



Introduction to Single-cell RNA-seq analysis

Harvard Chan Bioinformatics Core



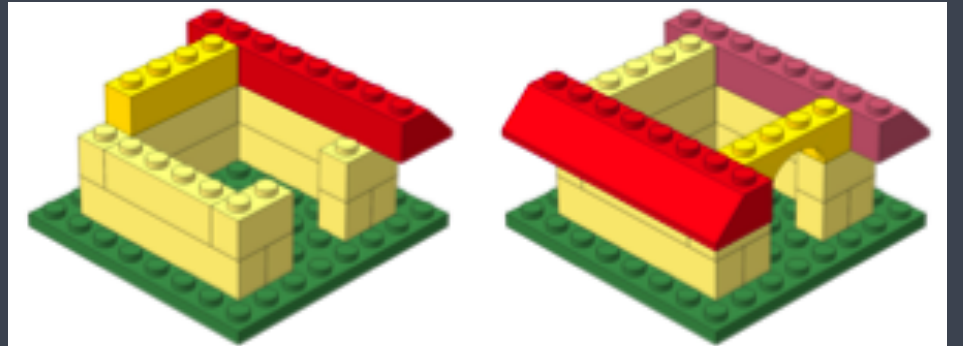
<https://tinyurl.com/hbc-scrnaseq-online>

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>

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. Arpita Kulkarni, Associate 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)

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