

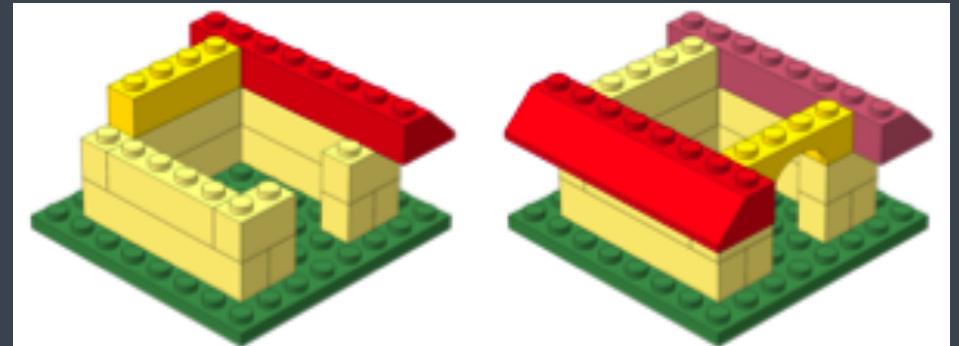
Introduction to Single-cell RNA-seq analysis

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

Computational packages for single-cell analysis:

[http://bioconductor.org/packages/devel/workflows/html/
simpleSingleCell.html](http://bioconductor.org/packages/devel/workflows/html/simpleSingleCell.html)

<https://satijalab.org/seurat/>

<https://scanpy.readthedocs.io/>

Comprehensive list of packages for single-cell and other analyses:

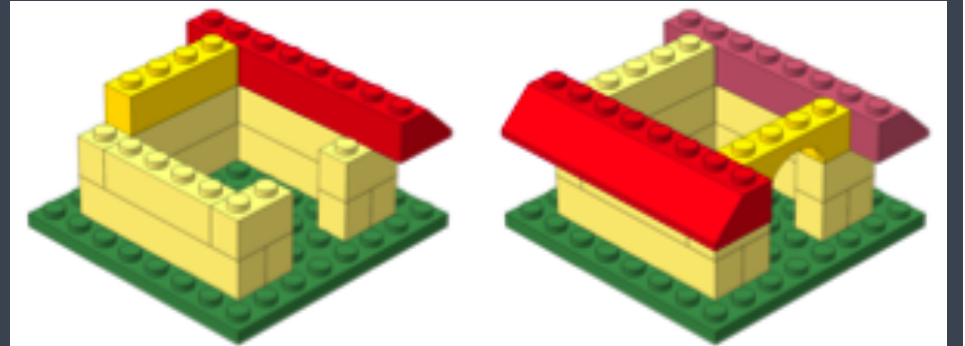
<https://github.com/seandavi/awesome-single-cell>

Online courses:

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

<https://github.com/SingleCellTranscriptomics>

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*

Date: **July 31th, 2019**

Time: **9:00 to 10:30 am**

Venue: **HSPH Building2 room 426**



Thanks!

- Sarah Boswell, HMS
- Ayshwarya Subramanian, Broad Institute
- HBC members

Contact us!

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

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