

# Introduction to Single-cell RNA-seq analysis

Harvard Chan Bioinformatics Core



<https://tinyurl.com/hbc-intro-to-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, clustering, and marker identification

# Useful Resources

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## 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>

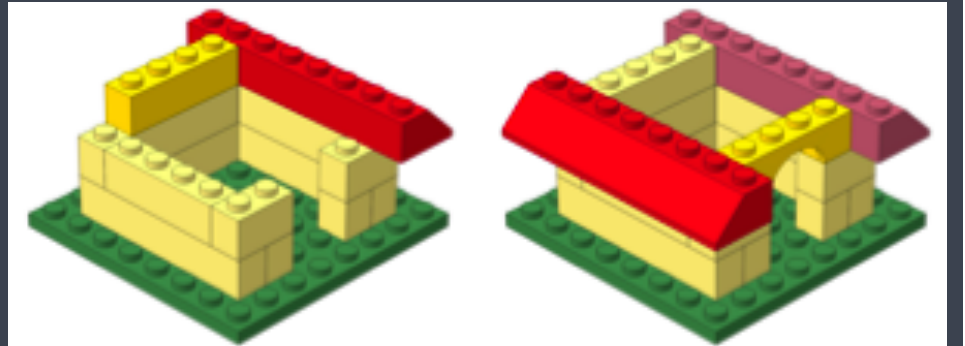
## Resources for scRNA-seq Sample Prep:

<https://www.protocols.io/>

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

<https://community.10xgenomics.com/>

# Survey



<https://tinyurl.com/scrnaseq-exit>



# Bioinformatics Community Networking Breakfast!

- *Free and open to the LMA community*
- *Food and seats are **first-come-first-served***
- ***Last Wednesday** of every month*

December 18th

HMS' Jeffrey Modell Center for Immunology, Room 100A

# Thanks!

- Sarah Boswell, HMS
- HBC members

# Contact us!

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