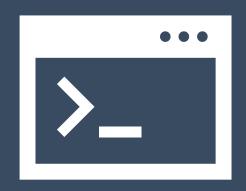


Differential expression analysis of Single Cell RNA-seq

https://tinyurl.com/DGE-analysis-scRNAseq



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



Will Gammerdinger



Noor Sohail



Elizabeth Partan



Alex Bartlett



Emma Berdan



James Billingsley



Zhu Zhuo



Maria Simoneau



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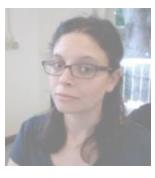
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Consulting

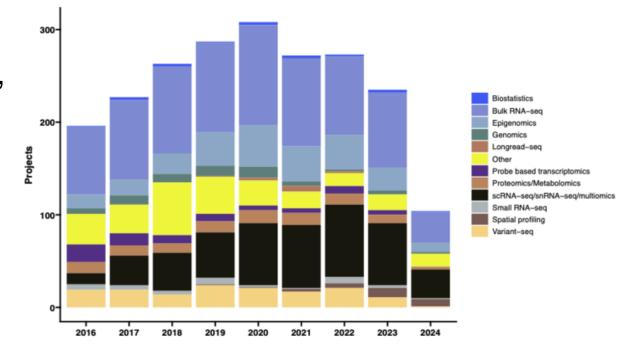
Transcriptomics: Bulk, single cell, small RNA

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



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THE HARVARD CLINICAL
AND TRANSLATIONAL
SCIENCE CENTER



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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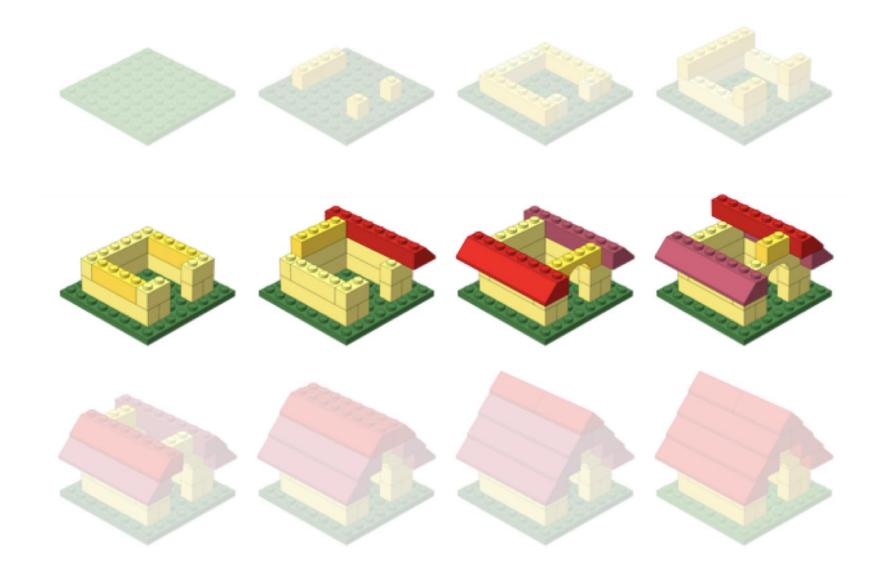




THE HARVARD CLINICAL AND TRANSLATIONAL SCIENCE CENTER



Workshop scope



Bioinformatic Data Analysis

What is NOT covered in this workshop

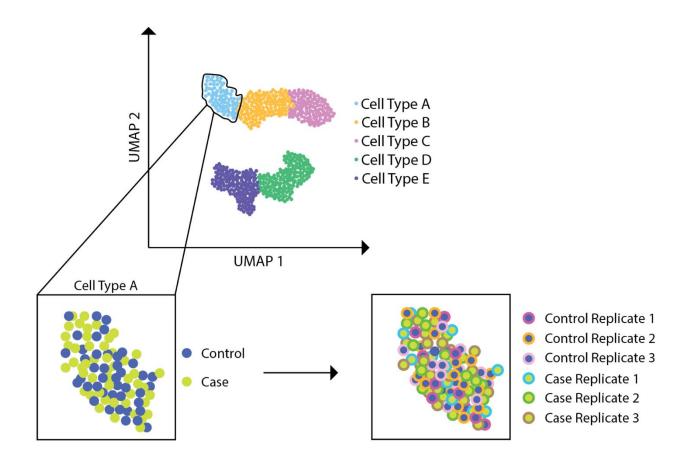
PRE-PROCESSING Raw data processing Normalization Count depth Data correction (e.g. batch) Highly variable **DOWNSTREAM ANALYSIS**

Marker identification

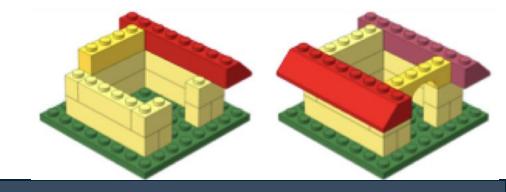
Luecken, MD and Theis, FJ. Current best practices in single-cell RNA-seq analysis: a tutorial, Mol Syst Biol 2019 (doi: https://doi.org/10.15252/msb.20188746)

EMBC

What IS covered in this workshop



Workshop Scope



- Understanding considerations for when to use different DGE algorithms on scRNA-seq data
- Using FindMarkers to evaluate significantly DE genes
- Aggregating single cell expression data into a pseudobulk counts matrix to run a DESeq2 workflow
- Evaluating expression patterns of differentially expressed genes at the pseudobulk and single cell level
- Application of methods for evaluating differential proportions of cells between conditions



Course schedule

Day 1

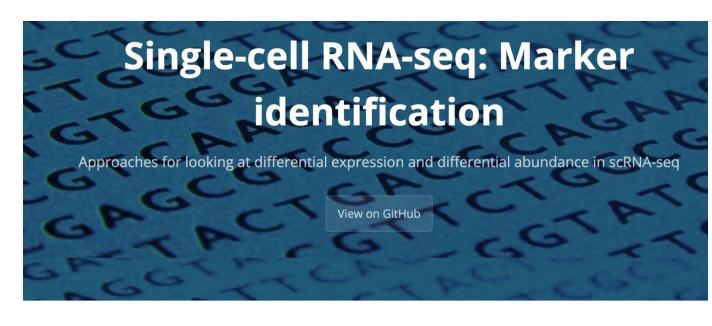
Time	Topic	Instructor
09:30 - 09:45	Workshop introduction	Noor
09:45 - 10:30	Project setup and data exploration	Noor
10:30 - 10:40	Break	
10:40 - 11:45	Differential expression analysis using FindMarkers()	Meeta
11:45 - 12:00	Overview of self-learning materials and homework submission	Meeta

Before the next class:

- I. Please **study the contents** and **work through all the code** within the following lessons:
 - 1. Aggregating counts by celltype using pseudobulk approach Click here for a preview of this lesson
 - 2. DE analysis of pseudobulk data using DESeq2 Click here for a preview of this lesson

Course materials

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



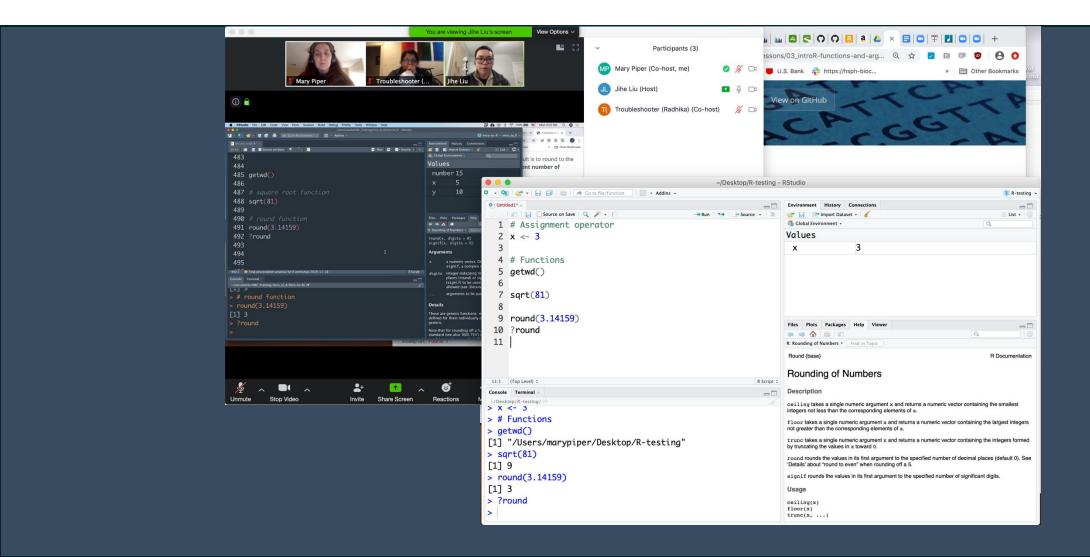
Approximate time: 75 minutes

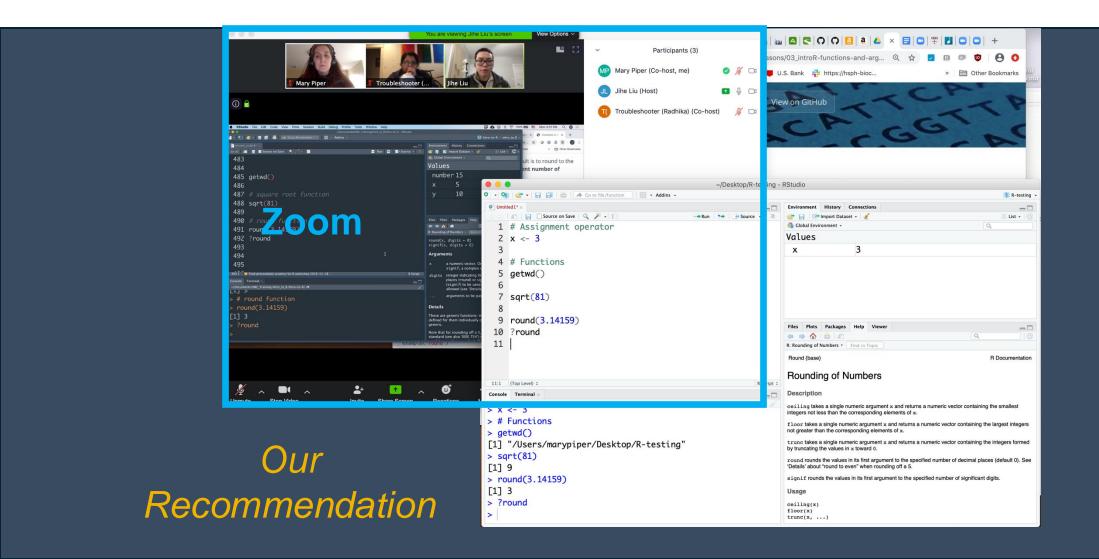
Learning Objectives:

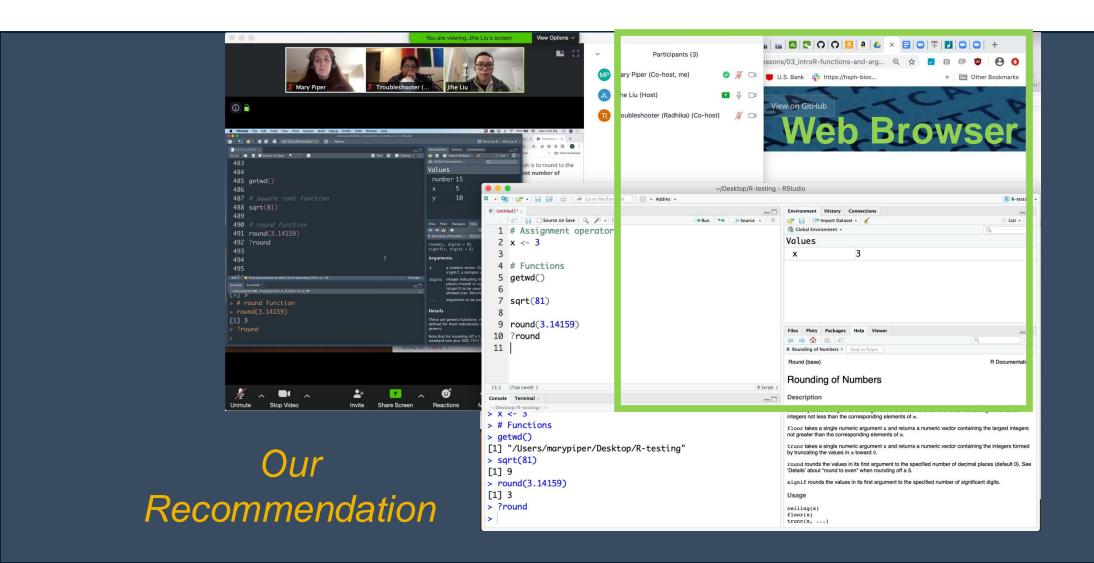
- Evaluate differential gene expression between conditions using a Wilcoxon rank sum test
- Create visualizations for differentially expressed genes
- Discuss other statistical tests for differential expression analysis

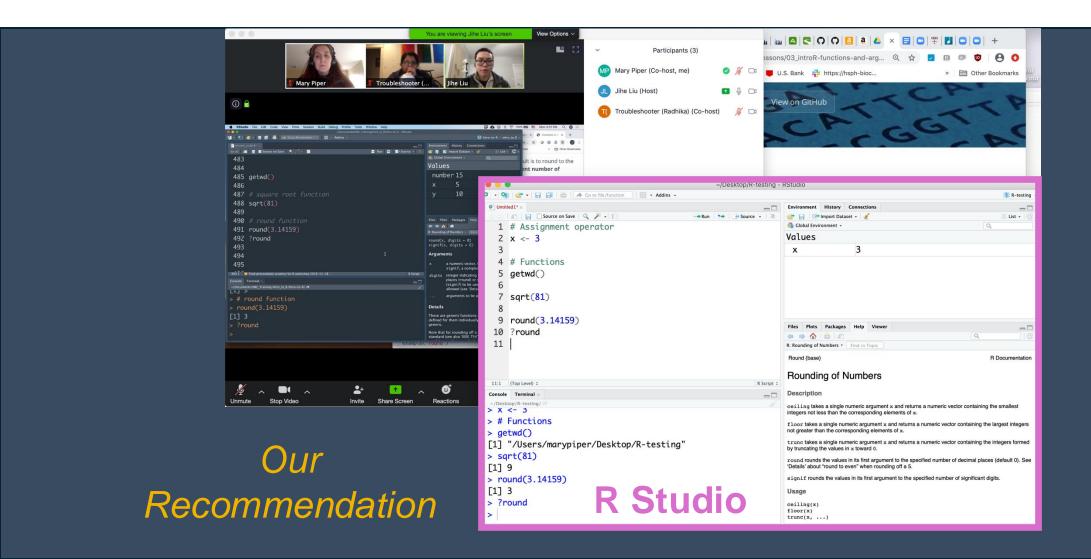
Differential expression between conditions using FindMarkers()

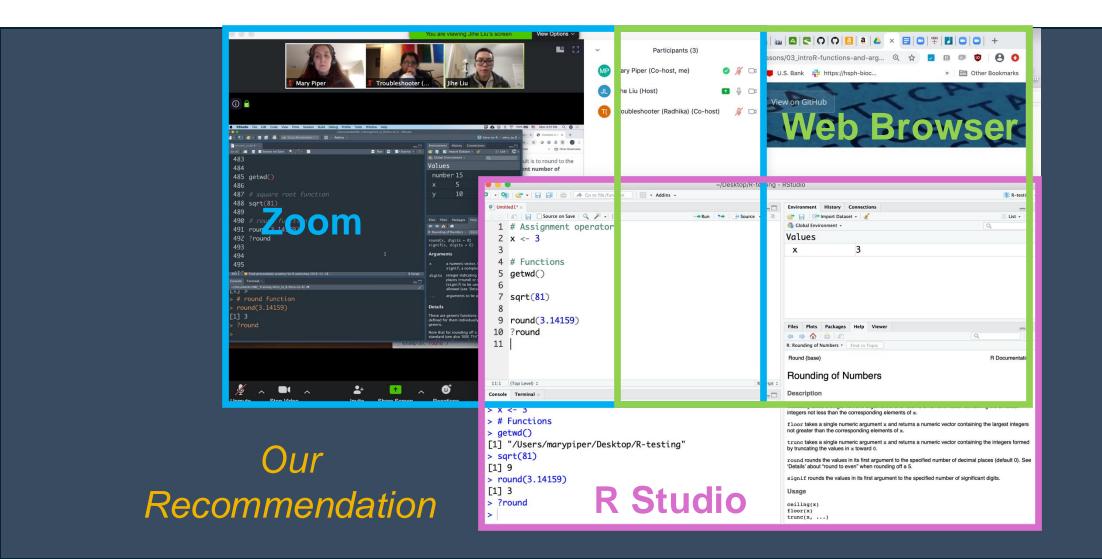
In our current UMAP, we have merged samples across the different conditions and used integration to align cells of the same celltype across samples. Now, what of we were interested in a particular celltype and **understanding how gene expression changes across the different conditions?**





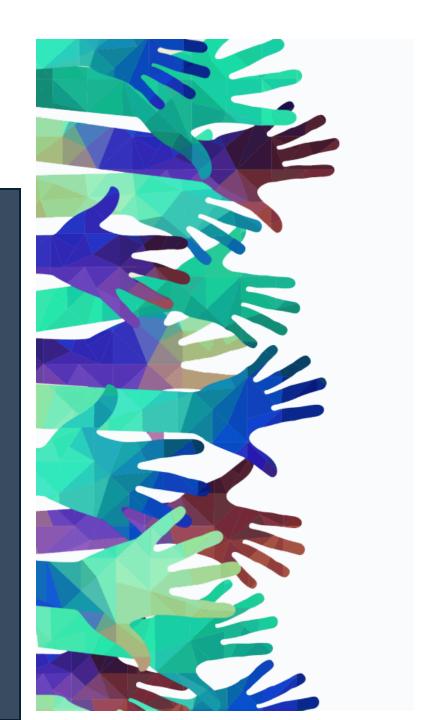






Course participation

- 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