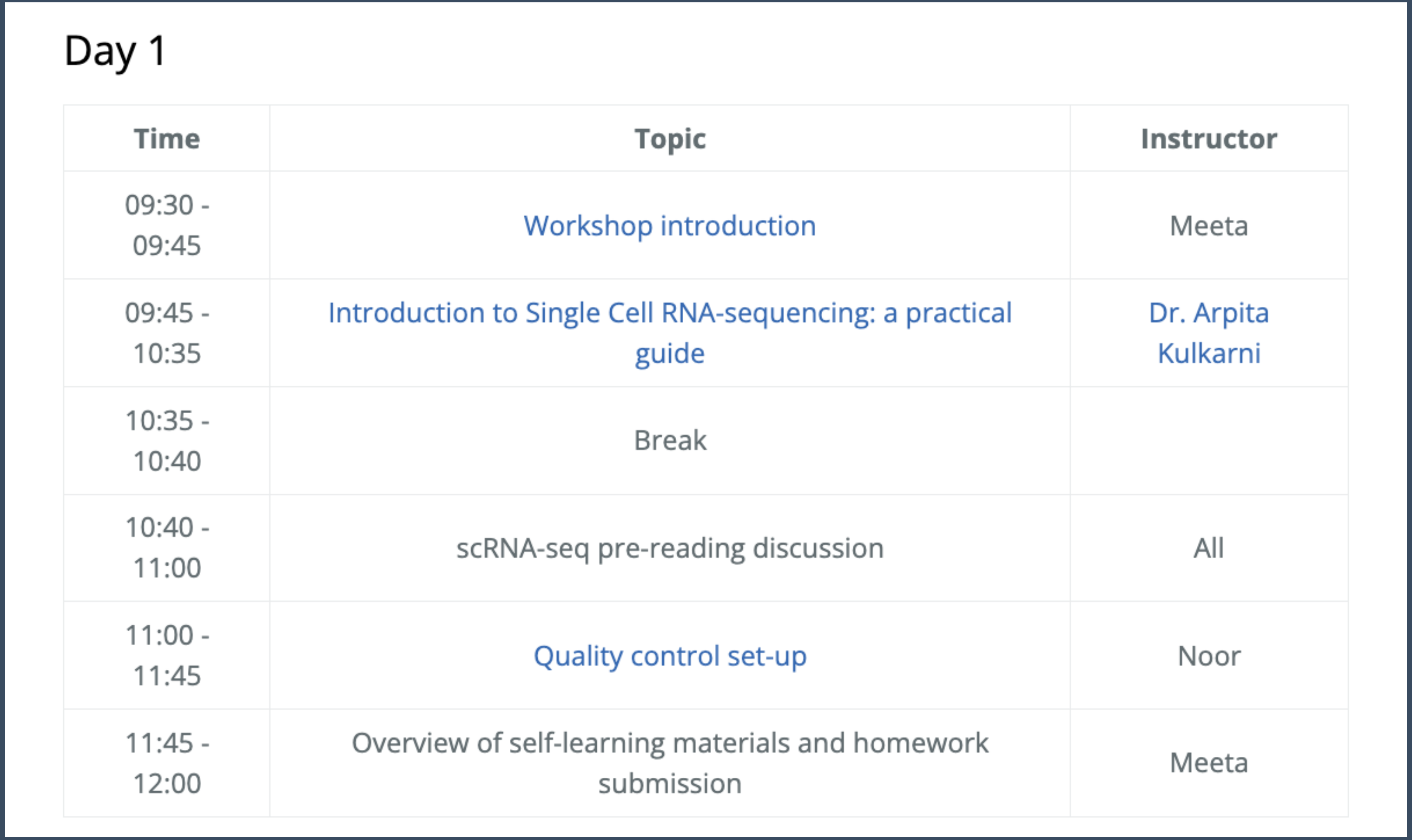
Workshop Scope



- 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
- Understand practical considerations for performing scRNA-seq, rather than in-depth exploration of algorithm theory

Logistics

Course schedule



Day 1

Time	Topic	Instructor
09:30 - 09:45	Workshop introduction	Meeta
09:45 - 10:35	Introduction to Single Cell RNA-sequencing: a practical guide	Dr. Arpita Kulkarni
10:35 - 10:40	Break	
10:40 - 11:00	scRNA-seq pre-reading discussion	All
11:00 - 11:45	Quality control set-up	Noor
11:45 - 12:00	Overview of self-learning materials and homework submission	Meeta

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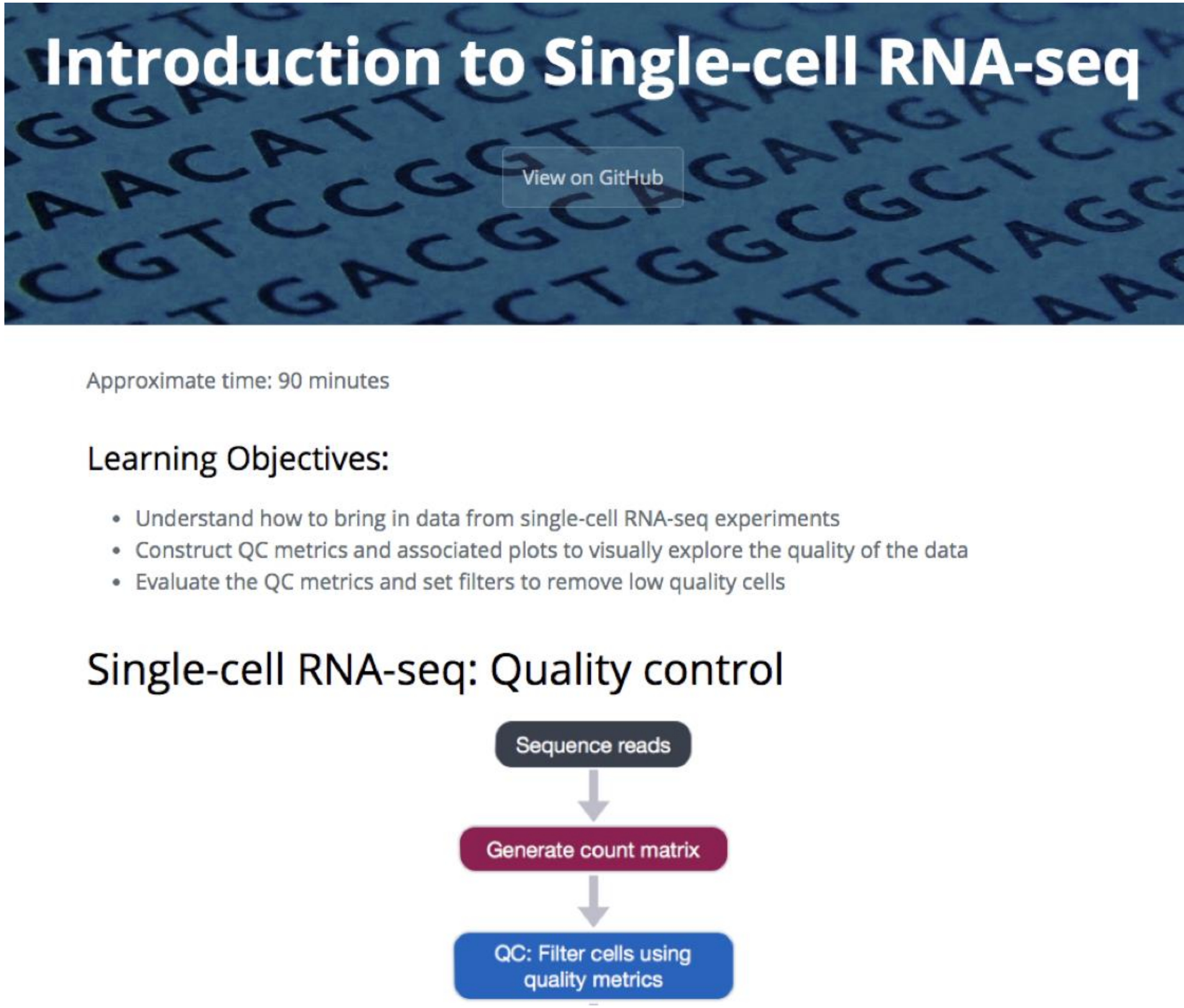
Course materials

- We continuously update our materials to reflect changes in the field/software



Introduction to Single-cell RNA-seq

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

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Course participation

- Mandatory review of self-learning lessons and assignments
- Attendance required for all classes
- Your questions and active participation drive learning
- **We look forward to all of your questions!**

Course participation

- At-home lessons and exercises after each session
- Cover material not previously discussed
- Provides us feedback to help pace the course appropriately
- 3-5 hours to complete
- Homework load is heavier in the beginning of this workshop series and tapers off

Using AI for Assignments

- Do
    - Try to resolve error messages with it
    - Test code written by AI on a dataset where you have expected results
    - Take the time to review the generated code line-by-line
- Don’t
    - Implement it in replacement to learning
    - Write code that you don’t understand
    - Assume the output from an AI process is correct

Odds & Ends

- Quit/minimize all applications that are not required for class
- Name tags
- Post-its
  - 🟩 green - I am all set
  - 🟥 red - I need time/help
- Phones on vibrate/silent
- Bathrooms

Contact Us

- *HBC training team:* hbctraining@hsph.harvard.edu
- *HBC consulting:* bioinformatics@hsph.harvard.edu