Dros26 Workshop
Organizer: Hongjie Li lab, Baylor College of Medicine

Date/Time: Thursday, March 5, 2026/8:00 - 10:00 pm

Title: Single-cell sequencing resource in Drosophila: generating grant and publication figures without coding.

Program Description: In the past decade, single-cell technology has revolutionized Drosophila research, yielding numerous valuable datasets from individual labs and initiatives like the Fly Cell Atlas. However, many researchers struggle to navigate platforms such as SCope, UCSC Cell Browser, EPFL ASAP, EBI Single Cell Atlas, and CZI CellxGene platforms. This workshop will highlight a hands-on training to generate grant and publication figures without coding using available public data based on CellxGene platform.

Agenda:

8:00 pm: **Hongjie Li**, Baylor College of Medicine
Title: Overview of single-cell research and resources in Drosophila

8:10 pm: **Ye-Jin Park** and **Niccole Auld**, Baylor College of Medicine
Title: Basic functions of CellxGene: cell type, gene expression, DEG analysis and more.

8:40 pm: **Tyler Jackson** and **Bo Sun**, Baylor College of Medicine
Title: The VIP functions of CellxGene: plotting figures.

9:10 pm: **Tzu-Chiao Lu** and **Zhiyong Yin**, Baylor College of Medicine
Title: Key steps of analyzing your own single-cell data using CellxGene

9:40 pm: All speakers
Open questions and Hands-on training

Below are useful materials for this workshop

1. CellxGene link:

Workshop demo data (temporarily available during fly meeting):
Additional sample data: https://cellxgenevip-ms.bxgenomics.com/
Aging fly cell atlas: https://agingflycellatlas.ds.czbiohub.org/headbody

Additional fly scRNA-seq resources from Hongjie Li lab:
https://hongjielilab.org/resources/

2. How to use CellxGene basic function?
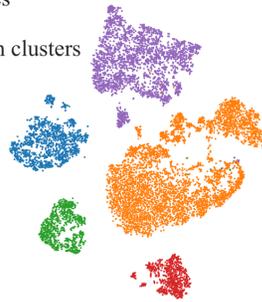
3. How to use CellxGene VIP (visualization in plugin) function?
   ○ Compare gene expression
   ○ Plot figures

4. How to analyze your own data using CellxGene?
   ○ Online tutorial of CellxGene_VIP plugin:
      https://interactivereport.github.io/cellxgene_VIP/tutorial/docs/
   ○ Install CellxGene with CellxGene_VIP plugin:
      https://github.com/interactivereport/cellxgene_VIP

   slides by Zhiyong Yin PhD and Tzu-Chiao Lu, PhD (next pages)
   ○ Instill CellxGene
   ○ Load your data

How to **analyze your own data** using CellxGene?

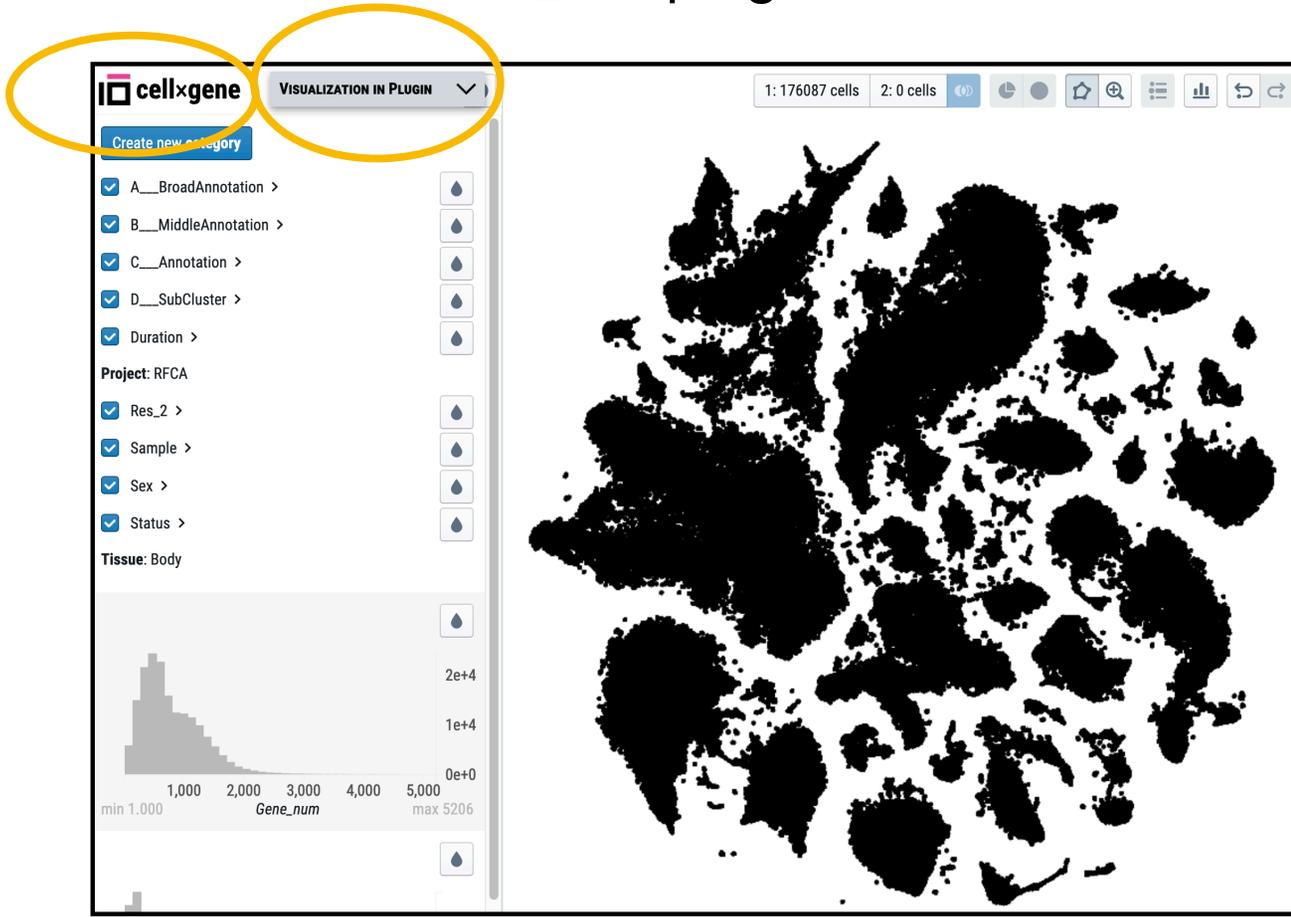How to **install** and **launch** CellxGene with CellxGene_VIP plugin?

Zhiyong Yin

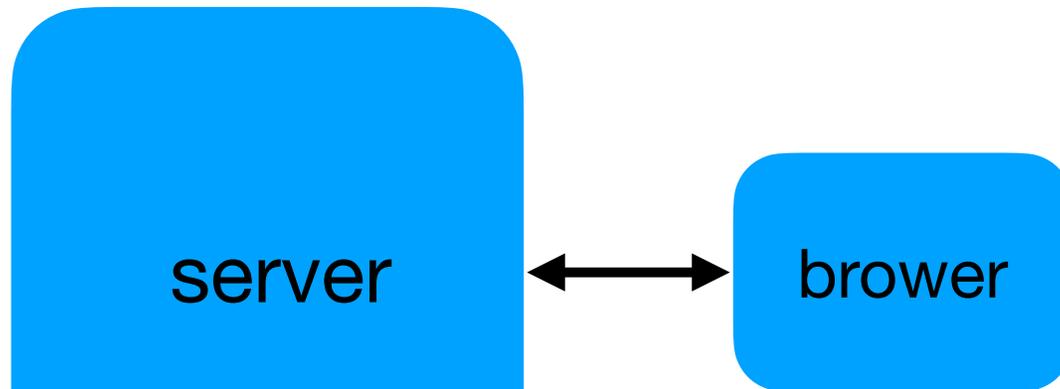A postdoctoral associate under the supervision of **Professor Hongjie Li**.
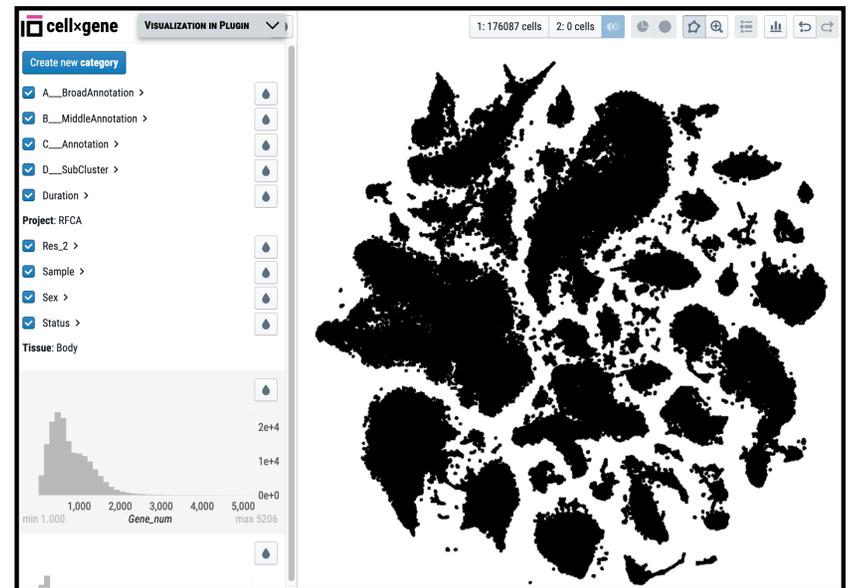
March 5, 2026

How CellxGene and CellxGene_VIP plugin works?

server ←→ brower

hold the data and launch CellxGene
with CellxGene_VIP plugin

Please go to this GitHub portal to download:

SCAN ME

https://github.com/interactivereport/cellxgene_VIP

3. Create and enable conda environment

```
git clone https://github.com/interactivereport/cellxgene_VIP.git
cd cellxgene_VIP

source <path to Anaconda3>/etc/profile.d/conda.sh (Default: /opt/anaconda3/etc/profile.d/conda.
conda config --set channel_priority flexible
conda env create -n <env name, such as: VIP> -f VIP.yml (system-wide R) or VIP_conda_R.yml (loc

For Mac User, conda env create -n <env name, such as: VIP> -f VIP.macOS.yml

conda activate <env name, such as: VIP>
or
source activate <env name>
```

4. Install cellxgene by running config.sh in "cellxgene_VIP" directory

```
./config.sh
For Mac User, ./config.macOS.sh
```

👁 **6** watching

ᛘ **52** forks

Report repository

Releases 12

🏷 v3.1 (Latest)
on Feb 27, 2024

+ 11 releases

Deployments 80

✓ github-pages last year

+ 79 deployments

years ago
years ago
years ago
months ago
years ago
last year
years ago
months ago
years ago

Currently, the CellxGene_VIP supports to install in:

Linux system (like Ubuntu, CentOS)

Mac Unix system (both Intel and Apple Silicon).

For PC user, Ubuntu virtual machine can be installed first
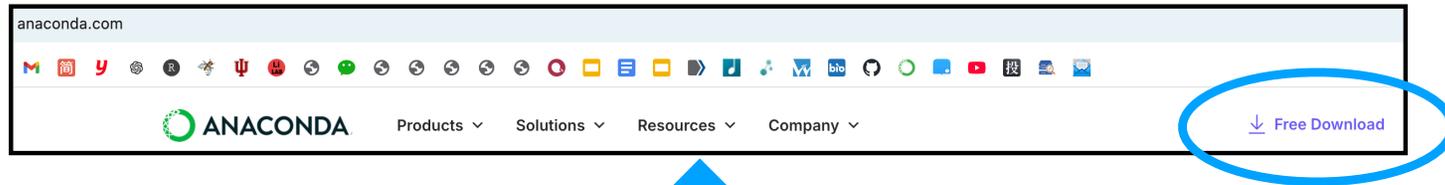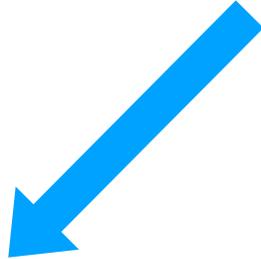and then install CellxGene_VIP in this virtual Ubuntu.
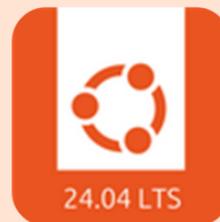
Ubuntu 24.04.1 LTS
Canonical Group Limited
24.04 LTS

Install anaconda:

www.anaconda.com

anaconda.com

ANACONDA

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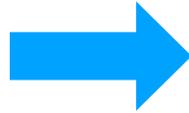
Choose Your Download

Windows   Mac   Linux

Anaconda Distribution

Complete package with 8,000+ libraries, Jupyter, JupyterLab, and Spyder IDE. Everything you need for data science.

↓ 64-Bit (Apple silicon) Graphical Installer

↓ 64-Bit (Apple silicon) Command Line Installer

Miniconda

Minimal installer with just Python, Conda, and essential dependencies. Install only what you need.

↓ 64-Bit (Apple silicon) Graphical Installer

↓ 64-Bit (Apple silicon) Command Line Installer

Install anaconda:

1 download

Anaconda3-2025.12-2-MacOSX-arm64.sh

2 install

```
bash Anaconda3-2025.12-2-MacOSX-arm64.sh
```

```
zhiyong@Mac-Studio ZZZZZZZ % bash Anaconda3-2025.12-2-MacOSX-arm64.sh

Welcome to Anaconda3 2025.12-2

In order to continue the installation process, please review the license
agreement.
Please, press ENTER to continue
>>> |
```
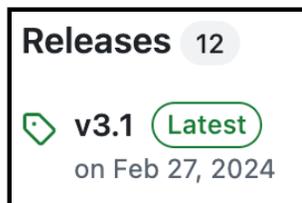
```
(base) zhiyong@Mac-Studio ZZZZZZZ %
```

How to install CellxGene with CellxGene_VIP plugin?
Take Ubuntu system (Linux) for an example:

1 download

Releases 12

🏷 **v3.1** (Latest)
on Feb 27, 2024

2 un-compress

```
tar -zxvf cellxgene_VIP-3.1.tar.gz
```

3 get into folder

```
cd cellxgene_VIP-3.1
```

4 configurate conda

```
source /opt/miniconda3/etc/profile.d/conda.sh
```

```
conda config --set channel_priority flexible
```

5 create conda environment

```
conda env create -n CellxGene_VIP -f VIP.yml
```

6 install cellxgene

```
./config.sh
```

How to launch CellxGene in your command line?

1 activate the conda environment with CellxGene_VIP:

```
Conda activate CellxGene_VIP
```

2 cellxgene launch —host 10.10.10.10 —port 1001 your_data.h5ad

IP of your computer/server

Port for this specific data set

You can launch cellxgene of different datasets with different port number

To avoid termination of cellxgene after you quit your terminal:

nohup cellxgene launch —host 10.10.10.10 —port 1001 your_data.h5ad
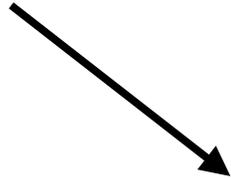
cellxgene will not hang up

But, if you restart your computer, you need to launch the cellxgene again.

How to start CellxGene in browser?

In Address Bar: IP:Port ➡️ 🌐 10.10.10.10:1001

SCAN ME
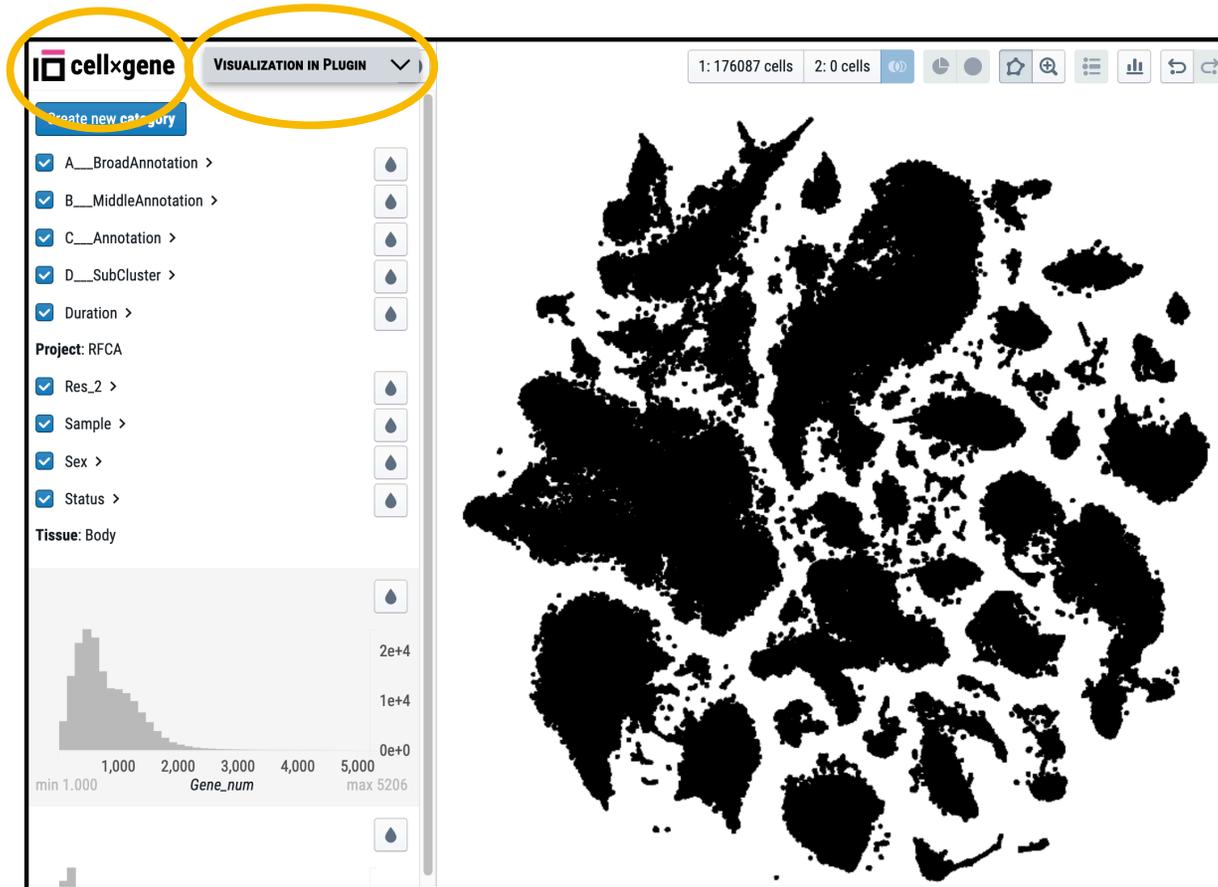
Thanks for your time!

Hongjie Li Lab @ Baylor College of Medicine

Running **CellxGene** on your computer:

prepare your **h5ad** file

SCAN ME

AFCA   **AD-FCA**   **Rapa-FCA**

Tzu-Chiao Lu

Baylor College of Medicine

Hongjie Li Lab

AFCA-head
https://agingflycellatlas.ds.czbiohub.org/head

AFCA-body
https://agingflycellatlas.ds.czbiohub.org/body
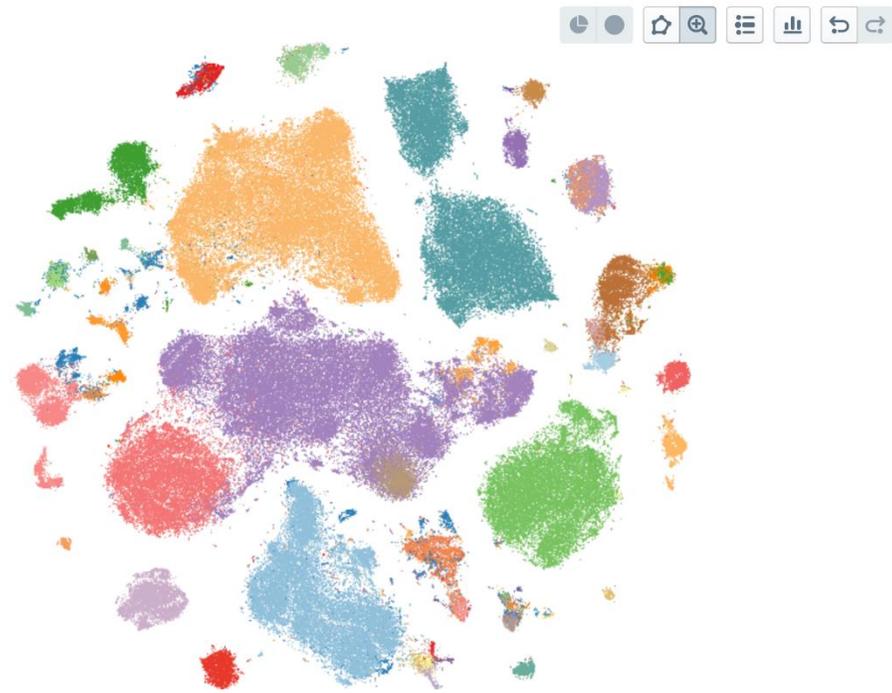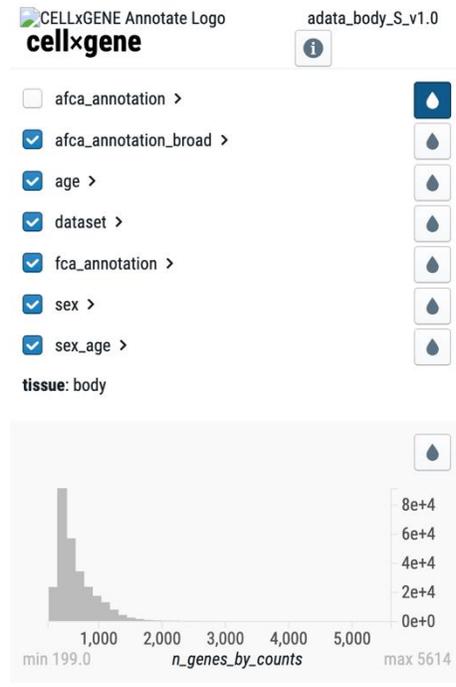
AFCA-head & body
https://agingflycellatlas.ds.czbiohub.org/headbody

Coming soon

AD-FCA   **Rapa-FCA**

Flowchart

CellxGene   Load .h5ad

Output h5ad files   Scanpy: output AnnData as h5ad file
                           Seurat: .rds → .h5ad

Process matrix files   Scanpy, Seurat

Expression matrix

FASTQ files

Flowchart

CellxGene   Load .h5ad

↑

Output h5ad files   Scanpy: output AnnData as h5ad file
Seurat: .rds → .h5ad

↑

Process matrix files   Scanpy, Seurat

↑

Expression matrix   Cell Ranger count: /CELLRANGER_SAMPLE/outs/

↑

FASTQ files   control_10_female_head_S3_L004_R1_001.fastq.gz
control_10_female_head_S3_L004_R2_001.fastq.gz

```
├──── analysis
│     ├──── clustering
│     ├──── diffexp
│     ├──── pca
│     ├──── tsne
│     └──── umap
├──── cloupe.cloupe
├──── filtered_feature_bc_matrix
│     ├──── barcodes.tsv.gz
│     ├──── features.tsv.gz
│     └──── matrix.mtx.gz
├──── filtered_feature_bc_matrix.h5
├──── metrics_summary.csv
├──── molecule_info.h5
├──── possorted_genome_bam.bam
├──── possorted_genome_bam.bam.bai
├──── raw_feature_bc_matrix
│     ├──── barcodes.tsv.gz
│     ├──── features.tsv.gz
│     └──── matrix.mtx.gz
├──── raw_feature_bc_matrix.h5
└──── web_summary.html
```
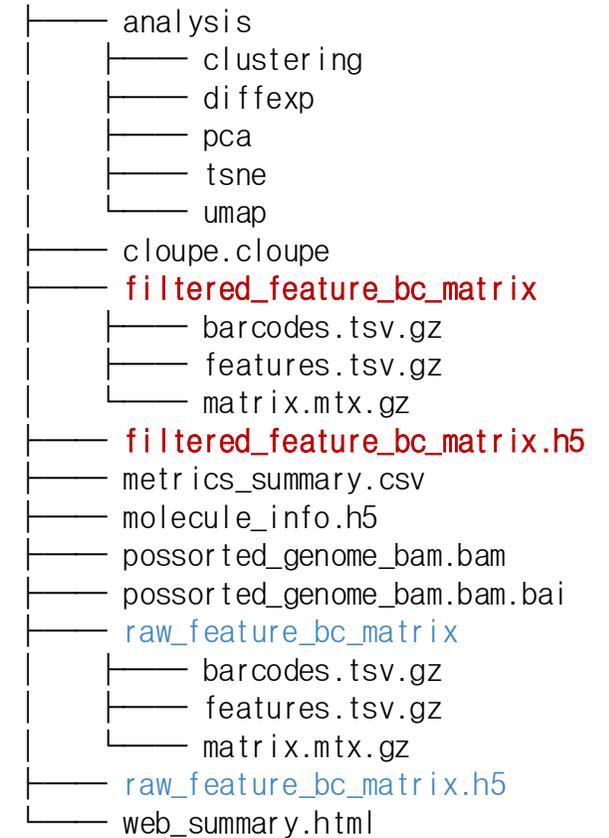
Convert .rds file to .h5ad (lots of compatibility issues)

Install Bioconductor (https://www.bioconductor.org/install/)
Install Seurat (https://satijalab.org/seurat/articles/install.html)

SeuratDisk (https://github.com/mojaveazure/seurat-disk)

```
if (!requireNamespace("BiocManager", quietly=TRUE)) {
        install.packages("remotes")
}
remotes::install_github("mojaveazure/seurat-disk")

### Seurat 5 user
seurat[["RNA"]] <- as(object = seurat[["RNA"]], Class = "Assay")

SaveH5Seurat(seurat, filename = " seurat.h5Seurat")
Convert(" seurat.h5Seurat", dest = "h5ad")
### may lose your metadata
```

Convert .rds file to .h5ad (lots of compatibility issues)

sceasy (https://github.com/cellgeni/sceasy) (recommended)

```r
devtools::install_github("cellgeni/sceasy")
library(sceasy)
library(reticulate)
sceasy::convertFormat(seurat_object, from="seurat", to="anndata", outFile='filename.h5ad')
### work well now
```

scDIOR (https://github.com/JiekaiLab/scDIOR) (not updated)

```r
```{r}
if (!requireNamespace("BiocManager", quietly=TRUE)) {
        install.packages("devtools")}
devtools::install_github("JiekaiLab/dior")
library(dior)
write_h5(seurat_obj, file = "data.h5", assay = "RNA")
```

$pip install diopy #in your conda env
```{python}
import diopy
import scanpy as sc
adata = diopy.read_h5("data.h5")
adata.write_h5ad("data.h5ad")
```
```

If these don't work, ask your:

Gemini
ChatGPT
Grok
Claude

How to covert .rds to .h5ad?

Create your h5ad file from scratch

CellxGene VIP: anndata <= 1.10

adata.var: "gene names"

anndata

adata.X: "LogNormalized data"

adata.obs (cell): all detailed information can be visualized on the left

adata.obsm: "X_umap", "X_tsne"