Introduction to Single-cell RNA-seq Analysis
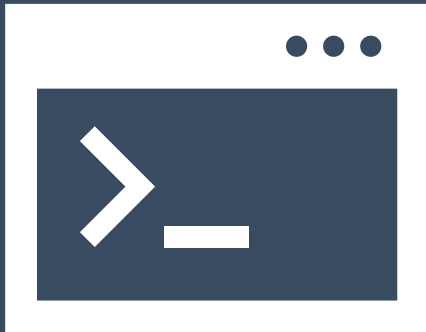
GEN349: Current tools for Gene Analysis
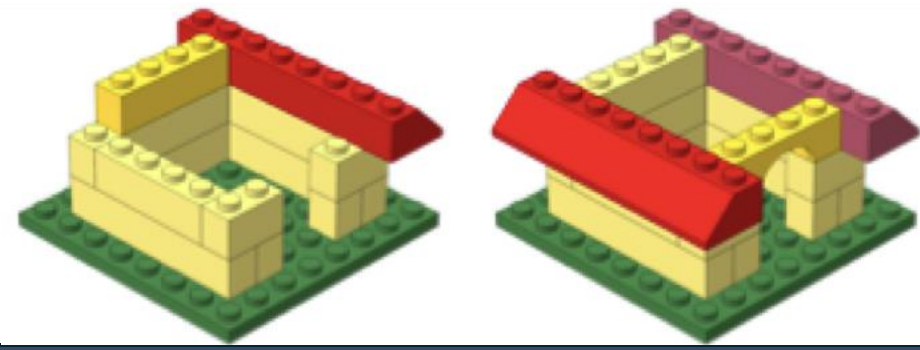
Harvard Chan Bioinformatics Core
February 25th, 2025

**https://tinyurl.com/hbc-GEN349-scRNAseq**

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

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

Exit survey

https://tinyurl.com/scRNAseq-online

Research Data Management (RDM)

BIOMEDICAL RESEARCH DATA LIFECYCLE
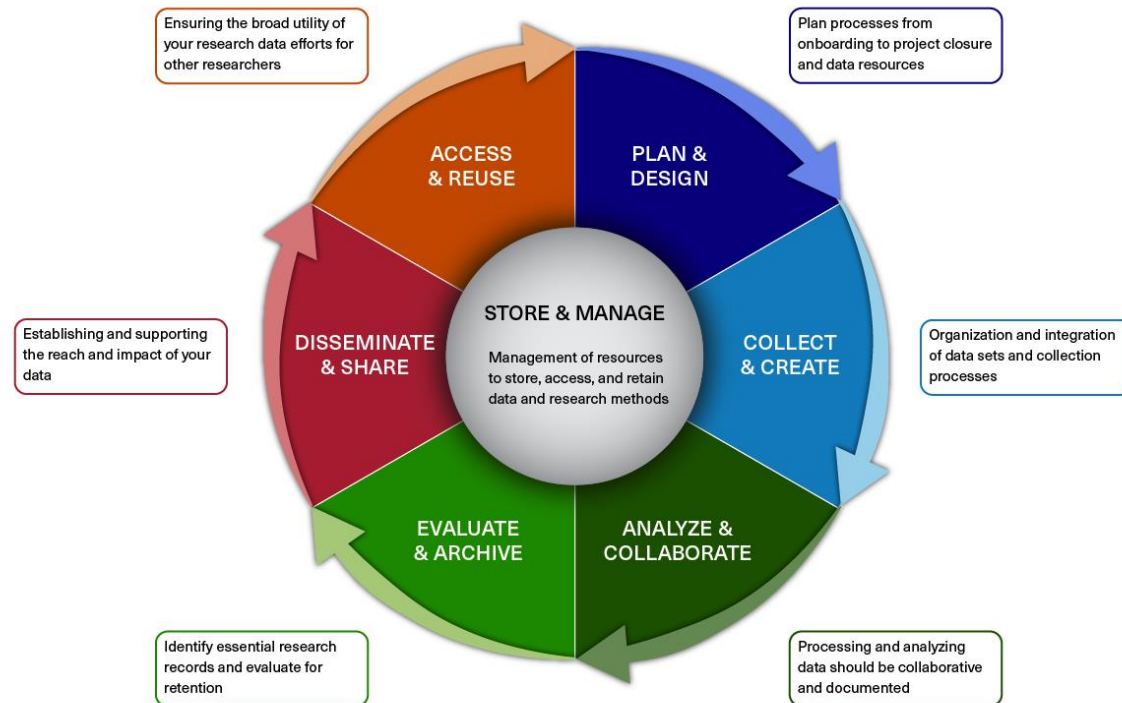
Better RDM practice benefits you

❖ **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/

Spring 2025 Data Lifecycle Training

Plan & Design

February 11 🖥
Data Management Offboarding for Research Projects

March 19 👥🖥
A Guide to Efficient Research Practices

March 26 👥🖥
Tips and Tricks for Writing an Actionable Data Management Plan

May 21 🖥
Research Data Stewardship Basics

Collect & Analyze

January 29 👥
Data Literacy: Introduction to GIS

February 19 🖥
Foundations in R

March 19 🖥
Reproducible Research using RMarkdown

April 16 🖥
An Introduction to Git and GitHub

May 21 🖥
Managing Conflicts on GitHub

Store & Evaluate

March 10 🖥
Introduction to the General Records Schedule

April 7 🖥
Managing Paper Records: Off-Site Records Storage

April 21 🖥
Managing Electronic Records: Shared Drives and Emails

Share & Publish

February 27 🖥
Research Management: Open Access Publishing

April 9 👥🖥
Research Management: Closing Out Your Research

April 23 🖥
Data Sharing with Harvard Dataverse

👥 In-person
🖥 Virtual

LONGWOOD
RESEARCH DATA MANAGEMENT

Learn More & Register
bit.ly/rdmwg-calendar

https://datamanagement.hms.harvard.edu/about/news-events/rdmwg-calendar

Keep building!
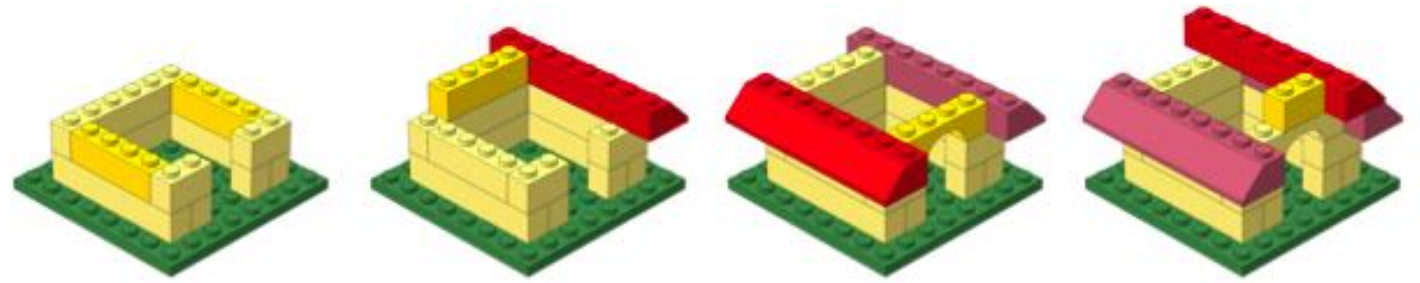
2025 schedule:

Topic	Pre-requisites	Date/Time	Time	Registration
Reproducible Research using Rmarkdown	R basics	3/19/25	1 - 4 pm	Register now!
"Track Changes" for Your Code: an Introduction to Git and GitHub	None	4/16/25	1 - 4 pm	Register now!
Coding with Others: Managing Conflicts on GitHub	"Track Changes" for your code: An Introduction to Git and GitHub	5/21/25	1 - 4 pm	Register now!

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

Keep building!
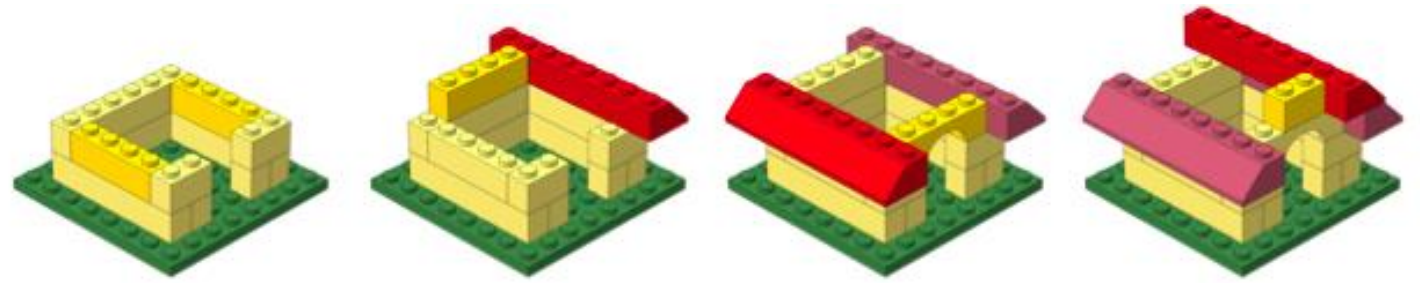
Topic	Category	Date	Duration	Prerequisites
Introduction to Differential Gene Expression Analysis	Advanced	March 18, 21, 25, 28	Four 2h sessions	R
Pseudobulk and related approaches for scRNA-seq analysis	Advanced	April 4, 8, 11	Three 2.5h sessions	R
Shell for Bioinformatics	Basic	April 22, 25, 29	Three 2.5h sessions	None
Investigating chromatin biology using ChIP-seq and CUT&RUN	Advanced	May 2, 6, 9	Three 2.5h sessions	Shell for Bioinformatics
Introduction to R	Basic	May 20, 23, 27, 30	Four 2h sessions	None
Peak Analysis	Advanced	June 17, 20, 24	Three 2.5h sessions	R

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

More Information

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

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

Sign up for our mailing list:

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

Talk to us early!

Involvement in study design to optimize experiments

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

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

Contact Us

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