

Introduction to Single-cell RNA-seq analysis

Harvard Chan Bioinformatics Core



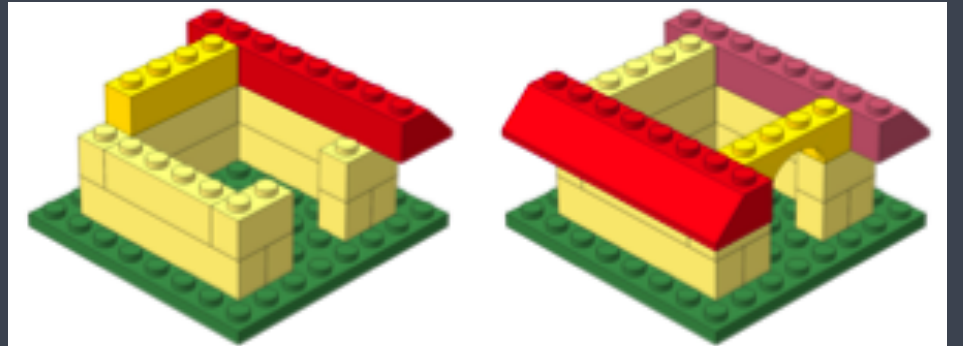
<https://tinyurl.com/hbc-scrnaseq-online>

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, clustering, and marker identification

Survey



<https://tinyurl.com/scRNAseq-online>

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/>

Interested in additional training?

All workshop materials are online: <https://hbctraining.github.io/main>

Sign up for our mailing list:

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

HBC Current Topics in Bioinformatics

Generating reports with Rmarkdown	Online R resource from Harvard Catalyst	10/5/2022	1 – 4pm	Register
Introduction to Shell	None	11/2/2022	1 – 4pm	Register
Version Control using Git/Github	Shell	12/7/2022	1 – 4pm	Register

Free and open to everyone at Harvard University
and its affiliates.
[Register online!](#)

Data Management

- HMS Data management : <https://datamanagement.hms.harvard.edu/>

[Click here to sign up for data management related emails](#)

- Countway Library [training schedule](#) for short workshops on Research Data Management

Thanks!

- Dr. Mandovi Chatterjee, Director, HMS Single Cell Core

Get (stay) in touch with us!

Training team ✉ : hbctraining@hsph.harvard.edu

Consulting ✉ : bioinformatics@hsph.harvard.edu

 [@bioinfocore](https://twitter.com/bioinfocore)

These materials have been developed by members of the teaching team at the Harvard Chan Bioinformatics Core (HBC). These are open access materials distributed under the terms of the Creative Commons Attribution license (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

