SCODA를 이용한 단일세포 RNA-seq 데이터 마이닝 실습
(조직/종양 미세환경 들여다보기)

윤석현

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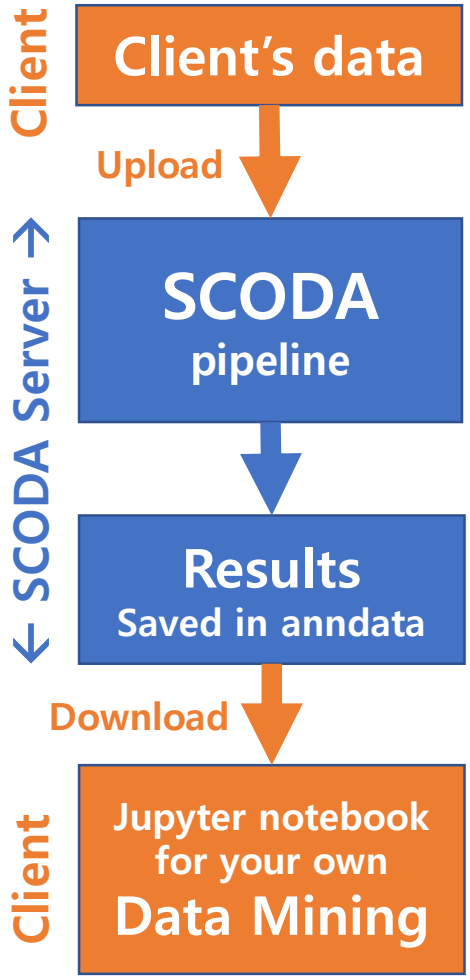
SCODA?

- 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
  - 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

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

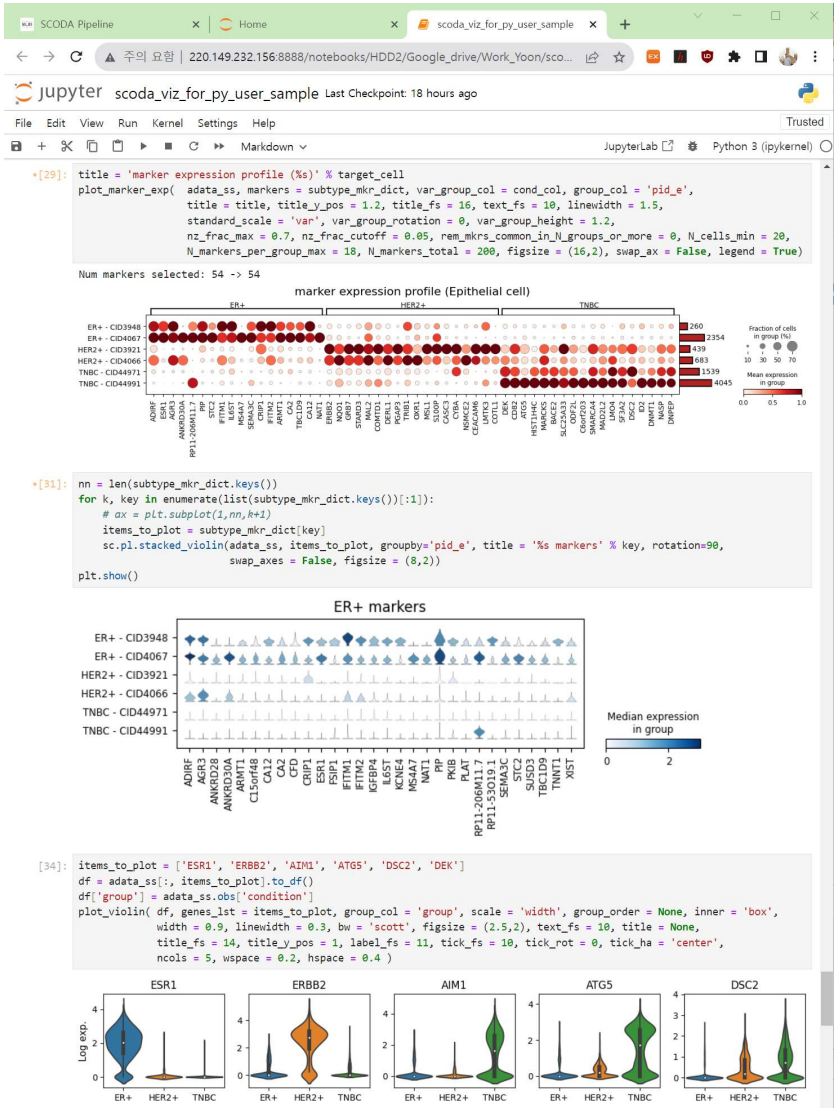
(3) Once it is done, you can download the result

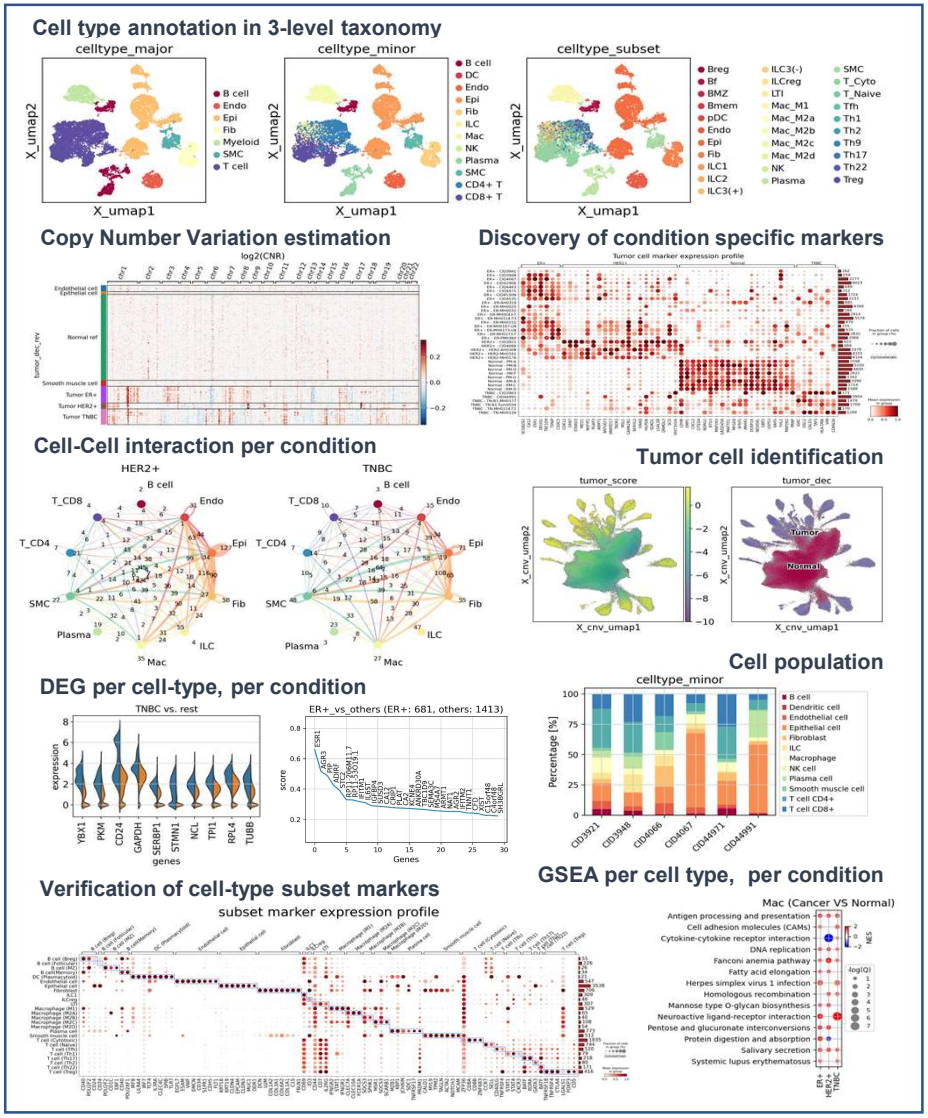
1. Saved in Anndata formatted h5ad file (tar.gz compressed)
2. It contains all the analysis results and the count matrix itself

(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





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

Tissue Sample → Library prep. → Sequencing → Sequence data pre-processing → Functional Analysis → Biologist investigation

(Data processing & analysis: Sequence data pre-processing, Functional Analysis)

(Data mining: Biologist investigation)

With SCODA

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

Tissue Sample → Library prep. → Sequencing → Sequence data pre-processing → Functional Analysis → Biologist investigation

Public data → Functional Analysis

You can concentrate more on your original jobs!!

Using SCODA

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

Related papers

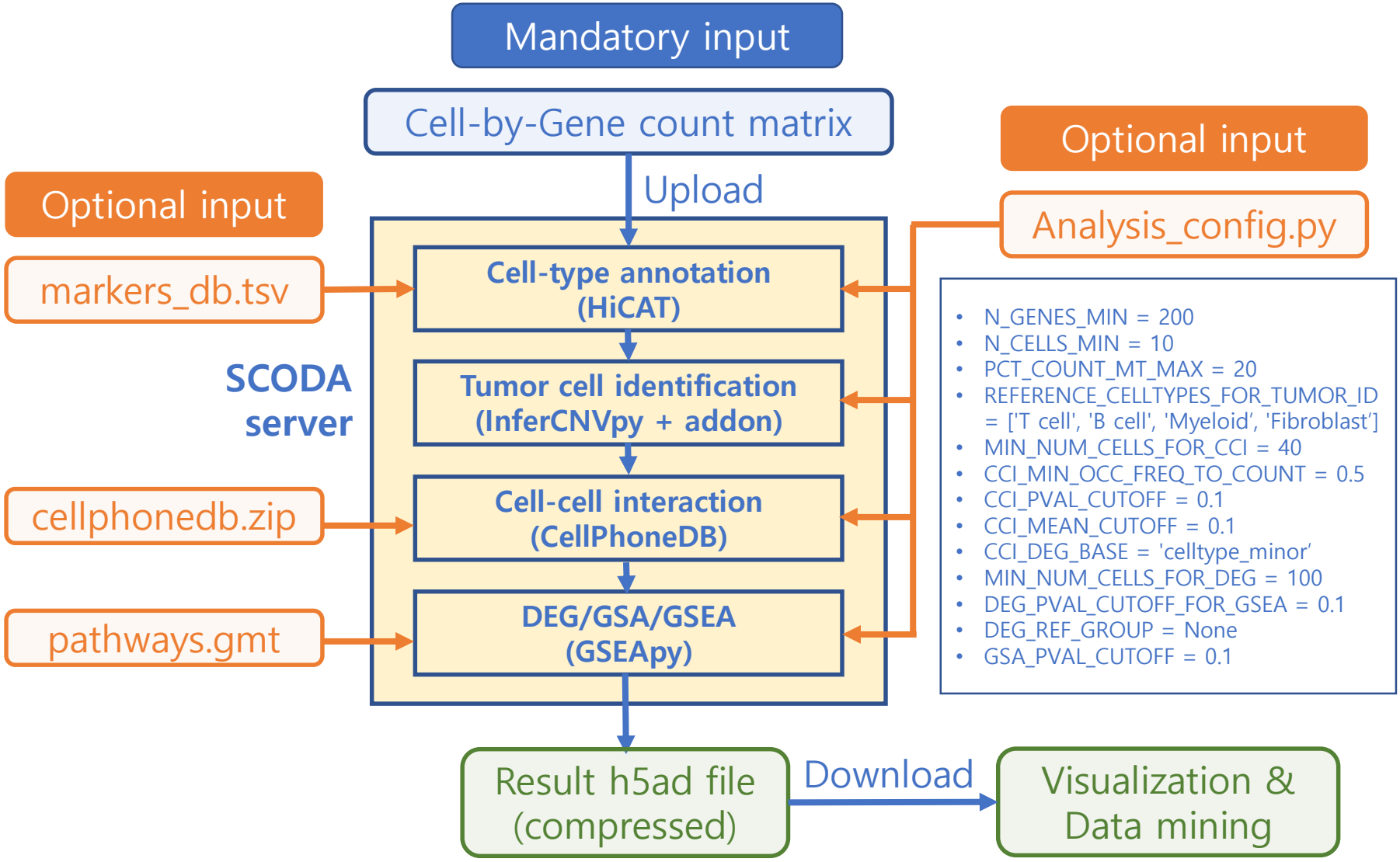
❑ HiCAT

- ❍ Hierarchical cell-type identifier accurately distinguishes immune-cell subtypes enabling precise profiling of tissue microenvironment with single-cell RNA-sequencing, **Briefings in bioinformatics, March 2023**

❑ Studies using SCODA

- ❍ Colon-Targeted eNAMPT-Specific Peptide Systems for Treatment of DSS-Induced Acute and Chronic Colitis in Mouse, **Antioxidants, Nov. 2022**
- ❍ Integrative analysis of ulcerative colitis progression using single-cell RNA-seq and microbiome, **Communications Biology, in revision**
- ❍ A Retrospective View on Triple Negative Breast Cancer Microenvironment: Novel Markers, Interactions, and Mechanisms of Tumor-Associated Components using public Single-cell RNA Seq Datasets, **Cancers, March 2024**

Optional configuration



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.

Cost & Service

❑ Pricing

- ❍ 유효 셀 당 ₩20 (unassigned 포함, 2024년 6월 30일 까지)
- ❍ 자동 결제 시스템 구축 중 (3월 중 오픈 예정)

❑ Our primary concern is client's satisfaction

- ❍ 동일 데이터에 대해 (optional configuration 등 변경하여) 추가 결재 없이 재분석 가능 (6개월 이내 8회)
- ❍ 3시간 무료 training workshop (주피터 노트북 사용법, 데이터 시각화 관련 내용)

❑ Suggestion & request

- ❍ SCODA 데모 페이지에서 먼저 보유하고 계신 데이터를 테스트 해보신 후 (대체적으로 예상되는 결과를 미리 보시고) Full Service 요청하면 좋을 듯 합니다.
- ❍ Full service 사용 전이라도 SCODA 데모 분석 결과에 대한 문의/의견 환영 합니다.
- ❍ 가능한 한 의견들 반영하여 당분간 지속적으로 업그레이드 할 예정입니다.

❑ Any inquiries?

- ❍ 070-7766-5841
- ❍ inquiry@mlbi-lab.com

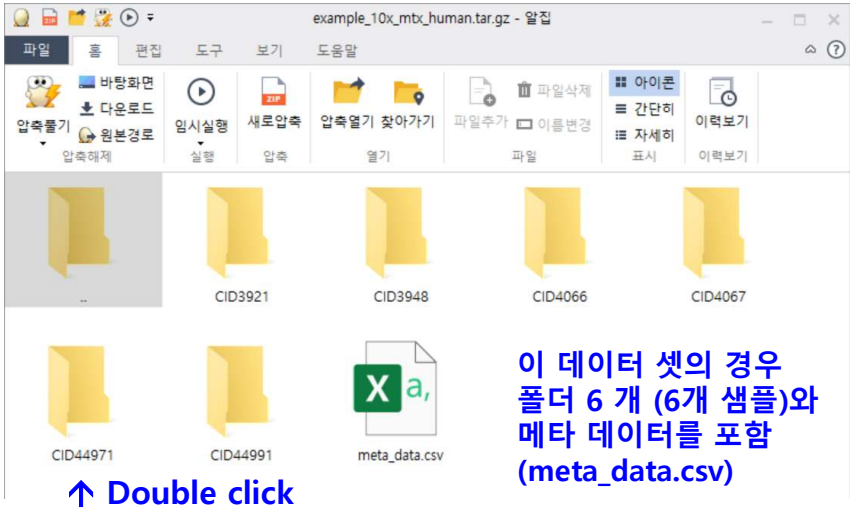
Thank you

Input data formatting (1) 10x_mtx

1. 압축된 예제 데이터셋을 알집으로 열어 보면

← 메인 폴더 Double click

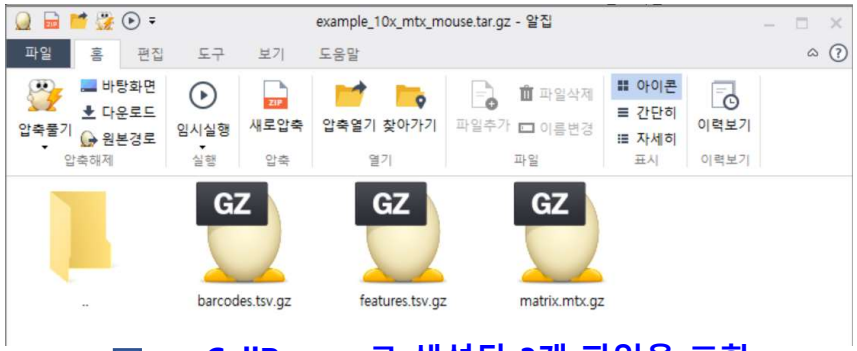
2. 메인 폴더를 더블 클릭해서 열면



↑ Double click

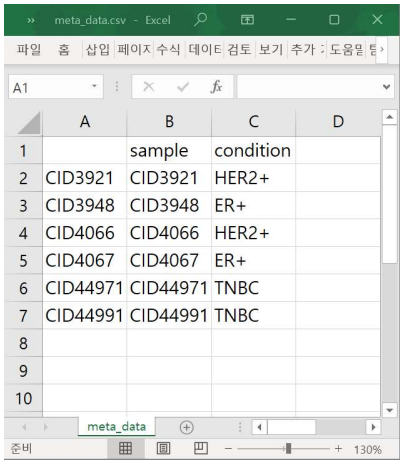
이 데이터 셋의 경우
폴더 6 개 (6개 샘플)와
메타 데이터를 포함
(meta_data.csv)

3. 각 데이터 폴더를 더블 클릭해서 열면



CellRanger로 생성된 3개 파일을 포함

4. meta_data.csv 파일을 엑셀로 열어 보면



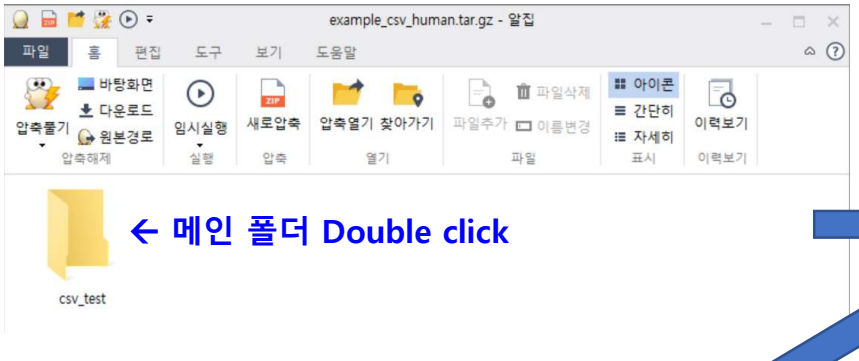
	A	B	C	D
1		sample	condition	
2	CID3921	CID3921	HER2+	
3	CID3948	CID3948	ER+	
4	CID4066	CID4066	HER2+	
5	CID4067	CID4067	ER+	
6	CID44971	CID44971	TNBC	
7	CID44991	CID44991	TNBC	
8				
9				
10				

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

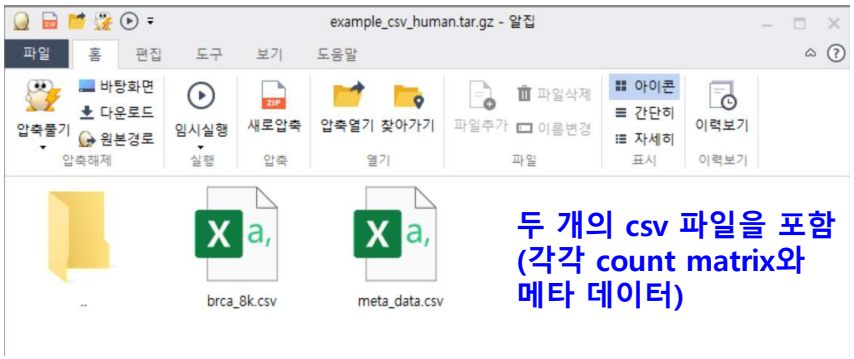
- 인덱스 열의 각 인덱스는 폴더 명과 일치해야 함.
- Sample name과 인덱스가 동일할 필요는 없음.
- Condition 열의 조건들을 대상으로 DEG, GSEA, cell-cell interaction 비교가 수행됨

Input data formatting (2) csv format

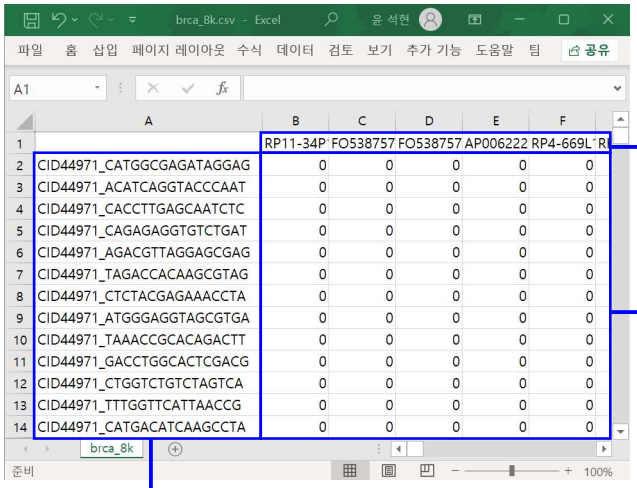
1. 압축된 예제 데이터셋을 알집으로 열어 보면



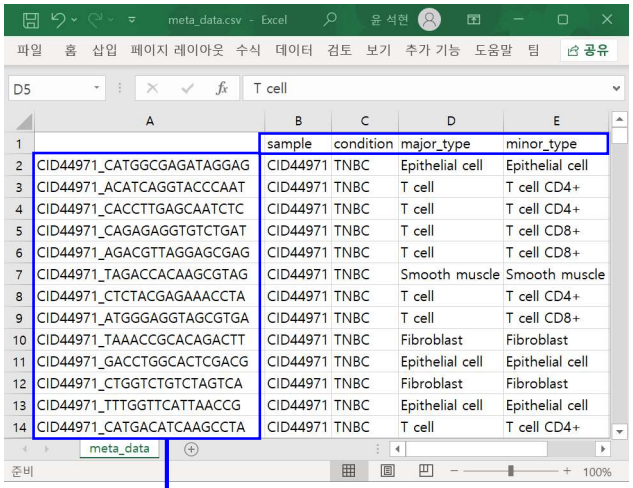
2. 메인 폴더를 더블 클릭해서 열면



3. 데이터 csv 파일



4. meta_data.csv 파일

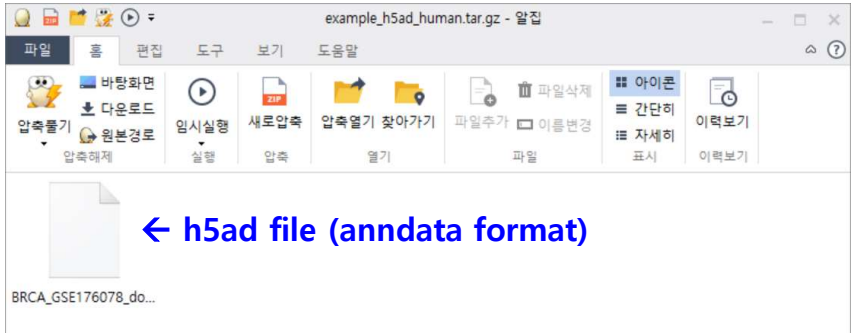


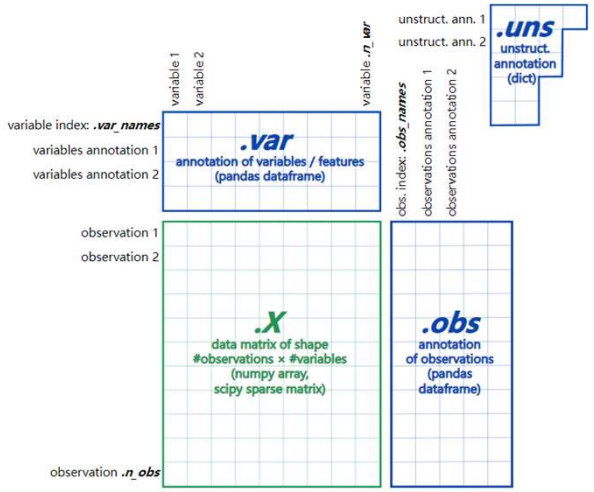
1열: 인덱스 열
2열: sample
3열: condition
4열~: optional items

- 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





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

2. h5ad file contents

```
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.