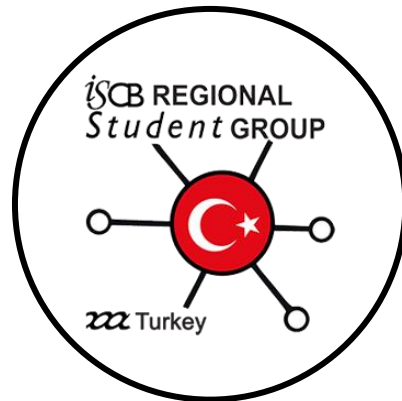


Overview of Data Formats

Single-cell Workshop
19-20 December 2020



h5ad

Loom

10x

SCE

h5ad

FILE FORMATS?

Seurat

Loom

SCE

h5ad

Seurat

FILE FORMATS?

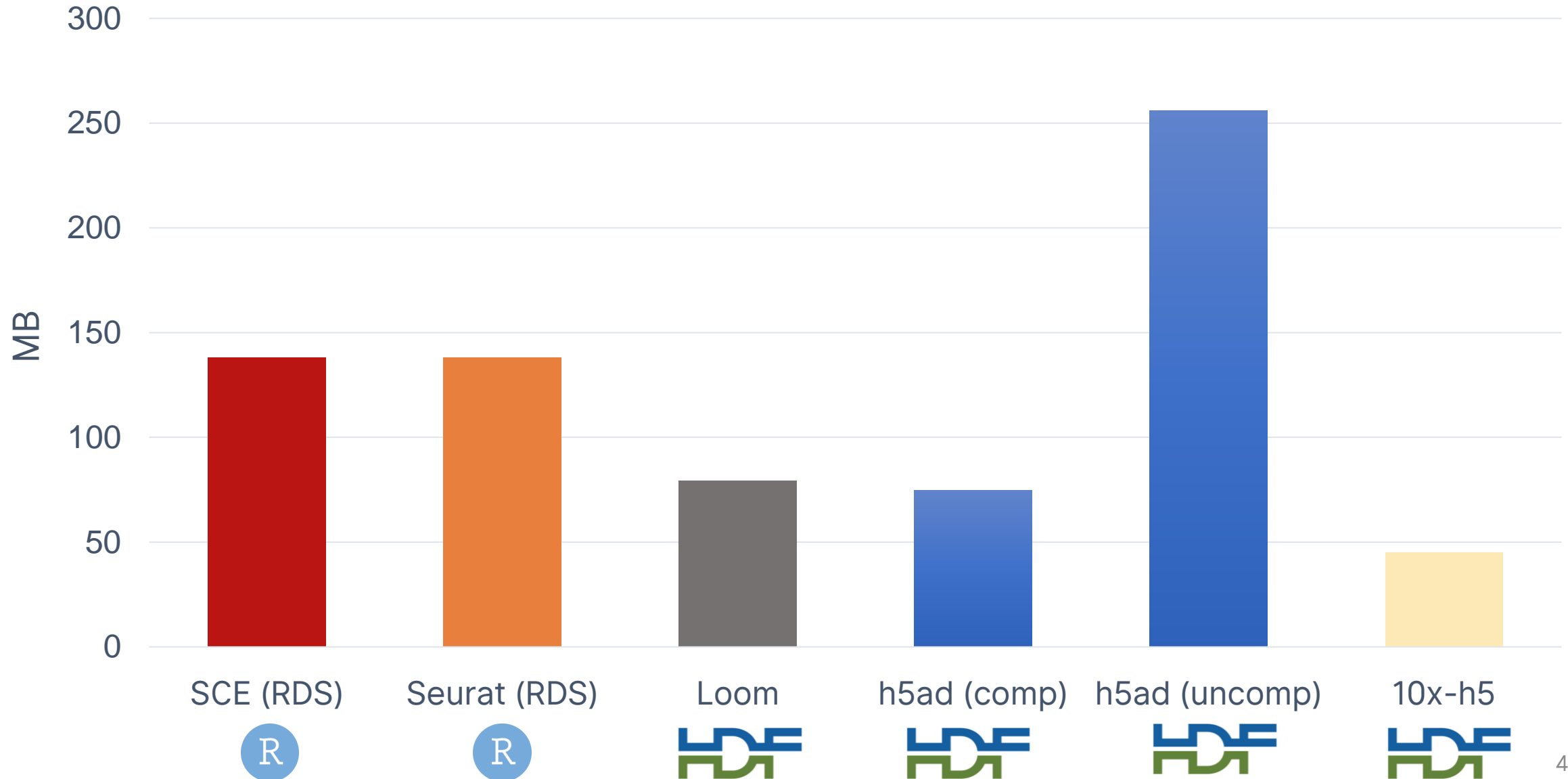


- designed for scanpy

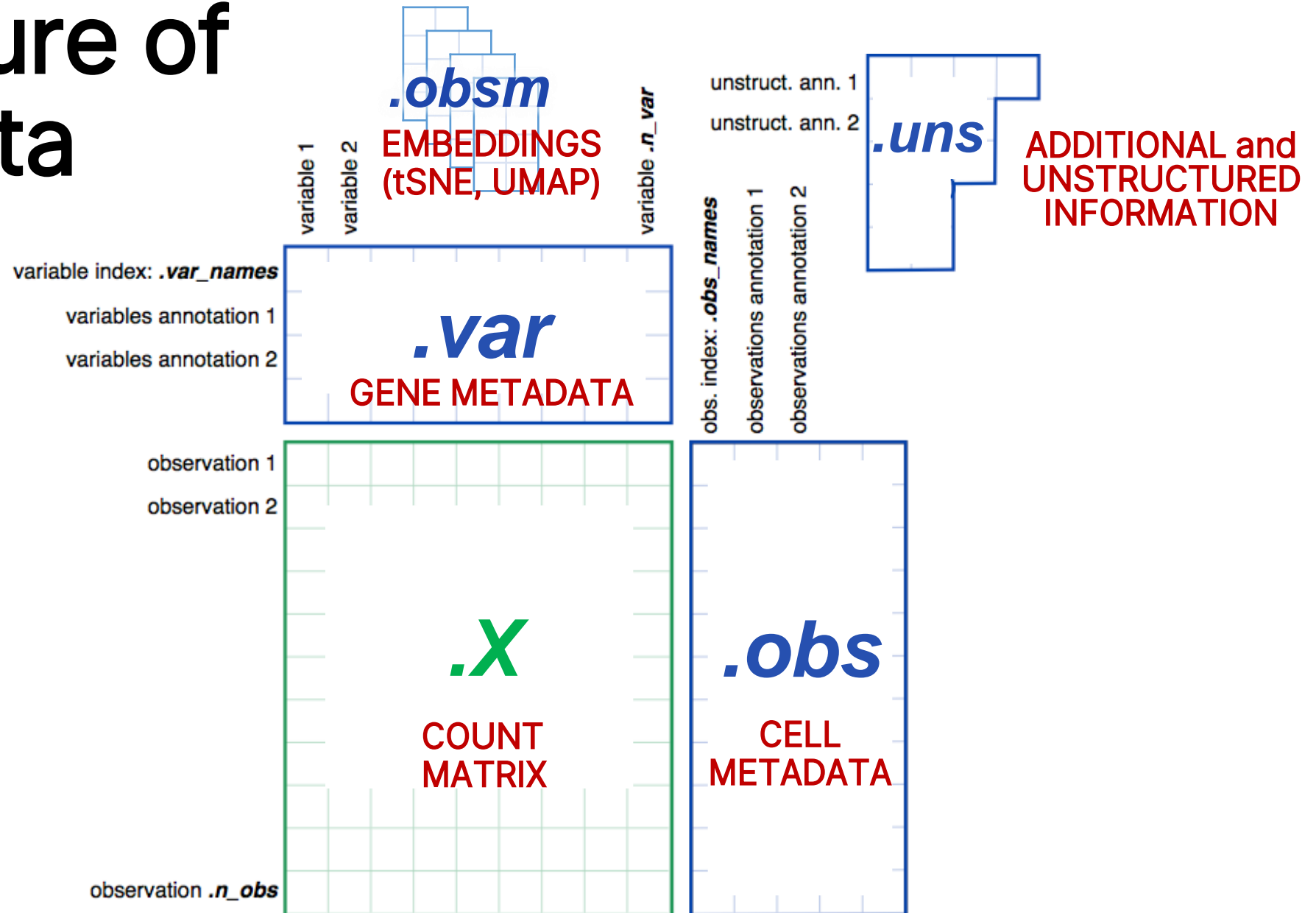
- designed to store and organize large amounts of data
- provides higher flexibility and on-demand loading

File size comparison

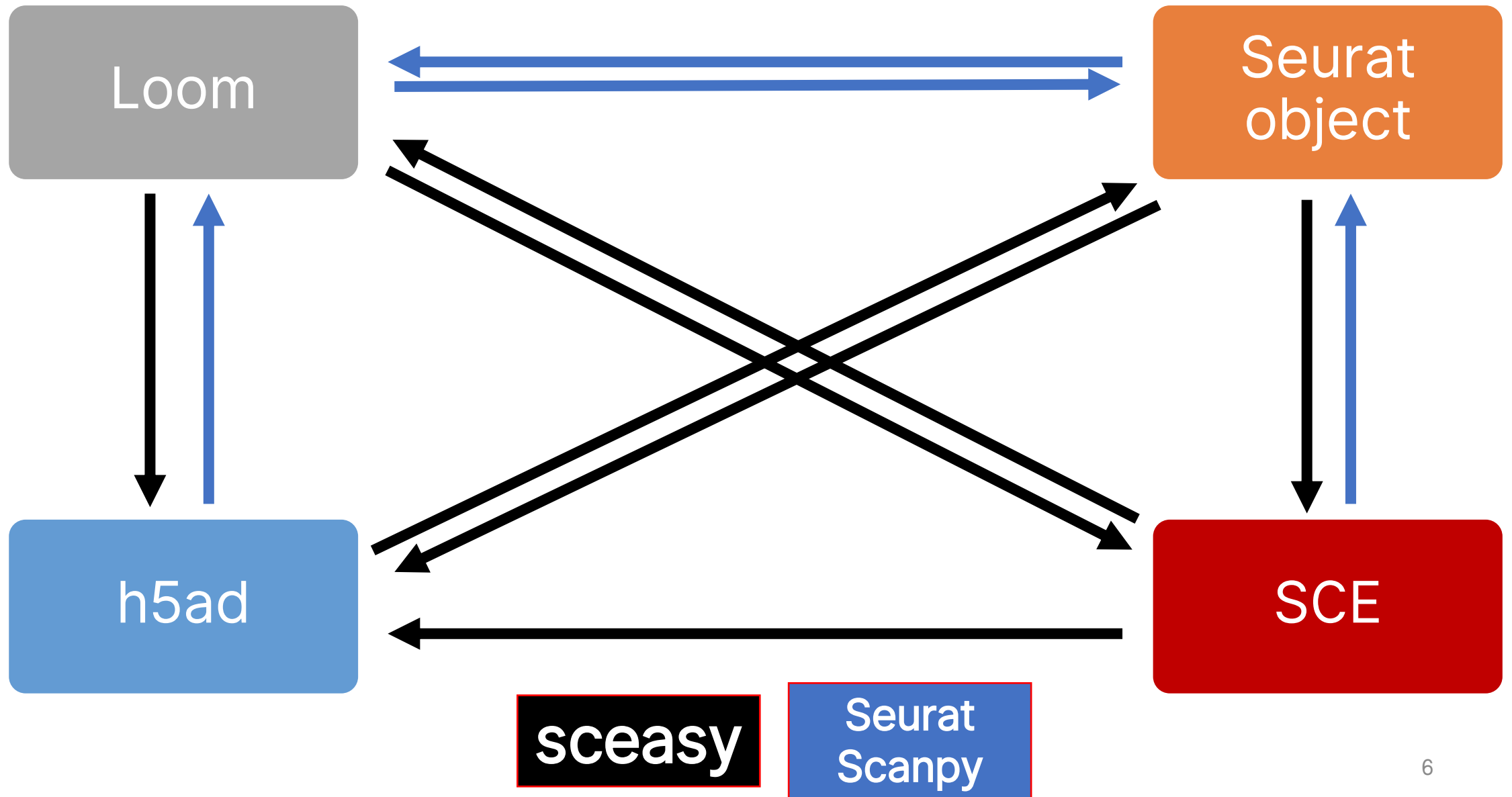
10k brain cells from an E18 mouse:
31053 genes × 11843 cells



Structure of AnnData



File format conversions



sceasy

sceasy is a package that helps easy conversion of different single-cell data formats to each other. Converting to AnnData creates a file that can be directly used in cellxgene which is an interactive explorer for single-cell transcriptomics datasets.

Warning

Before installing the conda packages below please first create a new conda environment EnvironmentName and activate it. Everything else can be installed in R.

Installation

sceasy is installable either as a bioconda package:

```
conda install -c bioconda r-sceasy
```

or as an R package:

```
devtools::install_github("cellgeni/sceasy")
```

which will require the biconductor packages BiocManager and LoomExperiment:


```
if (!requireNamespace("BiocManager", quietly = TRUE))
```

Interactive data visualization in single-cell RNAseq data



NAR Genomics and Bioinformatics

Comparison of visualization tools for single-cell RNAseq data

Batuhan Cakir, Martin Prete, Ni Huang, Stijn van Dongen, Pinar Pir, Vladimir Yu Kiselev 

NAR Genomics and Bioinformatics, Volume 2, Issue 3, September 2020, lqaa052,

<https://doi.org/10.1093/nargab/lqaa052>

Published: 29 July 2020 **Article history** ▼



PDF

Split View

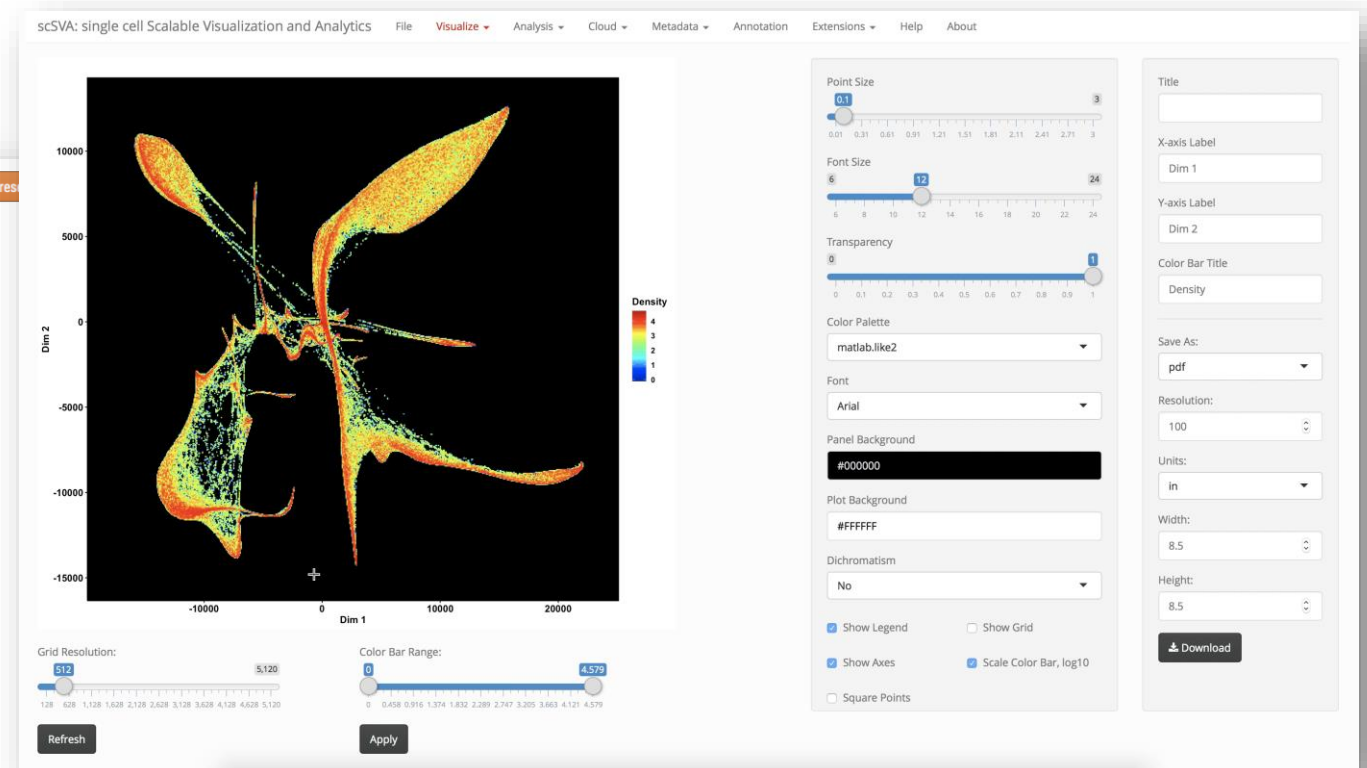
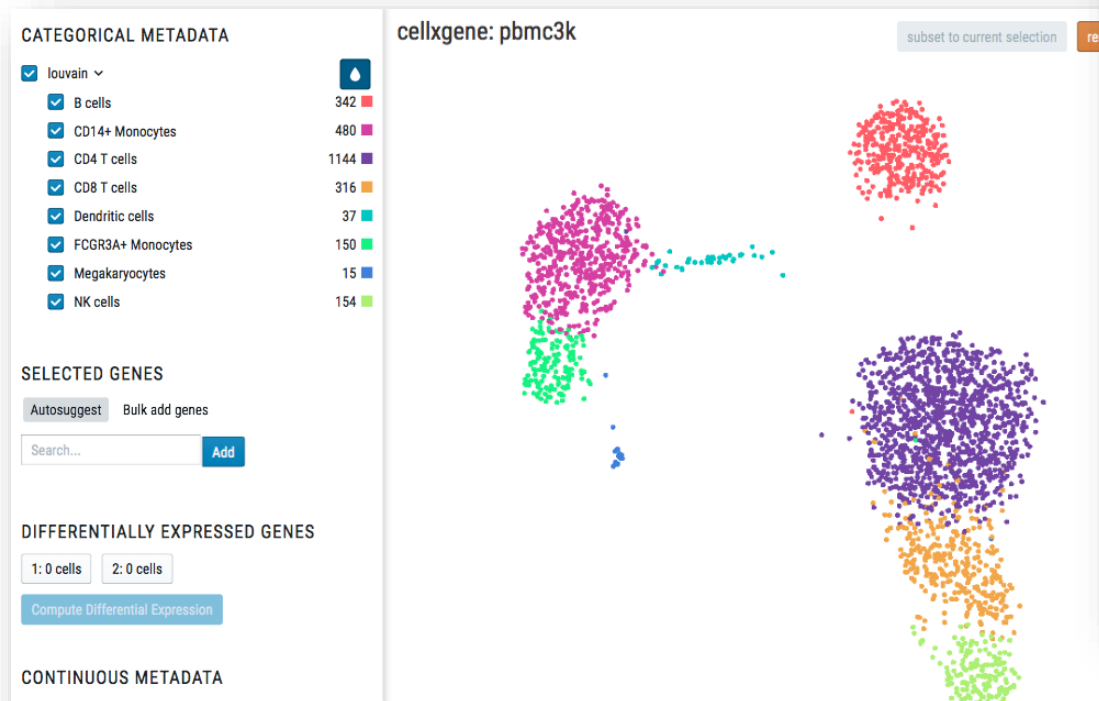
Cite

Permissions

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Why do we need an extra tool for visualization?

- Better exploration of the datasets
- Perfect way to present the cell atlases



	ASAP	Bbrowser	cellxgene	Granatum	iSEE	Loom viewer	Loupe Cell Browser	SCope	scSVA	scVI	Single Cell Explorer	SPRING	UCSC Cell Browser
Web Sharing	✓		✓		✓	✓		✓	✓		✓	✓	✓
Interactivity	✓	✓	✓		✓		✓	✓	✓		✓	✓	✓
Docker	✓		✓		✓			✓	✓				
Cloud Support			✓	✓				✓	✓			✓	
SaaS	✓			✓				✓			✓	✓	✓
Loom	✓				✓	✓		✓	✓	✓	✓		✓
h5ad		✓	✓						✓	✓	✓		✓
SCE					✓								
Seurat		✓									✓		✓
csv/txt	✓	✓		✓					✓	✓	✓	✓	✓
Platform	Java/ R	Desktop	Python	R	R	Python	Desktop	Python	R	Python	Python	Python	Python
Last updated*	>3 m	<1 m	<1 m	>12 m	<1 m	>6 m	>3 m	<1 m	>12 m	<1 m	>6 m	>12 m	<1 m
Number of contributors**	2	?	19	3	7	5	?	5	2	24	1	3	6
Number of active developers**	0	?	6	0	3	0	?	2	0	4	0	0	2
Reviewed Version	1.0	2.2.13	0.11.0	0.0.0.900	1.4.0	0.32.4	3.1.1	1.7.2	0.2.0	0.5.0	1.0.0	1.6.0	0.5.49

Last update in June 2020

	ASAP	Bbrowser	cellxgene	Granatum	iSEE	Loom viewer	Loupe Cell Browser	SCope	scSVA	scVI	Single Cell Explorer	SPRING	UCSC Cell Browser
Web Sharing	✓		✓		✓	✓		✓	✓		✓	✓	✓
Interactivity	✓	✓	✓		✓		✓	✓	✓		✓	✓	✓
Docker	✓		✓		✓			✓	✓				
Cloud Support			✓	✓				✓	✓			✓	
SaaS	✓			✓				✓			✓	✓	✓
Loom	✓				✓	✓		✓	✓	✓	✓		✓
h5ad		✓	✓						✓	✓	✓		✓
SCE					✓								
Seurat		✓									✓		✓
csv/txt	✓	✓		✓					✓	✓	✓	✓	✓
Platform	Java/ R	Desktop	Python	R	R	Python	Desktop	Python	R	Python	Python	Python	Python
Last updated*	>3 m	<1 m	<1 m	>12 m	<1 m	>6 m	>3 m	<1 m	>12 m	<1 m	>6 m	>12 m	<1 m
Number of contributors**	2	?	19	3	7	5	?	5	2	24	1	3	6
Number of active developers**	0	?	6	0	3	0	?	2	0	4	0	0	2
Reviewed Version	1.0	2.2.13	0.11.0	0.0.0.900	1.4.0	0.32.4	3.1.1	1.7.2	0.2.0	0.5.0	1.0.0	1.6.0	0.5.49

Last update in June 2020





**VIDEO CAN BE FOUND IN
RESOURCES LIST**



Gut Cell Atlas

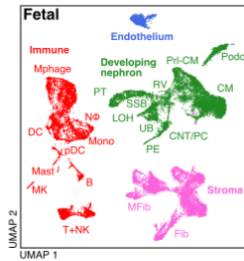
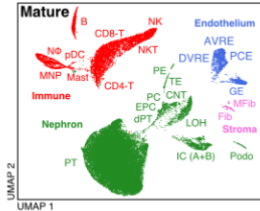
web portals created by
Cellular Genetics Informatics



Kidney Cell Atlas

An atlas of single-cell gene expression from fetal and mature human kidneys

Mature kidney dataset



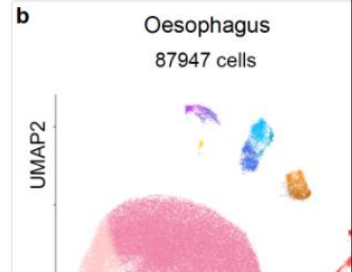
Tissue Stability Cell Atlas

The study containing this data was published in

[Genome Biology](#)

The sequence data generated in this study is available at

[accession code PRJEB3184](#)



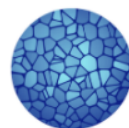
Development Cell Atlas

Murine Melanoma Atlas

COVID-19 Cell Atlas

Patient donors

Atlas of Anopheles Hemocytes



HUMAN
CELL
ATLAS



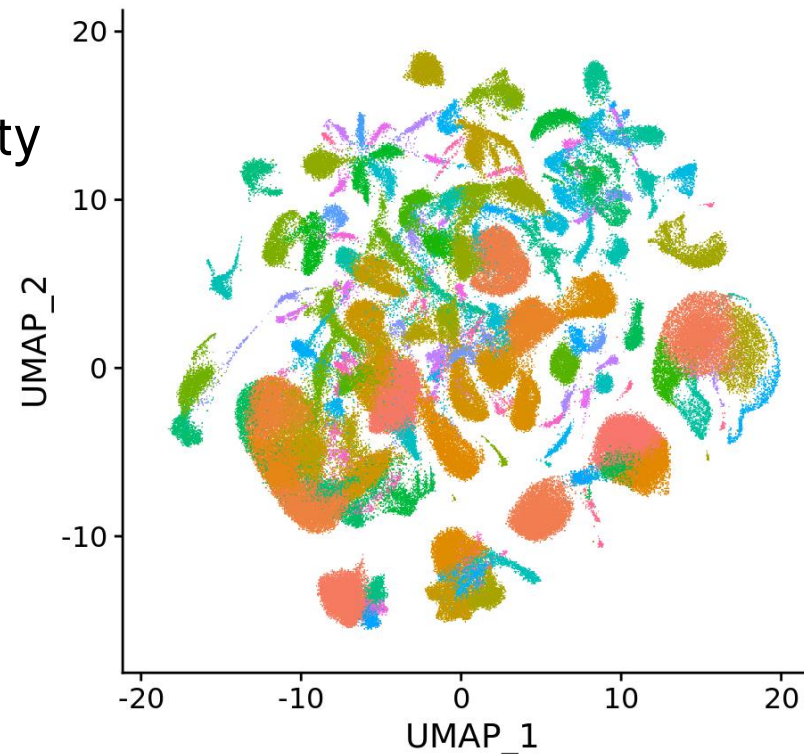
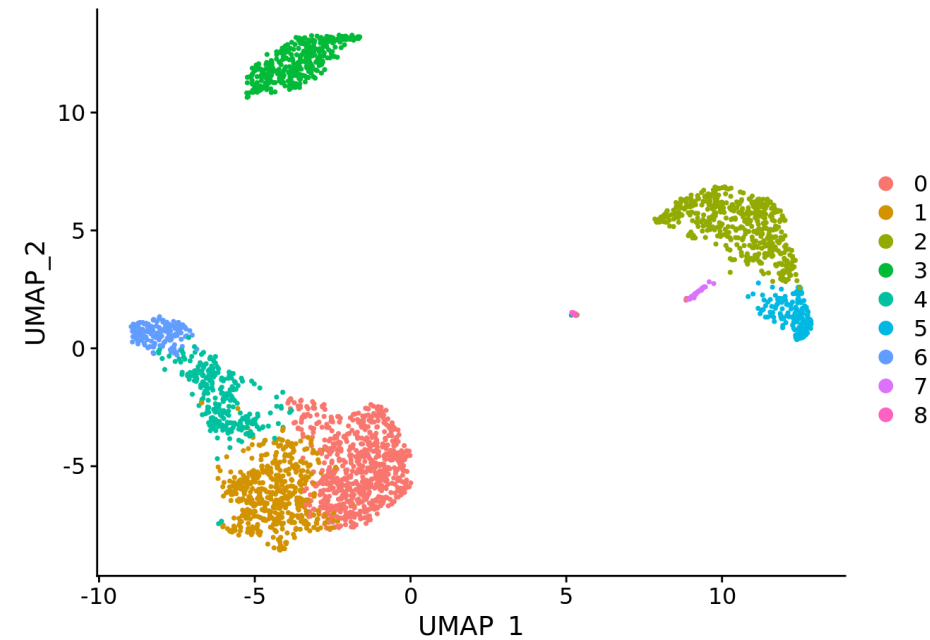
Seurat

- Developed by Satija Lab, New York Genome Center.
- R package designed for QC, analysis, and exploration of single-cell RNA-seq data.
- to identify and interpret sources of heterogeneity
- to integrate diverse types of single-cell data.

FOR MORE INFORMATION:

Butler, Andrew, et al. "Integrating single-cell transcriptomic data across different conditions, technologies, and species." *Nature biotechnology* 36.5 (2018): 411-420.

Stuart, Tim, et al. "Comprehensive integration of single-cell data." *Cell* 177.7 (2019): 1888-1902.



- ## **FOR MORE INFORMATION:**

Stuart, Tim, et al. "Comprehensive integration of single-cell data." *Cell* 177.7 (2019): 1888-1902.



Georges Seurat (1859-1891)

best known for developing pointillism

END OF THE PRESENTATION

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