

Single-cell RNA-Seq Analysis (2)

生物資訊與數據分析

10/20/2026

開課時間：2:00-4:00PM

上課地點：環變大樓6005室

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IMB Bioinformatics Core

Demo – Single-cell Data Analysis

Demo on Colab

<https://bit.ly/4jwQ2po>

<https://drive.google.com/drive/folders/1L79nD4uBud6ujEIXZvT4Axicl10R2MjS?usp=sharing>



Scverse - <https://scverse.org/>

Scverse is an open-source, community-governed ecosystem of packages for single-cell and spatial omics. Shared data structures like AnnData, MuData, and SpatialData let tools such as Scanpy, scvi-tools, and Squidpy coordinate single powerful analysis.



Scverse - <https://scverse.org/>



Core packages

scverse develops a set of interoperable packages spanning every step of single-cell and spatial omics analysis, from data structures to modeling.

[Browse the core packages ›](#)



Ecosystem

A broader ecosystem of packages builds on the scverse core, extending it with domain-specific models and analysis methods.

[Continue to scverse ecosystem ›](#)



Events

scverse hosts hackathons, workshops, and an annual conference to bring the community together throughout the year.

[See all scverse events ›](#)



Mission

Scverse builds the community that sustains foundational tools for omics data in the life sciences.

[Read more about scverse ›](#)



Team

Scverse is a community project currently governed by a core team. Please reach out if you'd like to be involved!

[Learn more about scverse community ›](#)



References

scverse tools are used in research and industry across the globe. If they are useful in your work, please cite the scverse paper along with the individual packages you used.

[Find each package's publication ›](#)



Getting started with AnnData

Explore the structure and content of single-cell analysis results stored in an .h5ad file.



Axes in AnnData and MuData

Operations on independent AnnData objects, and how several processing workflows can live in one MuData object.



Concatenation

Concatenate objects while keeping all sub-elements of each, stacked in an ordered way.



Concatenation of multimodal data

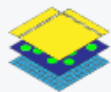
Concatenate two MuData objects representing complementary slices of a dataset, or two modalities, into one AnnData.

Scverse - Tutorials



Working with scverse objects in backed mode

Work with .h5ad and .h5mu files without loading the full dataset into memory.



Introduction to SpatialData

A tour of the SpatialData object: images, labels, points, shapes, tables and coordinate systems.



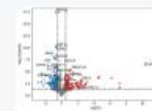
Preprocessing, clustering and cell-type annotation

Quality control, normalization, feature selection, dimensionality reduction, clustering and cell-type annotation.



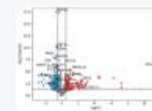
Batch-effect removal with scvi-tools

Fit a scvi-tools model to single-cell counts, correct batch effects, and run differential expression.



Single-cell enrichment analysis

Score transcription factor and pathway activities per cell, then compare them across cell types.



Pseudo-bulk differential expression and functional analysis

Pathway and TF enrichment on ~5k blood myeloid cells from healthy and COVID-19 patients.



Pseudotemporal ordering

Construct a pseudotime and compare different pseudotimes.



RNA velocity

Infer RNA velocity from single-cell RNA-seq data with scVelo.



Perturbation modeling

Augur to identify affected cell types, scGen to predict transcriptional response, Mixscape for CRISPR sensitivity.



Compositional analysis

Compositional analysis at cell identity cluster level, for known cell types or states affected by perturbations.



GPU-accelerated single-cell analysis with rapids-singlecell

A complete scRNA-seq workflow on the GPU, using rapids-singlecell as a drop-in replacement for scanpy.



Quantifying perturbation effects with distances

Measure how strongly a perturbation shifts cells with point-cloud distance metrics and permutation tests.



Perturbation spaces

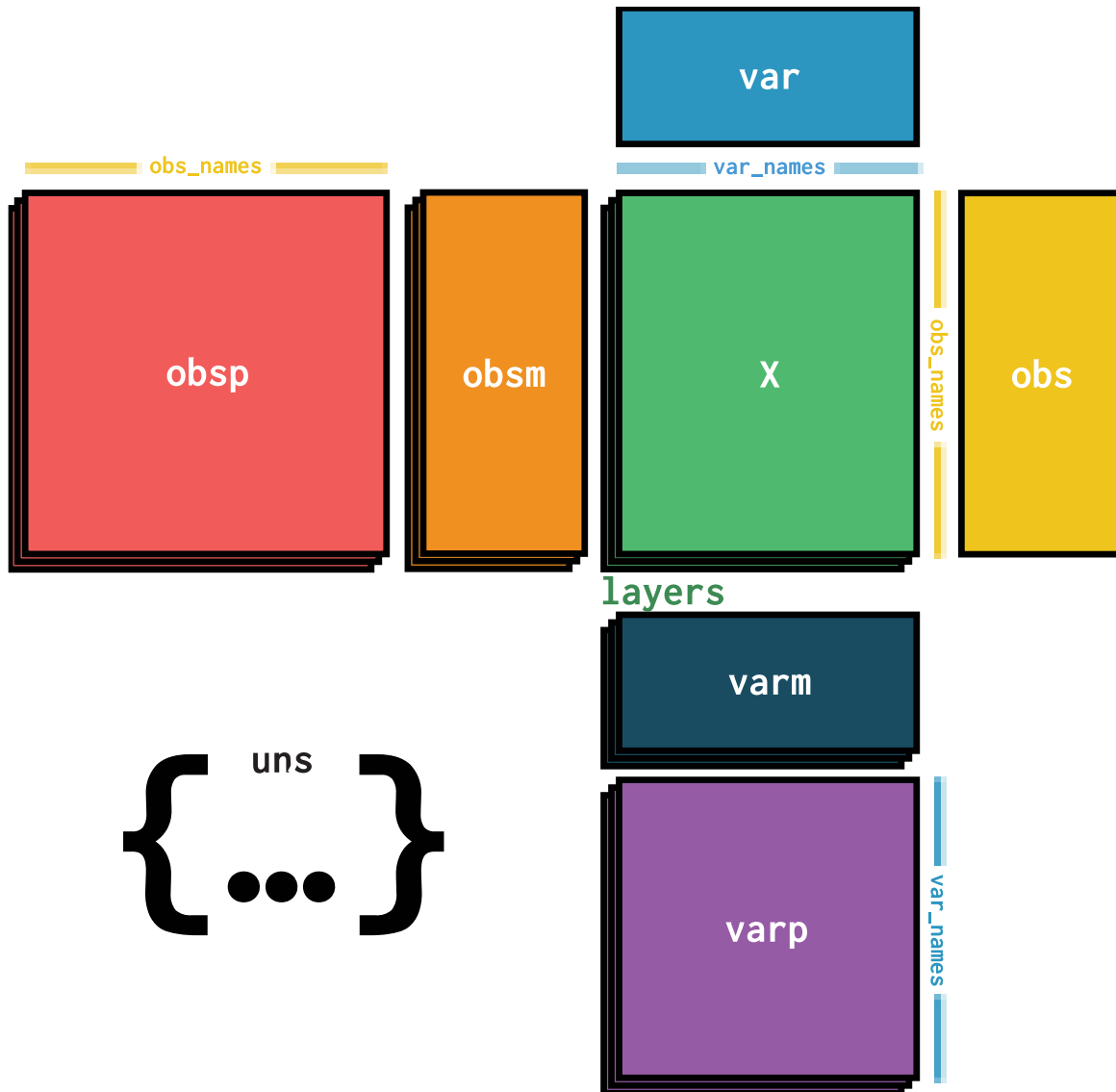
Summarize all cells of a perturbation into a single point, to compare whole perturbations rather than cells.



Perturbation efficacy in pooled CRISPR screens

Find which cells in a pooled CRISPR screen were effectively perturbed, with Mixscape and Mixscale.

AnnData object



X (matrix):

rows: **cells / observations (obs)**
columns: **genes / variables (var)**
raw counts, normalized counts ...

Annotations:

obs (observations): cell clusters, cell types, segmentation method, etc
var (variables): gene name, ensembl ID, etc

Multidimensional annotations:

obs: t-SNE, UMAP, etc

obsp and **varp**: Annotations for cell-cell and gene-gene pairs

uns: general metadata; unstructured annotation

The active data matrix in adata.X

adata

```
AnnData object with n_obs x n_vars = 2638 x 11505
  obs: 'n_genes', 'percent_mito', 'n_counts', 'louvain_cell_types'
  var: 'gene_names', 'n_cells', 'gene_ids'
  uns: 'louvain', 'louvain_colors', 'pca'
  obsm: 'X_pca', 'X_tsne', 'X_umap'
  layers: 'raw'
  obsp: 'distances_all'
```

adata.X

```
<Compressed Sparse Row sparse matrix of dtype 'float32'
  with 2076576 stored elements and shape (2638, 11505)>
```

