Differential expression analysis of Single Cell RNA-seq
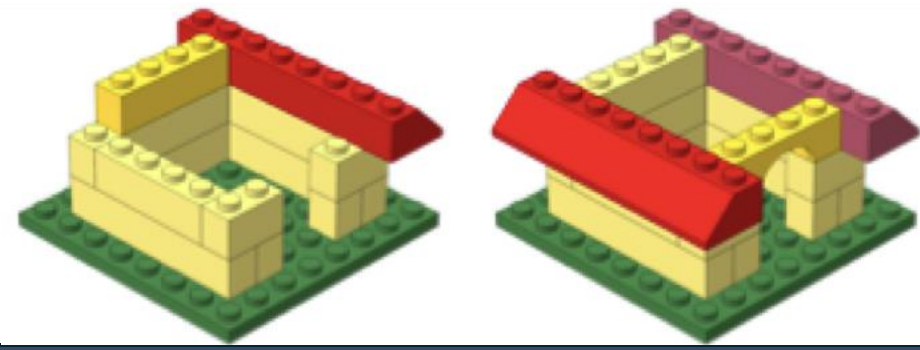
https://tinyurl.com/DGE-analysis-scRNAseq
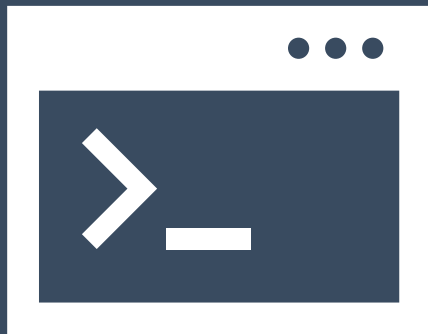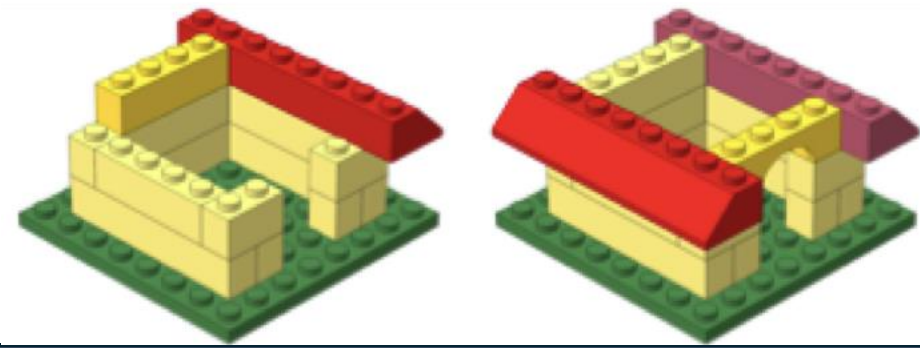
Harvard Chan Bioinformatics Core

Workshop Scope

❖ Understanding considerations for when to use different DGE algorithms on scRNA-seq data

❖ Using FindMarkers to evaluate significantly different genes

❖ Pseudobulking a counts matrix in order to run DESeq2 for a DGE analysis

❖ Visualizing and evaluating expression patterns of differentially expressed genes

❖ Calculating differential abundance with MiloR

Exit survey

Useful resources

❖ **Computational packages for single-cell analysis:**

❖ http://bioconductor.org/packages/devel/workflows/html/simpleSingleCell.html

❖ https://satijalab.org/Seurat/

❖ https://scanpy.readthedocs.io/

❖ https://github.com/seandavi/awesome-single-cell

❖ **Online courses:**

❖ https://hemberg-lab.github.io/scRNA.seq.course/

❖ https://github.com/SingleCellTranscriptomics

❖ **Resources for scRNA-seq Sample Prep:**

❖ https://www.protocols.io/

❖ https://support.10xgenomics.com/single-cell-gene-expression/sample-prep

❖ https://community.10xgenomics.com/

Research Data Management (RDM)

BIOMEDICAL RESEARCH DATA LIFECYCLE
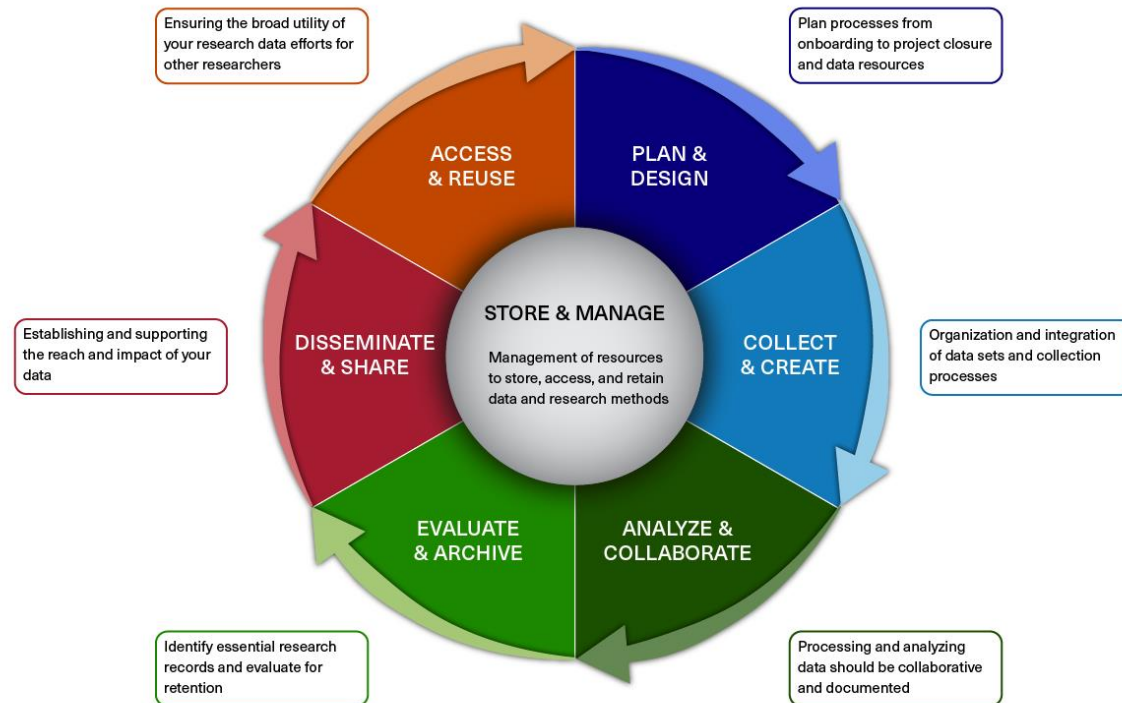
Better RDM practice benefits you

- ❖ **HMS Data Management LMA**

    - ❖ **Webpage:** https://datamanagement.hms.harvard.edu

    - ❖ **Sign up for quarterly email updates**

- ❖ **Harvard-wide Research data Management**

    - ❖ https://researchdatamanagement.harvard.edu/

Nov 20	1pm	**HBC: Basic Shell**	Zoom
Nov 20	1pm	**HMS CCB R/Stats Office Hours**	Countway Library, L1 Room 11
Nov 21	10am	**HMS RC: Intro to O2**	HMS TMEC
Nov 21	10am	**Managing Your Paper Records: Off-Site Records Storage**	Zoom
Nov 21	10am	**Trajectory inference in single cell data**	Hybrid
Nov 27	1pm	**HMS CCB R/Stats Office Hours**	Countway Library, L1 Room 11

Keep building!
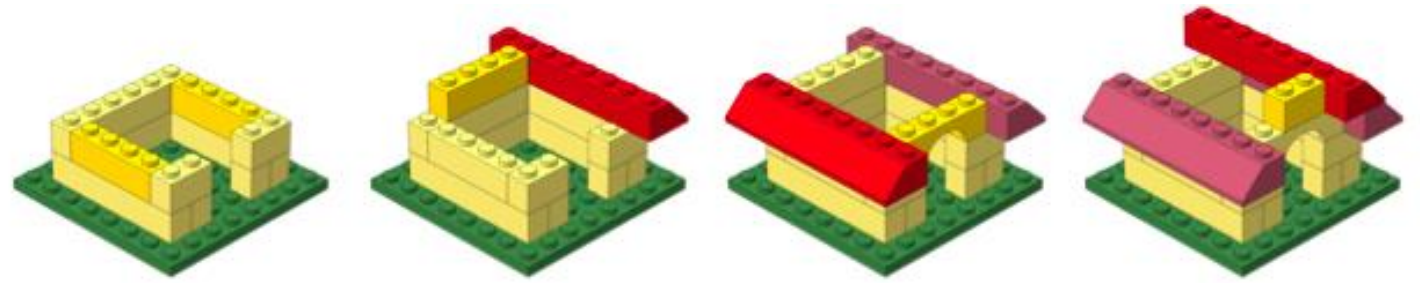
2024 schedule:

Topic	Pre-requisites	Date/Time	Time	Registration
Tips and Tricks on O2	Shell	12/11/24*	1 – 4pm	Register!

https://bioinformatics.sph.harvard.edu/current-bioinformatics-topics-workshops

Keep building!
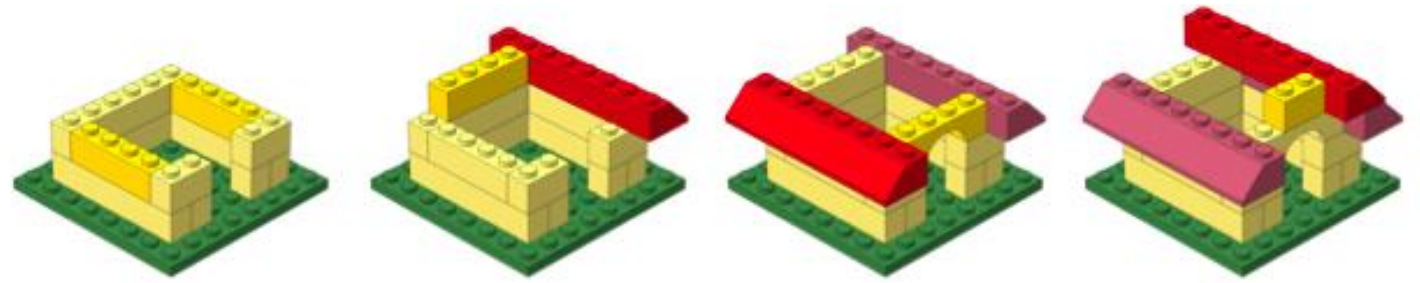
Topic	Category	Date	Duration	Prerequisites
Peak analysis	Advanced	December 3, 6, 10	Three 2.5h sessions	R

Tentative; 2025 Workshops:

Topic	Category	Date	Duration	Prerequisites
Shell for Bioinformatics	Basic	January 21, 24, 28	Three 2.5h session	None
Introduction to bulk RNA-seq data analysis Part I	Advanced	February 4, 7, 11	Three 2.5h session	Shell for Bioinformatics

https://bioinformatics.sph.harvard.edu/upcoming-workshops

Talk to us early!

Involvement in study design to optimize experiments

More Information

❖ *HBC training materials: https://hbctraining.github.io/main*

❖ *HBC website: http://bioinformatics.sph.harvard.edu*

Contact Us

Sign up for our mailing list:

https://tinyurl.com/hbc-training-mailing-list

❖ *HBC training team:* hbctraining@hsph.harvard.edu

❖ *HBC consulting:*   bioinformatics@hsph.harvard.edu