웹기반의 단일세포 RNA-seq 데이터 자동분석 서비스 SCODA™를 이용한 종양/조직 미세환경 연구

윤석현

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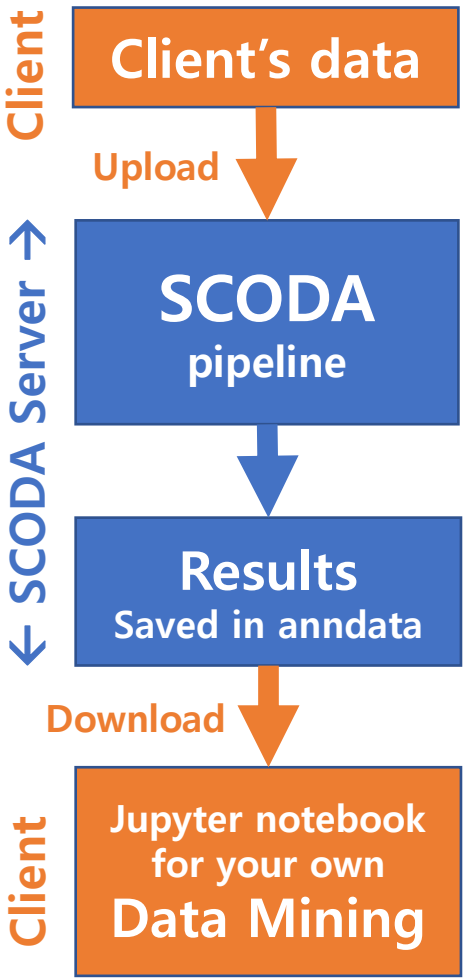
SCODA?

- Web-based, Fully-automated, all-in-one computing service for **S**ingle-**C**ell (transcript)**O**mics **D**ata **A**nalysis (single-cell RNA-seq)
- It is useful for
  - In-vivo tissue/tumor micro-environment (TME) study.
  - Immune cell profiling in many diseases, e.g., autoimmune disease & cancer

How SCODA works?



(1) Simply upload your data

1. Compressed 10x mtx files + optional meta_data.csv
2. Compressed CSV file + optional meta_data.csv
3. Compressed h5ad file (including meta data in obs field)

(2) Automated pipeline analyzes your data

1. Celltype annotation (HiCAT, MIT license)
2. DEG & GSA/GSEA (GSEApy, MIT license)
3. Cell-cell interaction (CellPhoneDB, MIT license)
4. Tumor cell identification (InferCNV, BSD-3c + icnv_addon)

❖ We use proven & standardized analysis tools
❖ The pipeline can be tailored with optional settings

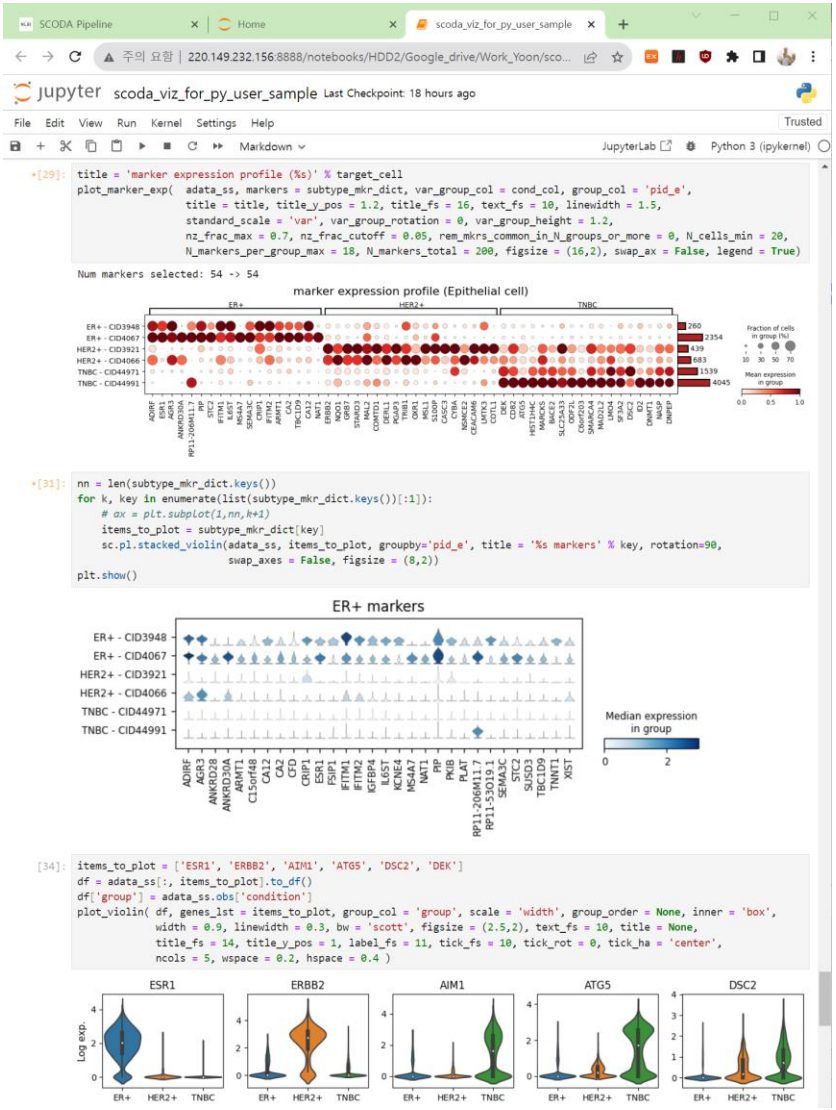
(3) Once it is done, you can download the result

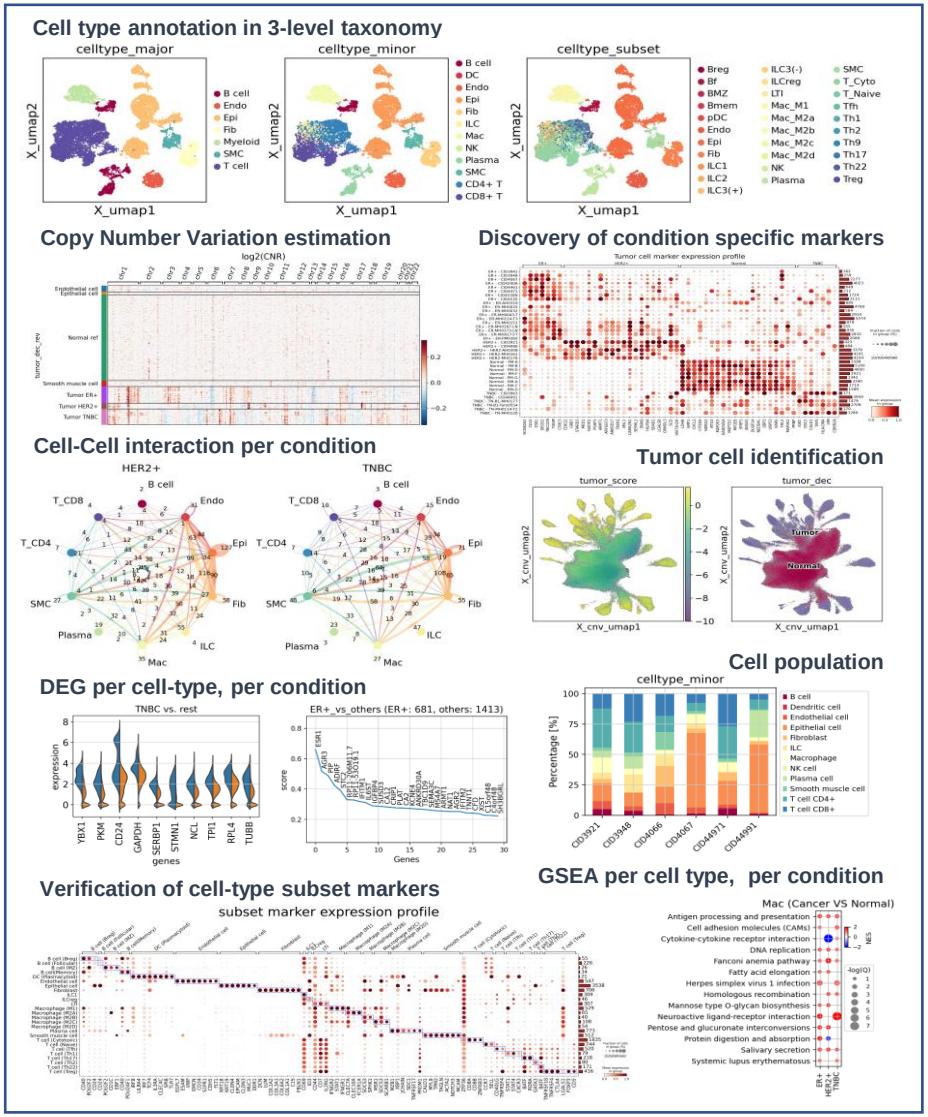
1. Saved in Anndata formatted h5ad file (tar.gz compressed)
2. It contains all the analysis results and the count matrix itself

(4) Explore the results by yourself on your web browser

1. We provide "jupyter notebook" with example codes
2. You can freely use SCODA-viz & SCANpy (free open SW)
3. With a little bit of programming, you can get deeper insight into the single-cell RNA-seq data you uploaded
4. We offer free workshop for data mining (upon request)

Visualization & data mining





Using SCODA

- SCODA homepage: https://mlbi-lab.net
- MLBI lab company homepage: https://mlbi-lab.com

Why SCODA?

Bio/Medical background

+

SCODA

with SCODA-viz tool

+

Little bit of programming skill
(Free Training workshop available)

||

Single-cell RNA-seq
데이터 분석 전문가

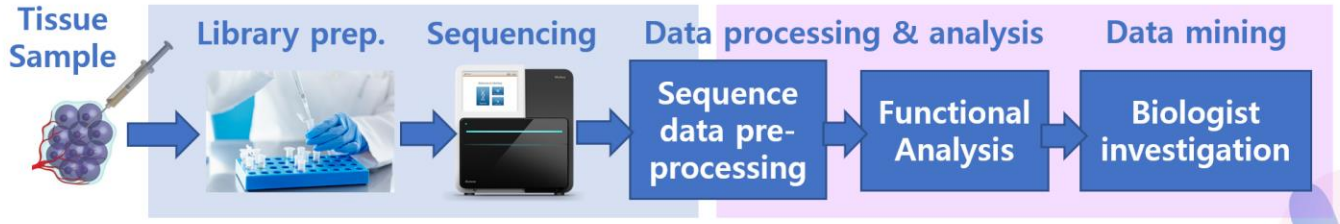
Why SCODA?

You must do something that is not your original job

It is time-consuming & sometimes embarrassing

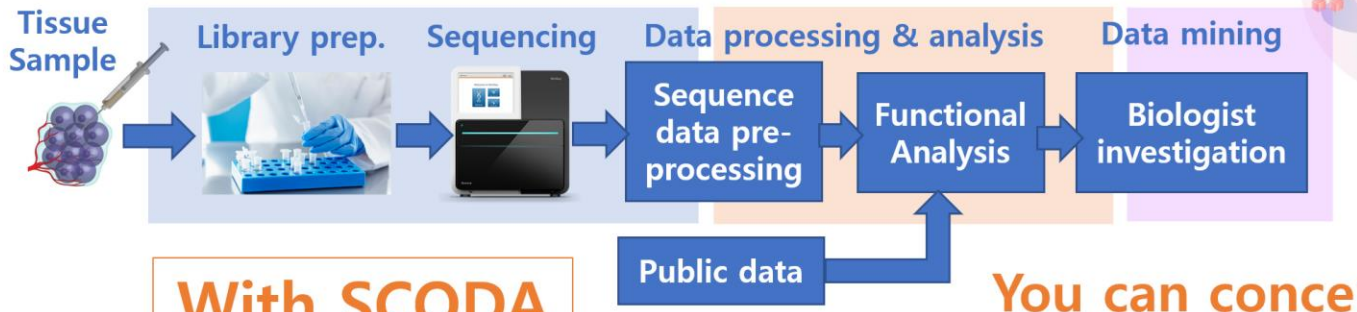
Without SCODA

Client → single-cell RNA-seq service → Client



With SCODA

Client → single-cell RNA-seq service → SCODA → Client



You can concentrate more on your original jobs!!

Related papers

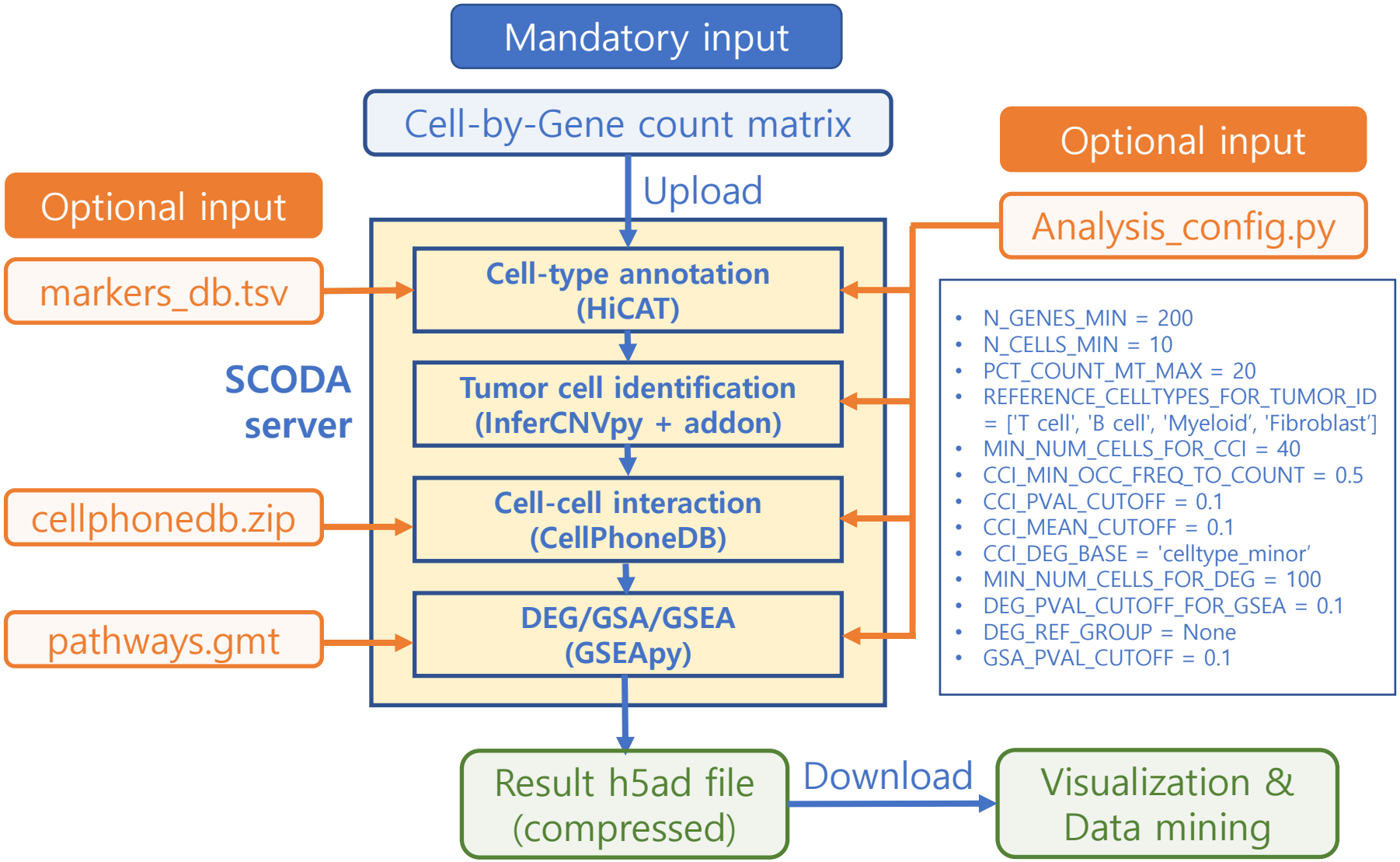
HiCAT

- J. Lee, M. Kim, K. Kang, CS Yang and S. Yoon, “Hierarchical cell-type identifier accurately distinguishes immune-cell subtypes enabling precise profiling of tissue microenvironment with single-cell RNA-sequencing,” Briefings in Bioinformatics, Jan. 2023. https://doi.org/10.1093/bib/bbad006

Studies using SCODA

- D. Hong, H. Kim, W. Yang, C. Yoon, M. Kim, CS Yang and S. Yoon, “Integrative analysis of single-cell RNA-seq and gut microbiome metabarcoding data elucidates macrophage dysfunction in mice with DSS-induced ulcerative colitis,” Communications Biology, June 2024. https://doi.org/10.1038/s42003-024-06409-w
- M. Kim, W. Yang, D. Hong, HS Won, S. Yoon, “A Retrospective View of the Triple-Negative Breast Cancer Microenvironment: Novel Markers, Interactions, and Mechanisms of Tumor-Associated Components Using Public Single-Cell RNA-Seq Datasets,” Cancers, Mar. 2024. https://doi.org/10.3390/cancers16061173
- JS Kim, HK Kim, M. Kim, S. Jang, E. Cho, S. Mun, J. Lee, D. Hong, S. Yoon and CS Yang,, “Colon-Targeted eNAMPT-Specific Peptide Systems for Treatment of DSS-Induced Acute and Chronic Colitis in Mouse,” Antioxidants, Nov. 2022. https://doi.org/10.3390/antiox11122376

SCODA Optional configuration



SCODA?

- **SCODA is useful for**
  - In-vivo tissue/tumor micro-environment (TME) study.
  - Immune cell profiling in many diseases, e.g., autoimmune disease & cancer
  - Discovery of diagnostic/prognostic markers
  - Discovery of druggable targets and its biological mechanism around pathological tissue
  - Exploring drug response and mechanism of action
- **But not suitable yet for**
  - Studies with cell line
  - Differentiation study

Summary

- **SCODA utilizes proven open-source software**
  - **HiCAT (MIT license)** for cell type annotation
  - **CellPhoneDB (MIT license)** for inferring cell-cell interaction
  - **InferCNVpy (BSC-3clause)** for CNV estimation
  - **GSEApy (BSC-3clause)** for gene set enrichment analysis
- **SCODA-viz package and example jupyter notebook freely available for visualization and data mining**
  - With a little bit of programming skill, you can create any kind of plots you want. (Free training workshop available upon request)
- **It accelerate your research with single-cell RNA-seq experiment, saving your time and the cost.**
  - Use SCODA first to get insight into the tissue of your interest.
  - Then, plan biological experiment to verify your hypothesis.

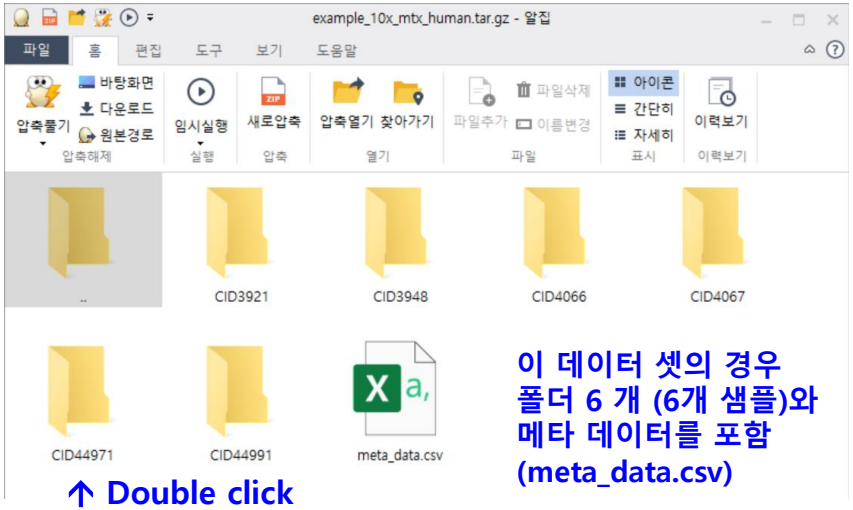
Input dataset formatting for using SCODA

Input data formatting (1) 10x_mtx

1. 압축된 예제 데이터셋을 알집으로 열어 보면

← 메인 폴더 Double click

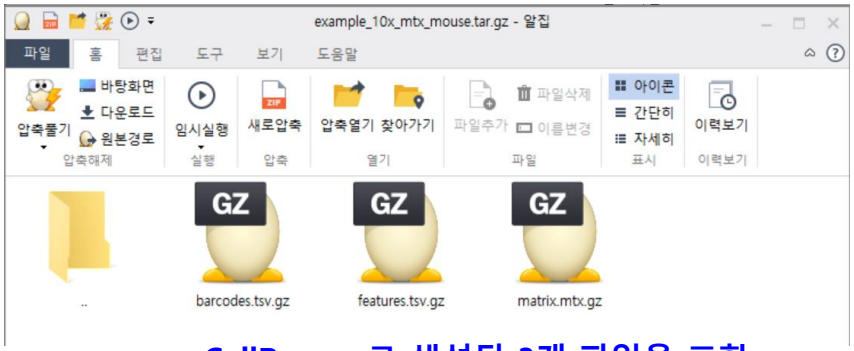
2. 메인 폴더를 더블 클릭해서 열면



↑ Double click

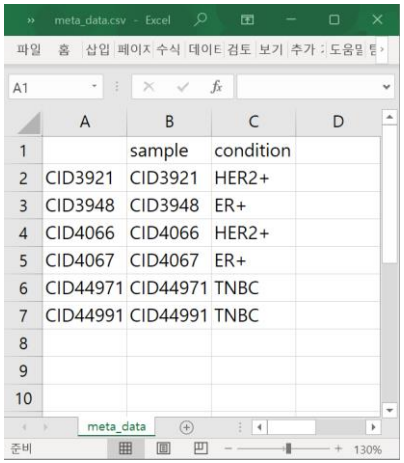
이 데이터 셋의 경우
폴더 6 개 (6개 샘플)와
메타 데이터를 포함
(meta_data.csv)

3. 각 데이터 폴더를 더블 클릭해서 열면



CellRanger로 생성된 3개 파일을 포함

4. meta_data.csv 파일을 엑셀로 열어 보면



	A	B	C	D
1		sample	condition	
2	CID3921	CID3921	HER2+	
3	CID3948	CID3948	ER+	
4	CID4066	CID4066	HER2+	
5	CID4067	CID4067	ER+	
6	CID44971	CID44971	TNBC	
7	CID44991	CID44991	TNBC	
8				
9				
10				

1열: 인덱스 열
2열: sample (name)
3열: condition

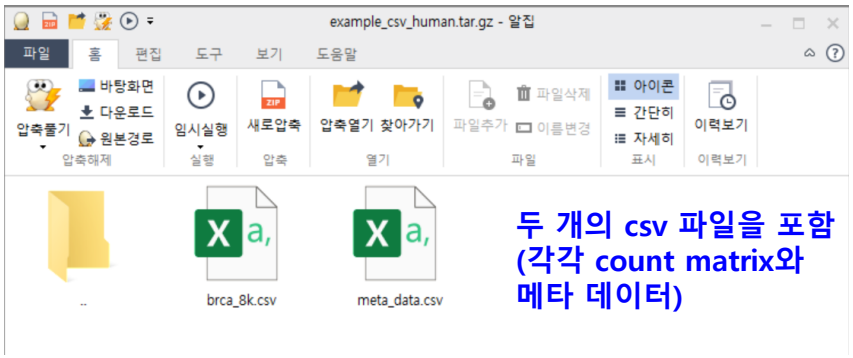
- 인덱스 열의 각 인덱스는 폴더 명과 일치해야 함.
- Sample name과 인덱스가 동일할 필요는 없음.
- Condition 열의 조건들을 대상으로 DEG, GSEA, cell-cell interaction 비교가 수행됨

Input data formatting (2) csv format

1. 압축된 예제 데이터셋을 알집으로 열어 보면

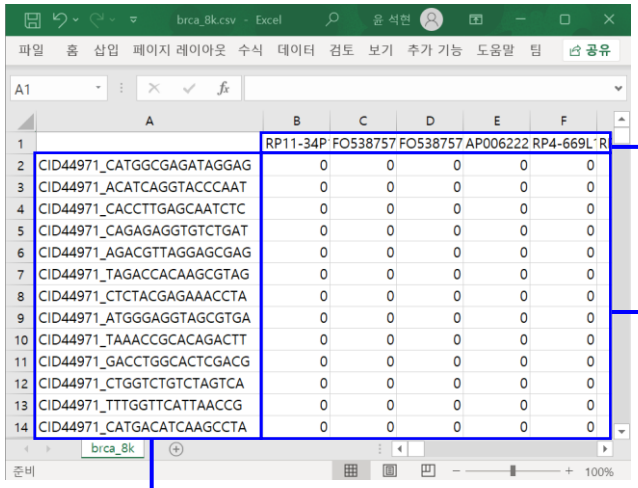
← 메인 폴더 Double click

2. 메인 폴더를 더블 클릭해서 열면



두 개의 csv 파일을 포함 (각각 count matrix와 메타 데이터)

3. 데이터 csv 파일

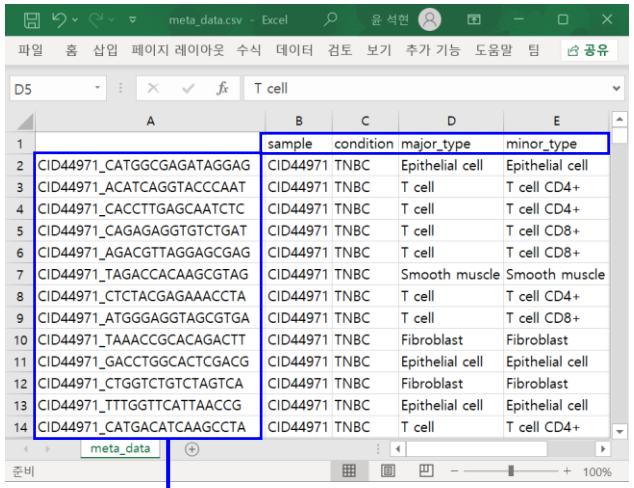


Hugo symbol

Count matrix

Cell barcode (cell ID)

4. meta_data.csv 파일



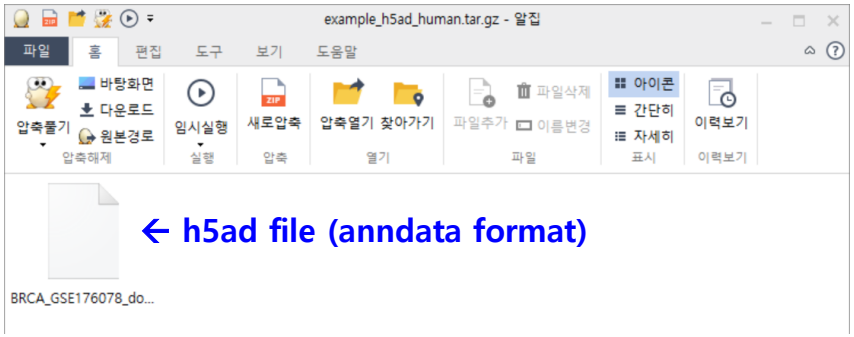
Cell barcode (cell ID)

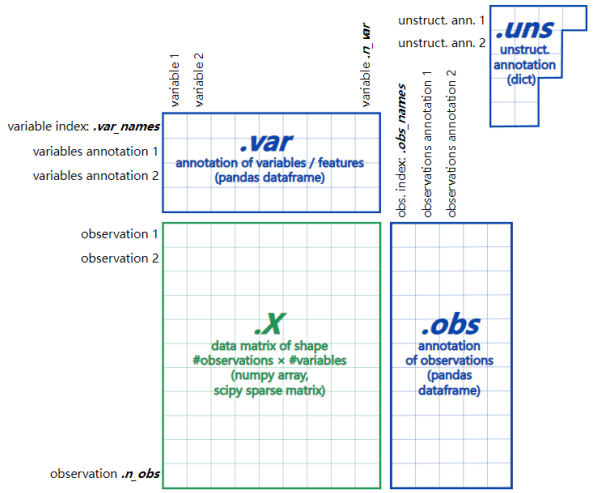
1열: 인덱스 열
2열: sample
3열: condition
4열~: optional items

- Count 데이터 파일과 메타 데이터 파일의 인덱스 열은 일치해야 함.
- Condition 열의 조건들을 대상으로 DEG, GSEA, cell-cell interaction 비교가 수행됨

Input data formatting (3) h5ad format

1. 압축된 예제 데이터셋을 알집으로 열어 보면





2. h5ad file contents

https://anndata.readthedocs.io/en/latest/

```
adata_t = sc.read_h5ad(file_h5ad)
adata_t
```

```
AnnData object with n_obs × n_vars = 12000 × 29733
    obs: 'Patient', 'Percent_mito', 'nCount_RNA', 'nFeature_RNA', 'Celltype_Major', 'Celltype_Minor', 'Celltype_Subset',
'subtype', 'gene_module', 'Calls', 'normal_cell_call', 'CNA_value', 'sample', 'condition'
    var: 'gene_ids'
```

- AnnData contains “sample” and “condition” columns to run DEG/GSEA. DEG/GSEA will not be performed if the obs field does not contain both “sample” and “condition” column.
- If the “sample“ column exists in the obs field, cell-cell interaction will be performed per-sample the same as in the above.