

Single-cell multi-omics dataset acquisition, model training, and analysis

Yi Jiang

Graduate Research Assistant

Department of Biomedical Informatics

The Ohio State University

12/1/24

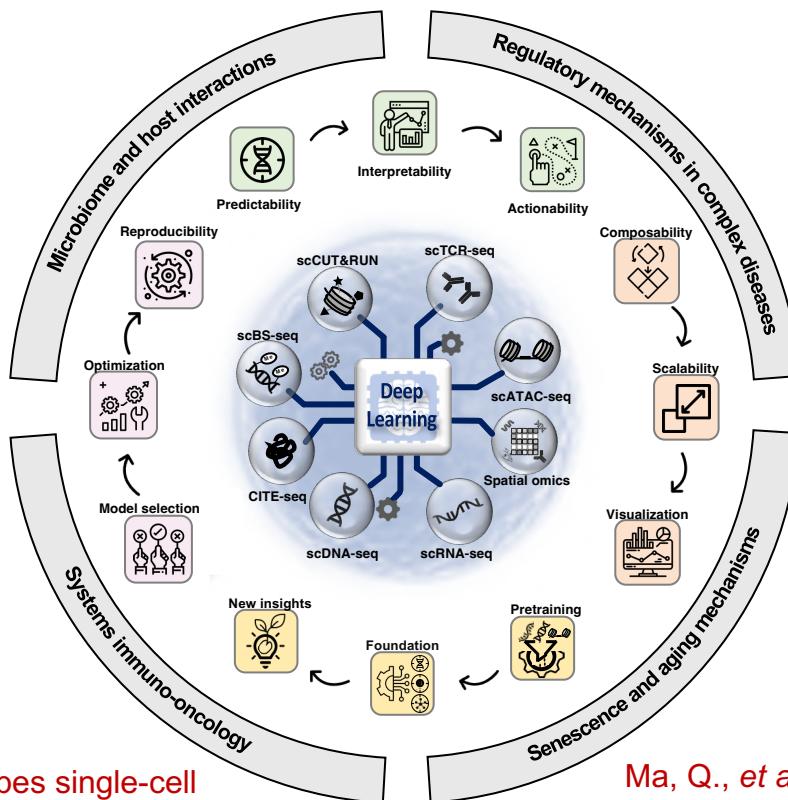


THE OHIO STATE UNIVERSITY

WEXNER MEDICAL CENTER



Develop DL methods for new hypothesis generation



Dr. Qin Ma
Professor, OSU

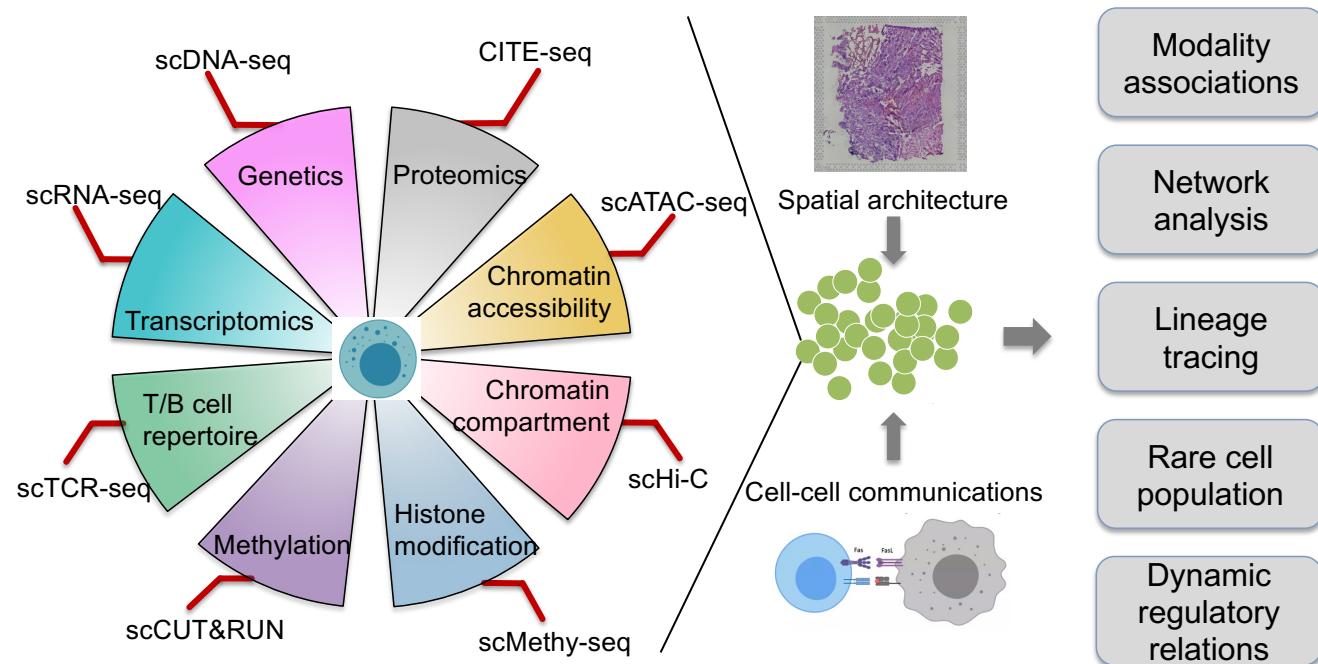


Dr. Dong Xu
Professor, MU

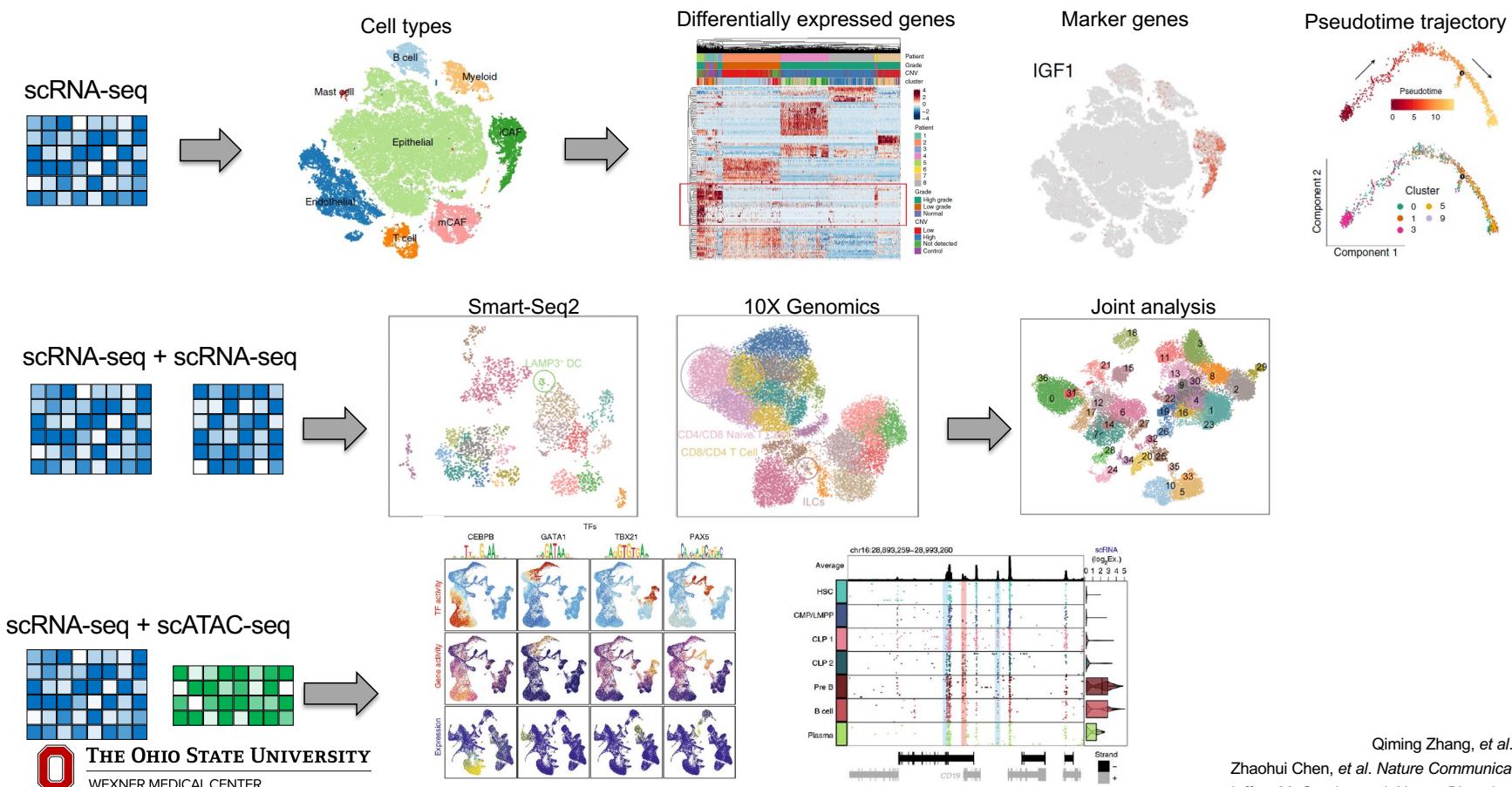
Ma, Q., et al. Deep learning shapes single-cell data analysis. *Nat Rev Mol Cell Biol* (2022)

Ma, Q., et al. Harnessing the deep learning power of foundation models in single-cell omics. *Nat Rev Mol Cell Biol* (2024)

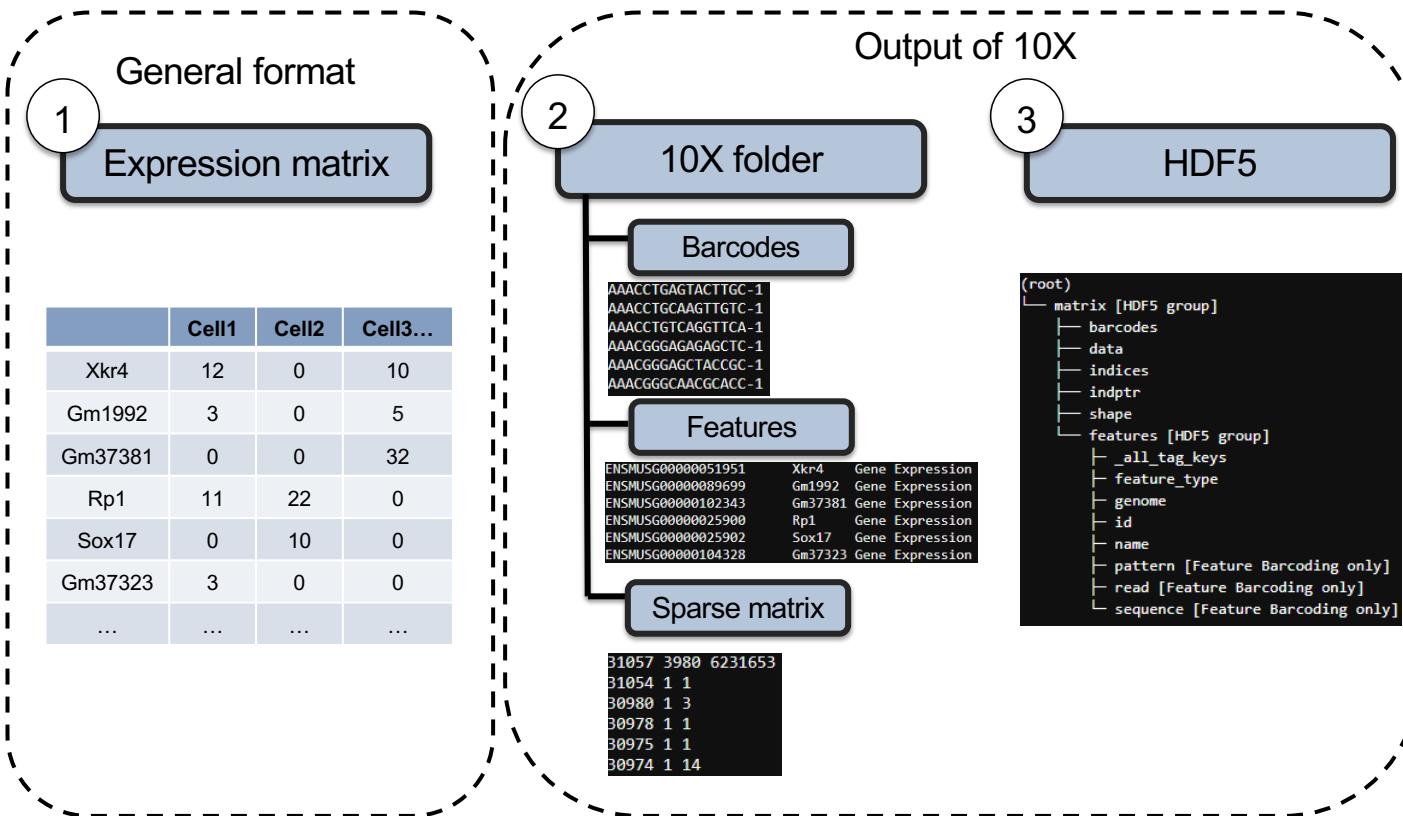
scMulti-omics enhance and enable various biological analyses



scMulti-omics analysis refines knowledge of cell heterogeneity



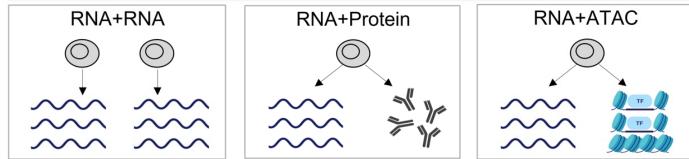
Single-cell common data format



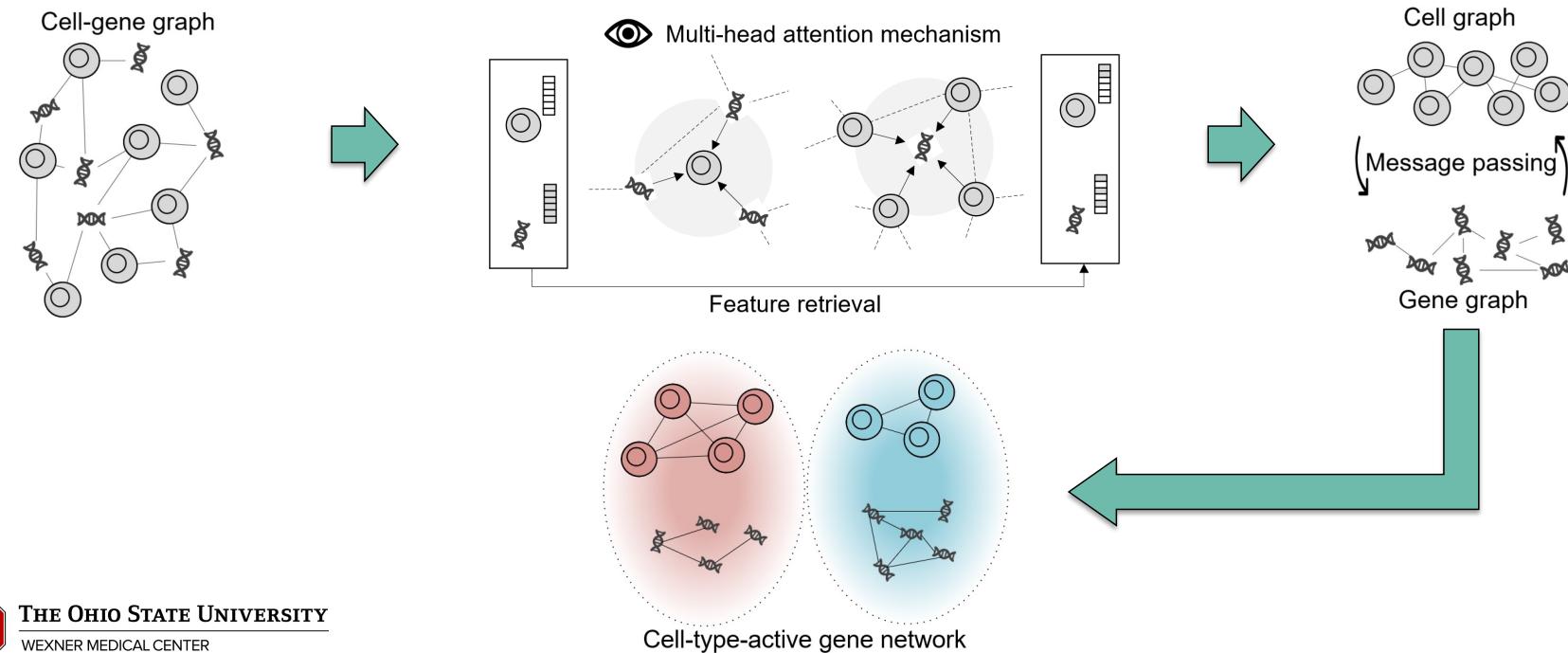
HDF5 detail can be found at: https://support.10xgenomics.com/single-cell-gene-expression/software/pipelines/latest/output/molecule_info

**Modeling, including deep learning models and
automated hyperparameter tuning**

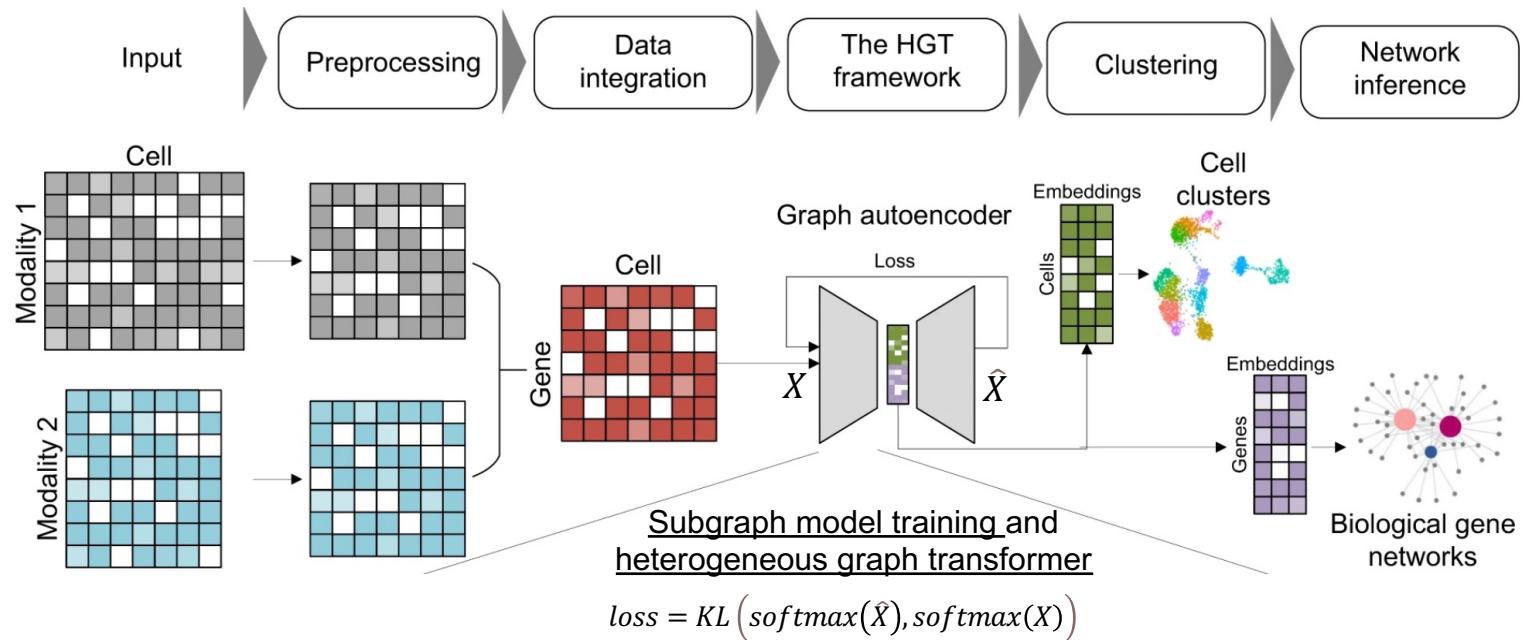
Overview of DeepMAPS framework



- Learn the **joint embedding** of cells and genes
- Calculate “**attention**” scores (importance) b/w cells and genes
- Learn cell clusters and gene clusters simultaneously



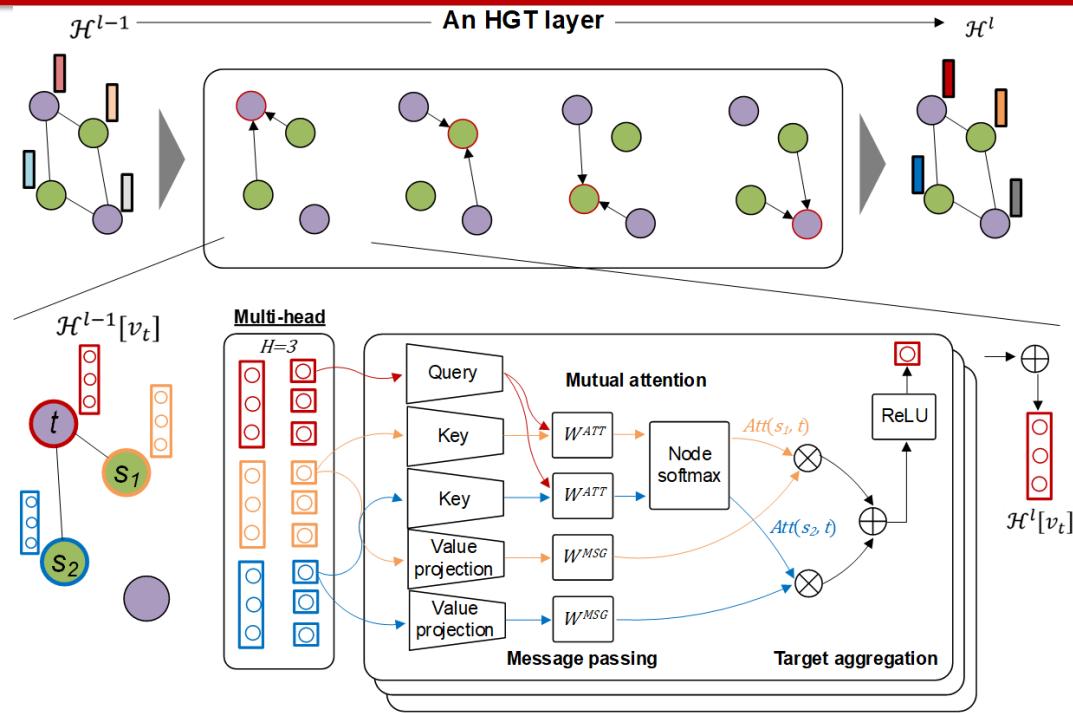
Overview of DeepMAPS framework



Note: ATAC peaks are annotated to corresponding genes based on distance-based regulatory potential score introduced in MAESTRO.

$$w_{ik} = \begin{cases} 0, & d_{ik} > 150\text{kb} \text{ or peak } k \text{ located in any nearby genes} \\ \frac{1}{Length(exon)}, & \text{peak } k \text{ located at the exon regions of the gene } j \\ 2^{-\frac{d_{ik}}{d_0}}, & \text{else} \end{cases}$$

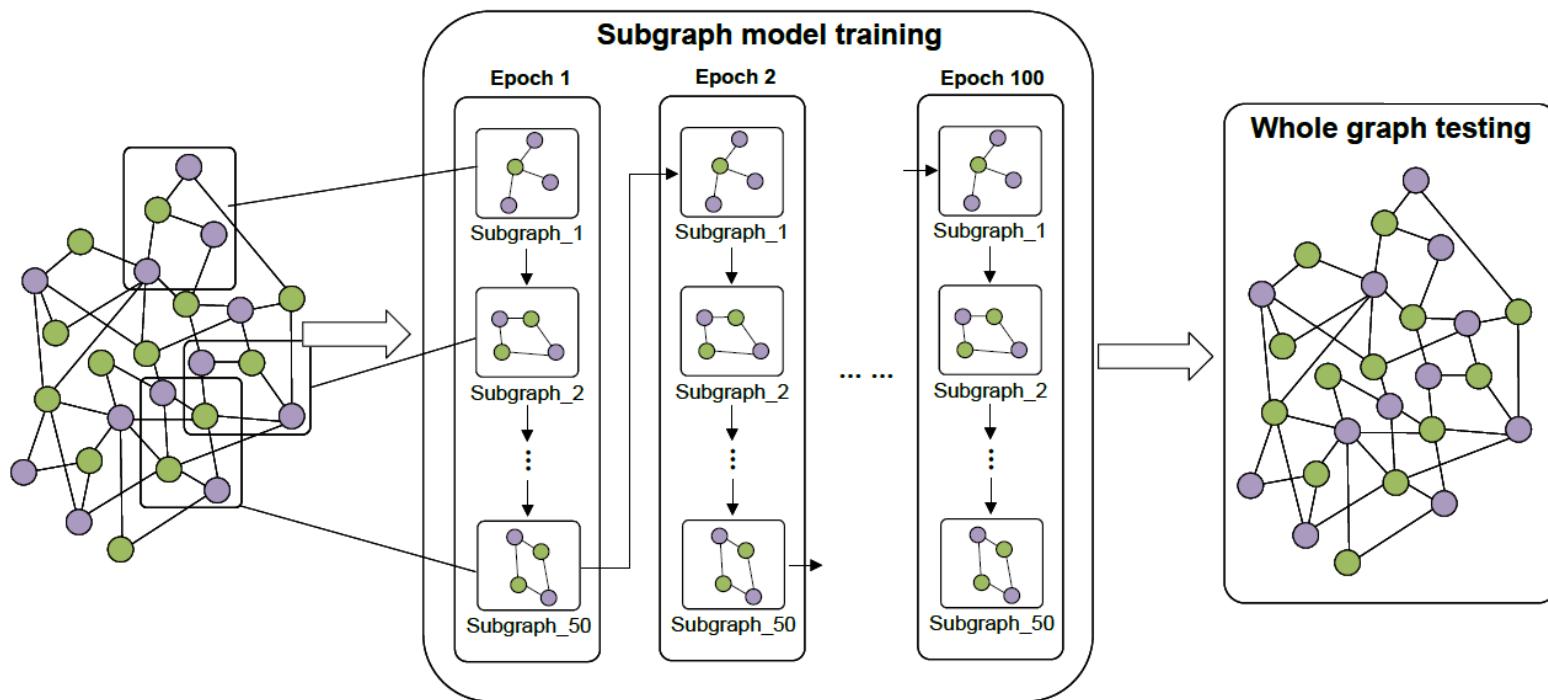
Detailed architecture of heterogeneous graph transformer



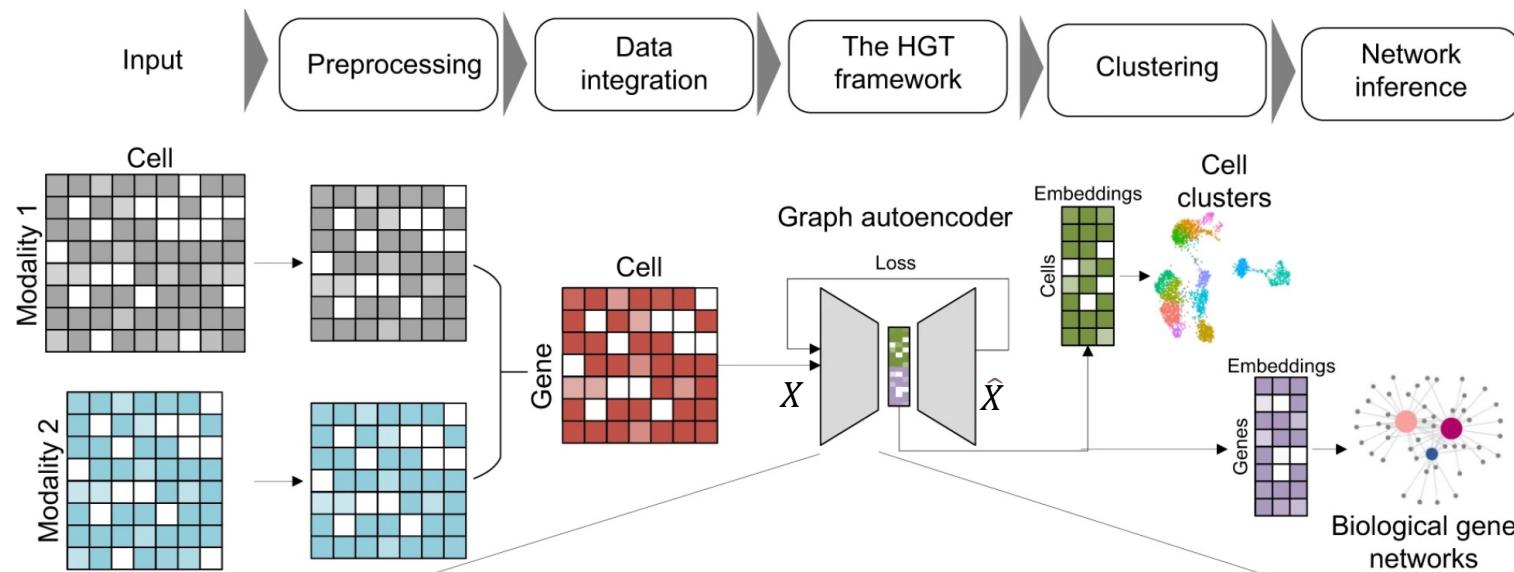
Advantages of heterogeneous graph transformer with multi-head mechanism:

- (1) Anti-noise, (2) increase discrepancies and similarity, (3) computing efficient, (4) interpretable

Subgraph training for large dataset



Overview of DeepMAPS framework

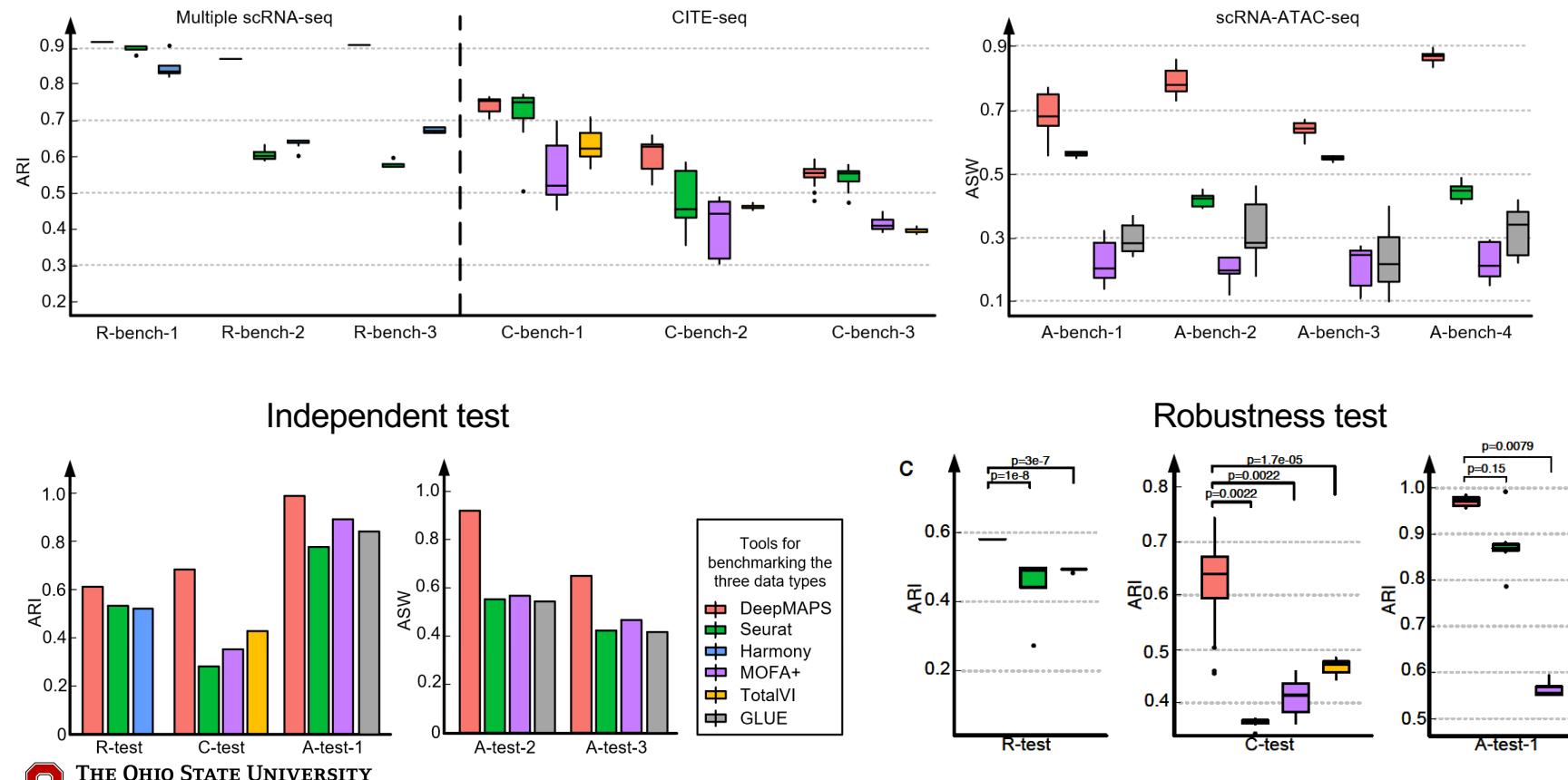


We used a Steiner Forest Problem (SFP) model to select genes that highly contribute to cell cluster characterization and construct cell cluster-active gene association networks.

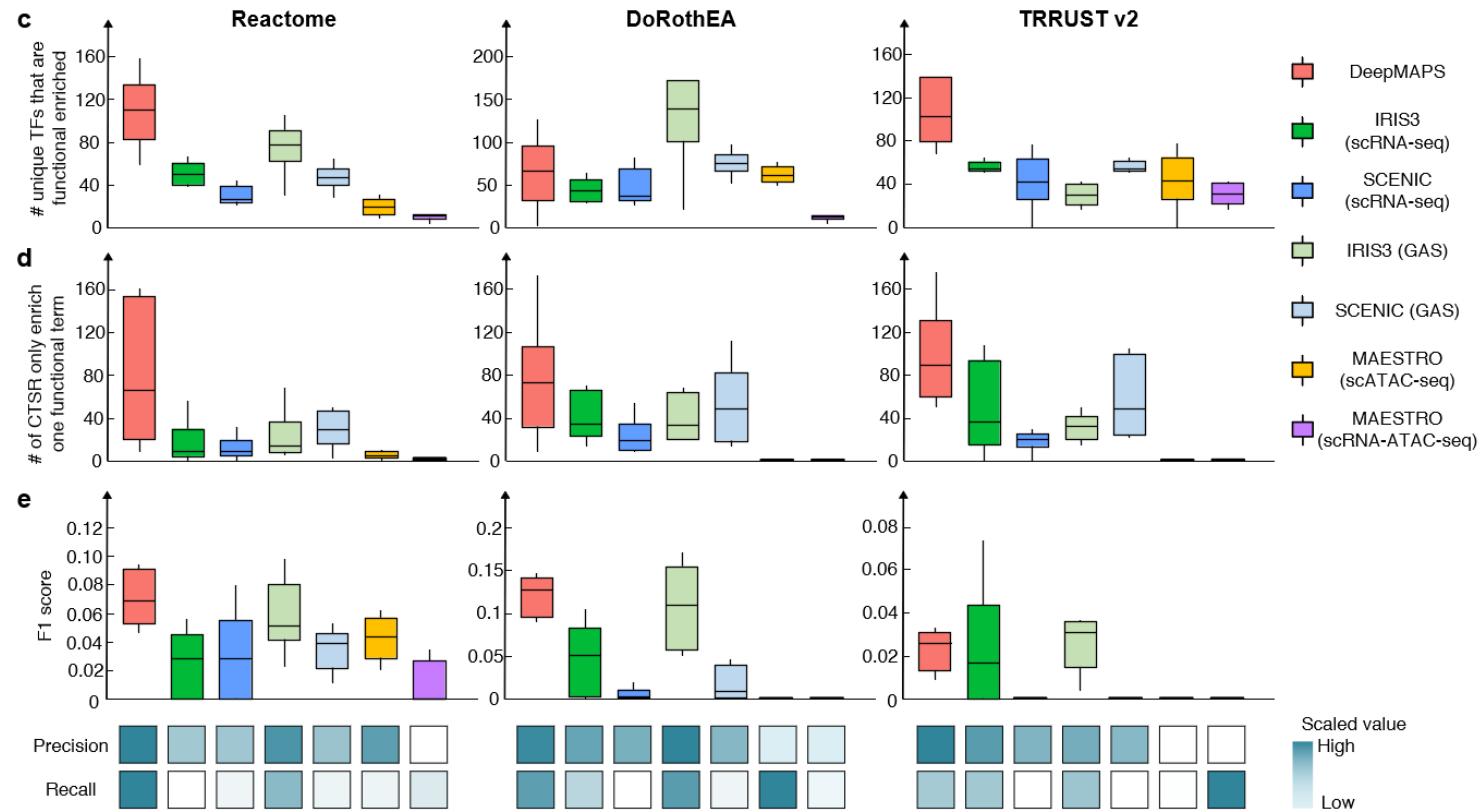
For GRN construction:
design a regulatory intensity (RI) score

$$s_{ij|q} = \sum_k b_{qk}^A \cdot r_{ik|j}$$

DeepMAPS benchmarking: better performance in cell clustering



DeepMAPS benchmarking: better performance in GRN inference



DeepMAPS Tutorial

Tutorial Objectives

- Get to know the DeepMAPS website: main page
- Start a new job
- Access example data
- Result tour for
 - matched scRNA-seq and scATAC-seq data
 - CITE-seq data
 - multiple scRNA-seq data
- User workspace

Main page navigation

The screenshot shows the DeepMAPS main page with several red boxes and arrows highlighting specific features:

- New project**: Points to the "New project" button in the top left.
- Browse public projects**: Points to the "Browse public projects" link in the top left.
- DeepMAPS**: Points to the DeepMAPS logo in the top left.
- EXPLORE**: Points to the EXPLORE menu item.
- TUTORIAL**: Points to the TUTORIAL menu item.
- NEWS**: Points to the NEWS menu item.
- ABOUT**: Points to the ABOUT menu item.
- Search project ID**: Points to the search bar for project IDs.
- LOGIN**: Points to the LOGIN button.
- We are working intensively to upgrade DeepMAPS (0.22.0) workflow. Please let us know if there are any bugs, issues, or suggestions via qin.ma@osumc.edu.**: Points to a blue banner at the top.
- Welcome to DeepMAPS**: Points to the main title.
- Deep learning based Multi-omics Analysis Platform for Single cells**: Points to the subtitle.
- Start a new project or load example data**: Points to the "New project" section.
- View example results**: Points to the "View Examples" section.
- Access users' workspace. All your previous jobs will show up here. Login required.**: Points to the "View workspace" section.
- Search an existing project with ID**: Points to the search bar for project IDs.
- Login or signup**: Points to the LOGIN button.
- Diagram illustrating the DeepMAPS workflow**: A detailed diagram showing the architecture and components of DeepMAPS, including the Server, Package, Docker, and Workspace, and their integration through a Heterogeneous graph transformer to perform tasks like Feature retrieval, Message passing, and Biological representation.
- Cite us:** Ma, A. et al. (2021) Biological network inference from single-cell multi-omics data using heterogeneous graph transformer. bioRxiv. <https://doi.org/10.1101/2021.05.10.443812>
- URL**: <https://bmblx.bmi.osumc.edu>

1.1 Matched scRNA-seq and scATAC-seq data submission

SCRNA-SEQ SCRNA-SEQ AND SCATAC-SEQ CITE-SEQ

Data upload

Feature barcode matrix
Support format: *.h5, *.hdf5
0 files

scATAC-seq fragments (optional)
Support format: *fragments.tsv.gz
0 files

scATAC-seq fragments index (optional)
Support format: *fragments.tsv.gz.tbi
0 files

Metadata (optional)
Support format: *.csv, *.txt
0 files

RNA velocity matrix (optional)
Support format: *.csv, *.txt
0 files

EXAMPLE

Project information

Project title
0 / 100

Species

Project description (optional)

E-mail

Optional: The running time could takes a few hours if the dataset is large. Hence, we strongly recommend you to leave your email, and you will be notified by email when the job is done.

START

A h5 or hdf5 file. (Required)

Used for scATAC-seq peak annotation

User defined cell meta-information (optional)

An RNA velocity matrix. Can be generated via CellRank using scRNA-seq fastq file. Without this file, cell clustering and only performed via Seurat. (optional)

Load example (10X Human lymphoma 14k cells)

Download data: Human lymphoma 14k cells (h5)

Download data: Human lymphoma 14k cells (velocity matrix)

Download data: Human lymphoma 14k cells (fragments)

Download data: Human lymphoma 14k cells (fragments index)

For more information, please check:
<https://www.10xgenomics.com/resources/datasets/fresh-frozen-lymph-node-with-b-cell-lymphoma-14-k-sorted-nuclei-1-standard-2-0-0>

1.1 Matched scRNA-seq and scATAC-seq data submission

SCRNA-SEQ SCRNA-SEQ AND SCATAC-SEQ CITE-SEQ

Data upload

Feature barcode matrix
Support format: *.h5, *.hdf5
0 files

scATAC-seq fragments (optional)
Support format: *fragments.tsv.gz
0 files

scATAC-seq fragments index (optional)
Support format: *fragments.tsv.gztbl
0 files

Metadata (optional)
Support format: *.csv, *.txt
0 files

RNA velocity matrix (optional)
Support format: *.csv, *.txt
0 files

EXAMPLE

Project information

Project title

Species: Human

Please select the right sample species. (required)

Human
Mouse

Project description (optional)

0 / 100

Once everything is ready, let's get started!

START

Give a name to your project

Take some notes for the project. E.g., library preparation, related paper, experiments, etc. (optional)

We recommend you leave your email. Some steps may take a while. A notice will send to you once the job is done.

1.2 CITE-seq data submission

SCRNA-SEQ SCRNA-SEQ AND SCATAC-SEQ CITE-SEQ

Data upload

Feature barcode matrix
Support format: *.h5, *.hdf5 0 files

Metadata (optional)
Support format: *.csv, *.txt 0 files

EXAMPLE ←

Project information

Project title
0 / 100

Species

Project description (optional)

E-mail

Optional: The running time could takes a few hours if the dataset is large. Hence, we strongly recommend you to leave your email, and you will be notified by email when the job is done.

START

Only need one feature barcode matrix. (required)

Load example (CITE-seq PBMC & Lung 3.8k cells)

[Download data: \(CITE-seq PBMC & Lung\)](#)

1.3 Multiple scRNA-seq data submission

SCRNA-SEQ SCRNA-SEQ AND SCATAC-SEQ CITE-SEQ

Data upload

Gene expression matrix 1
Support format: *.csv, *.txt, *.h5 0 files

Gene expression matrix 2
Support format: *.csv, *.txt, *.h5 0 files

ADD A ROW **REMOVE A ROW**

Metadata (optional)
Support format: *.csv, *.txt 0 files

EXAMPLE

Project information

Project title
0 / 100

Species

Project description (optional)

E-mail

Optional: The running time could takes a few hours if the dataset is large. Hence, we strongly recommend you to leave your email, and you will be notified by email when the job is done.

START

Add 2 or more scRNA-seq files

For more datasets, use add a row button.

Load example (Human IFNB PBMCs, 2800 cells)

[Download gene expression matrix: Human IFNB \(sample 1\)](#)

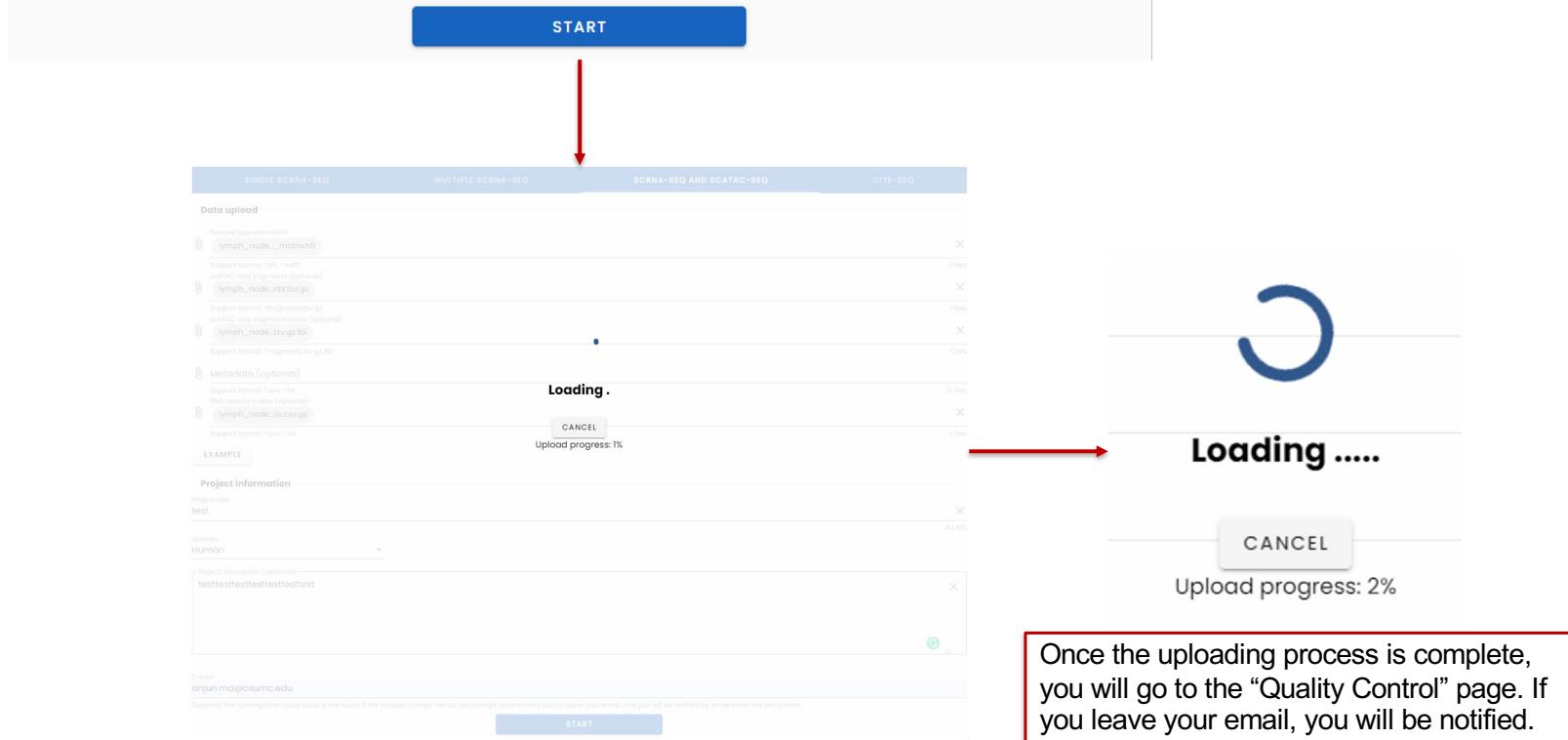
[Download gene expression matrix: Human IFNB \(sample 2\)](#)

[Download metadata file: Human IFNB](#)

1.4 Waiting for uploading

E-mail

Optional: The running time could takes a few hours if the dataset is large. Hence, we strongly recommend you to leave your email, and you will be notified by email when the job is done.



The screenshot shows a user interface for file upload. At the top, there's a red 'START' button. Below it is a navigation bar with tabs: SINGLE SCRNA-SEQ, MULTIPLE SCRNA-SEQ, SCRNA-SEQ AND SCATAC-SEQ, and CITE-SEQ. The CITE-SEQ tab is selected. The main area contains several input fields for 'Data upload' (including matrix files and GCT files), 'Metadata (optional)', and 'EXAMPLE'. A 'Project information' section includes fields for 'Project title' (set to 'test'), 'Species' (set to 'Human'), and 'Project description (optional)' (containing the text 'testtesttesttesttesttesttest'). At the bottom, there's an 'Email' field with the value 'anjun.ma@osumc.edu' and a note about optional email notifications. A red arrow points from the 'START' button down to the 'Loading...' status message, which is followed by a blue circular loading icon and the text 'Loading'. Another red arrow points from the 'Loading' message to a progress bar indicating 'Upload progress: 2%'. A 'CANCEL' button is visible next to the progress bar.

Once the uploading process is complete, you will go to the "Quality Control" page. If you leave your email, you will be notified.

2. How to get access to the example result

View Examples

Browse showcase datasets

→

You have two ways to navigate our example results

The first one is to click the “View Example” button on the main page, and choose on of your interest.

Public datasets

Filters:

Species
Human

Results:

Human IFNB-Stimulated and Control PBMCs

Type Multiple scRNA-seq dataset
Species: Human
Tissue: blood
Number of cells: 2741
Update on: 2022-01-16
Creator: admin

BROWSE

Human PBMC and lung tumor leukocytes

Type CITE-seq
Species: Human
Tissue: PBMC & Lung
Number of cells: 3485
Update on: 2022-01-16
Creator: admin

BROWSE

Fresh Frozen Lymph Node with B-cell Lymphoma (14k sorted nuclei)

Type scRNA-seq and scATAC-seq
Species: Human
Tissue: lymph
Number of cells: 13510
Update on: 2022-01-16
Creator: admin

BROWSE

2. How to get access to the example result

New project

Create a project from your data

→

The second one is to in the new project, you can load the example data and start.

SCRNA-SEQ SCRNA-SEQ AND SCATAC-SEQ CITE-SEQ

Data upload

Feature barcode matrix
Support format: *.h5, *.hdf5 0 files

scATAC-seq fragments (optional)
Support format: *fragments.tsv.gz 0 files

scATAC-seq fragments index (optional)
Support format: *fragments.tsv.gz.tbi 0 files

Metadata (optional)
Support format: *.csv, *.txt 0 files

RNA velocity matrix (optional)
Support format: *.csv, *.txt 0 files

Load example (10X Human lymphoma 14k cells)

Download data: Human lymphoma 14k cells (h5)
Download data: Human lymphoma 14k cells (velocity matrix)
Download data: Human lymphoma 14k cells (fragments)
Download data: Human lymphoma 14k cells (fragments index)

E-mail

Optional: The running time could takes a few hours if the dataset is large. Hence, we strongly recommend you to leave your email, and you will be notified by email when the job is done.

START

3. Example data illustration

Next, we will go through the result pages using the matched scRNA-seq and scATAC-seq example data.

Three steps are included:

- 3.1. data quality control,
- 3.2. data integration and cell clustering,
- 3.3. network construction

DeepMAPS provides real-time parameter changing and result observations.

3.1 Quality control

Expand to see project information

Select data for preprocessing

Original and preprocessed data statistics

Choose parameters

Move mouse to one figure will show figure illustration and download options

Step indicator

Preprocessing results and general data statistic visualizations

Top variable genes

Number of total read counts per cell

Number of expressed genes per cell

Number of read counts per cell

Number of cells among each expressed gene

Quality control

Cell clustering

Network construction

Project summary

SCRNA-SEQ ASSAY SCATAC-SEQ ASSAY

Original data statistics

Cells: 8770
Genes: 21477
Average expression level: 0.1172
Zero expression percentage: 0.0595

Current data statistics

Cells: 8770
Genes: 21477
Average expression level: 0.1172
Zero expression percentage: 0.0595

Preprocessing

Max counts per cell: 20000
Min cells per gene: 0.001
Mitochondrial counts ratio: 0.1
Ribosomal counts ratio: 0.5
 Remove outlier cells
Normalization method: LogNormalize

UNLOCK PARAMETERS

LOAD

Download PNG

Download JPG

Download file (CSV)

Number of total read counts per cell: 6,000
Number of expressed genes per cell: 1,500
Number of read counts per cell: 2,500
Number of cells among each expressed gene: 1,500

Gene: CEMIP, Residual variance: 13.90, Standard deviation: 4.96, Mean: 0.04, Max: 6.05
Gene: FTL, Residual variance: 10.84, Standard deviation: 17.29, Mean: 0.49, Max: 5.99
Gene: CCSERI, Residual variance: 9.70, Standard deviation: 4.02, Mean: 0.17, Max: 5.07
Gene: HDAC9, Residual variance: 9.33, Standard deviation: 5.37, Mean: 0.23, Max: 5.49
Gene: SEMA3A, Residual variance: 7.86, Standard deviation: 0.75, Mean: 0.04, Max: 4.98
Gene: SLCBA1, Residual variance: 6.79, Standard deviation: 23.13, Mean: 0.44, Max: 5.67
Gene: TFEC, Residual variance: 6.74, Standard deviation: 6.43, Mean: 0.28, Max: 4.80
Gene: RIMS1, Residual variance: 6.61, Standard deviation: 2.35, Mean: 0.18, Max: 5.06
Gene: CCL4L2, Residual variance: 6.45, Standard deviation: 3.00, Mean: 0.23, Max: 5.34
Gene: A1126AFA.1, Residual variance: 6.20, Standard deviation: 1.50, Mean: 0.19, Max: 5.10

3.2.1 Cell clustering – Data integration and cell clustering

Integrative clustering

Integrative clustering

Method

Velocity weighted method

Clustering resolution
0.5

CALCULATE

Cell identity

Cell labeling

Cell selection

Velocity weighted method

Seurat-WNN

Users can choose to use either the velocity weighted integration method in DeepMAPS or the weighted nearest neighbor (WNN) method in Seurat 4.0

Note that, a velocity matrix is needed as input for using the velocity weighted integration. If you do not provide such velocity data, please use WNN instead.

You will then asked to select number of principle components to be used for data integration (for WNN only), and the clustering resolution in Louvain clustering method (for both)

Click “calculate” button to continue.

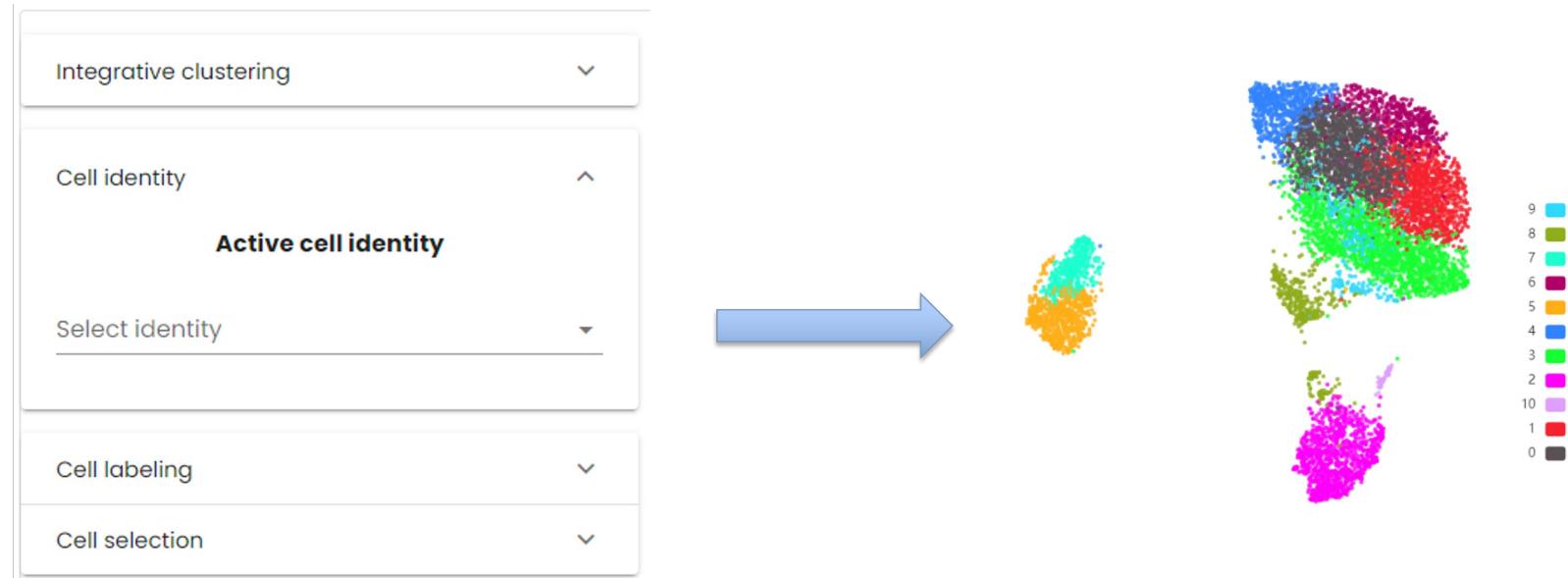
An email will be sent to you once the clustering step is done.

3.2.3 Cell clustering – UMAP



3.2.2 Cell clustering – Change active cell identity

If you have uploaded a metadata file, you can switch the active cell identity to observe different cell labels on the UMAP, e.g., treatment, sample id, male/female. By default, the clustering results will be selected.



3.2.4 Cell clustering – Rename existing cell labels

Cell labeling

Rename clusters

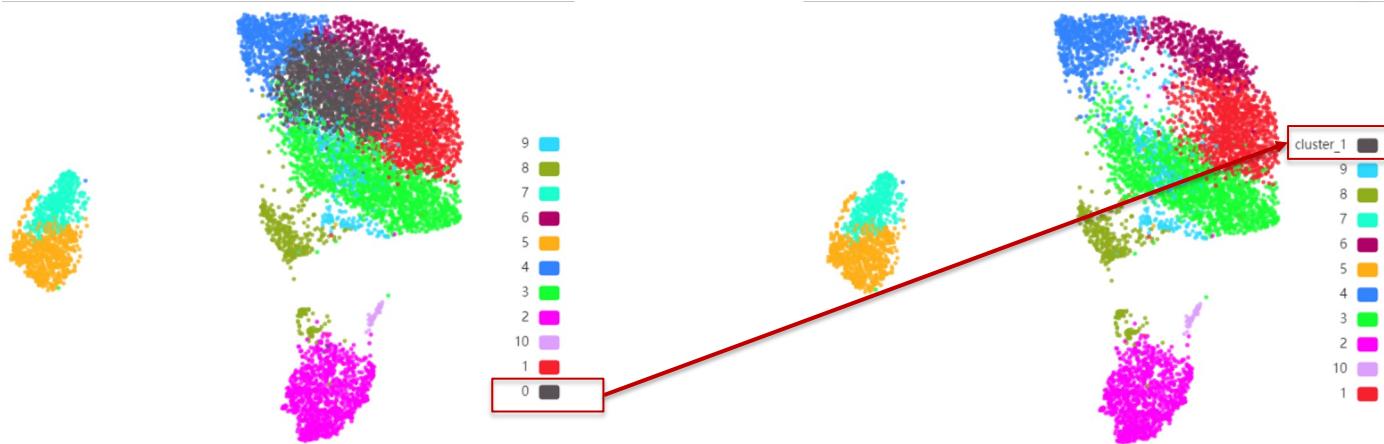
Old cluster name
0

New cluster name
cluster_1

RENAME

Once you decided the name of each predicted cell cluster, you can use the “Rename clusters” function to manually annotate the name. Here as an example, cluster 0 is renamed as “cluster_1”.

Please remember to change to the right active cell identity before rename clusters.



3.2.5 Cell clustering – Cluster merge and create new cell labels

Custom cell labeling

Step 1: Create cell filters

1. Choose a label type → Category: Cluster

2. Choose clusters you want to merge → Cluster: Add t

For reselection, remove all rules first → REMOVE ALL

Delete rule if you select it wrong

3. Give a name to your new label group → Set new category: new_type_2

4. Give a new cell type label → Add new label: test_type1

ASSIGN CELLS

Step 2: Assign cells to new label

5. Confirm and see result

Cell identity

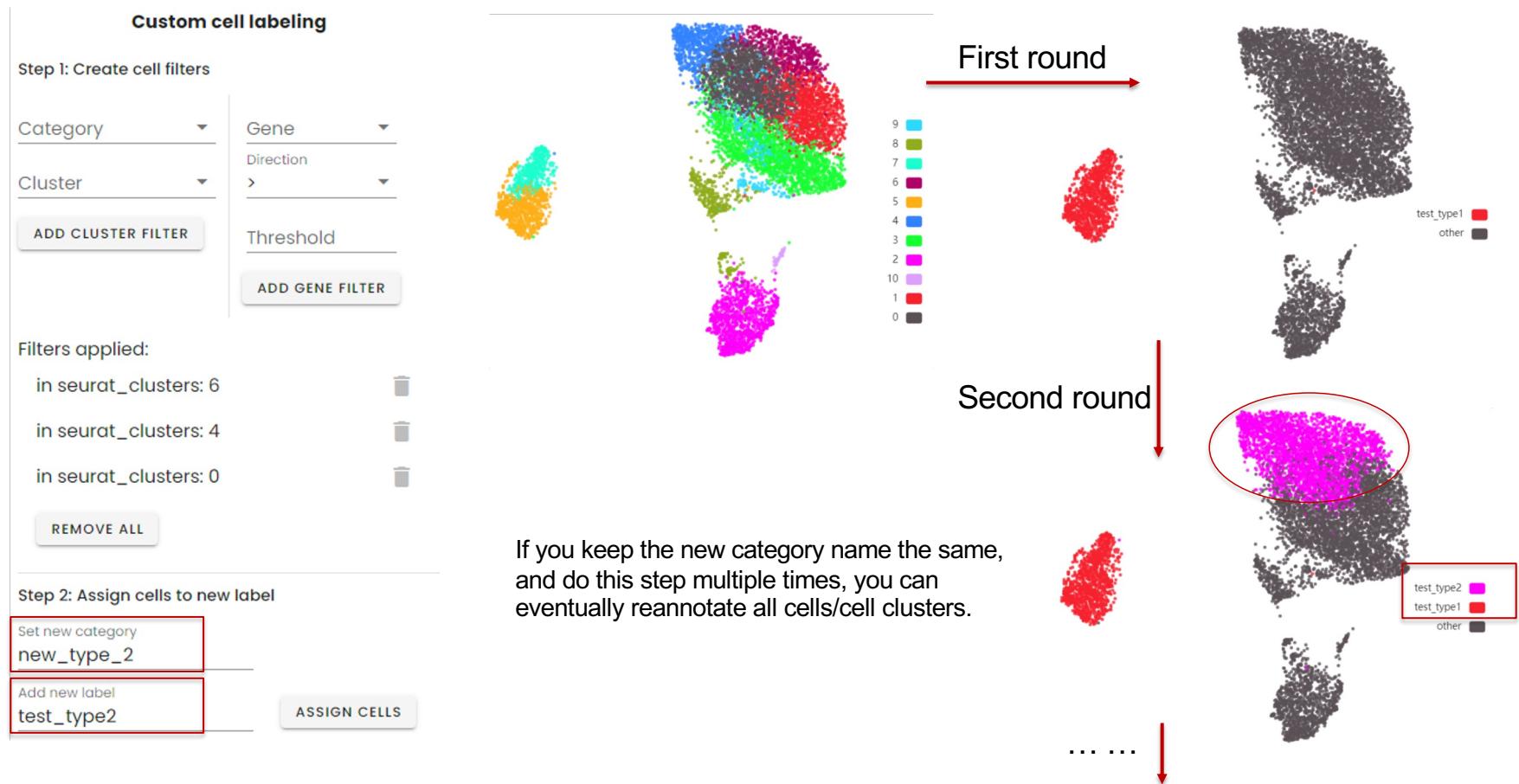
Active cell identity

Select identity

- seurat_clusters
- cell_type
- new_type
- new_type_2**

The screenshot shows the 'Custom cell labeling' interface. On the left, under 'Step 1: Create cell filters', there are dropdown menus for 'Category' (set to 'Cluster') and 'Gene' (set to 'test_type1'). Below these are 'Direction' (set to '>') and 'Threshold' fields. A red box highlights the 'Cluster' dropdown. A button 'ADD CLUSTER FILTER' is above a text input 'Add t'. Another button 'ADD GENE FILTER' is below it. To the right, a legend shows 11 color-coded categories from 0 to 9. Below the legend are two scatter plots: one with a red circle highlighting a cluster of points, and another with a red circle highlighting a different cluster. A text box states: 'You can merge your cells by different rules (multiple clusters) or specific gene expression. Create a new label group and name cell types in your way!' On the right, under 'Cell identity' and 'Active cell identity', a tree view shows 'Select identity' with 'seurat_clusters', 'cell_type', 'new_type', and 'new_type_2' listed. 'new_type_2' is highlighted in blue. At the bottom, a large red arrow points from the 'Assign Cells' button to the 'Active cell identity' section.

3.2.5 Cell clustering – Cluster merge and create new cell labels



3.2.6 Cell clustering – Subset cells/cell clusters

Cell selection

Cell selection

Category new_type_2	Gene
Cluster test_type1, test_type2	Direction >
	Threshold

ADD CLUSTER FILTER **ADD GENE FILTER**

Selections applied:

new_type_2: test_type2



new_type_2: test_type1

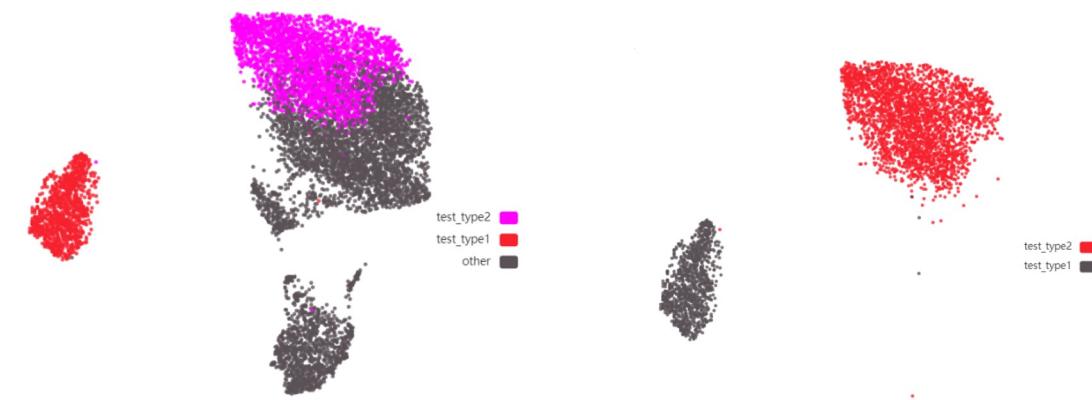


REMOVE ALL

SUBSET CELLS

RESET

To remove any unwanted cells or perform cell sub-clustering, you can use the “Cell selection” function. Similar as the previous one to set rules and subset.



3.2.7 Cell clustering – DEG analysis

The screenshot shows a user interface for performing differential gene expression (DEG) analysis. At the top, there are dropdown menus for 'Group 1' (set to '0') and 'Group 2' (set to '1 (+9 others)'). A 'Direction' dropdown is set to 'all'. Below these are input fields for 'p-value threshold' (0.05), 'min cell percentage' (0.1), and 'logFC threshold' (0.25). A 'CALCULATE' button is present. To the right, a red box highlights the 'Direction' dropdown, which has three options: 'up', 'down', and 'all' (which is selected). A red arrow points from the text 'Whether you want both positive and negative DEGs, or just one direction.' to this dropdown.

Whether you want both positive and negative DEGs, or just one direction.

DEG analysis uses Wilcoxon rank test. You need to select the two groups to be compared, either a normal comparison (1 vs all) or a 1 vs 1 comparison. Note that, switch to the right active cell identity first, otherwise you may not see the right cell labels.

Gene	pct_1	pct_2	logFC ↓	adjusted p-value
AGAPI	0.615	0.29	1.1754	7.9405e-158
GNYL	0.508	0.317	1.0507	5.4977e-54
MEAK7	0.367	0.177	0.9993	2.1002e-69
RNF213	0.974	0.875	0.9046	7.704e-227
AC139720.1	0.415	0.229	0.8641	7.5721e-56
CADM1	0.694	0.387	0.8623	1.535e-115
GZMK	0.431	0.223	0.8523	2.2284e-69
TIAM1	0.453	0.263	0.8464	1.7529e-56
BCL11B	0.793	0.498	0.8412	6.6515e-125

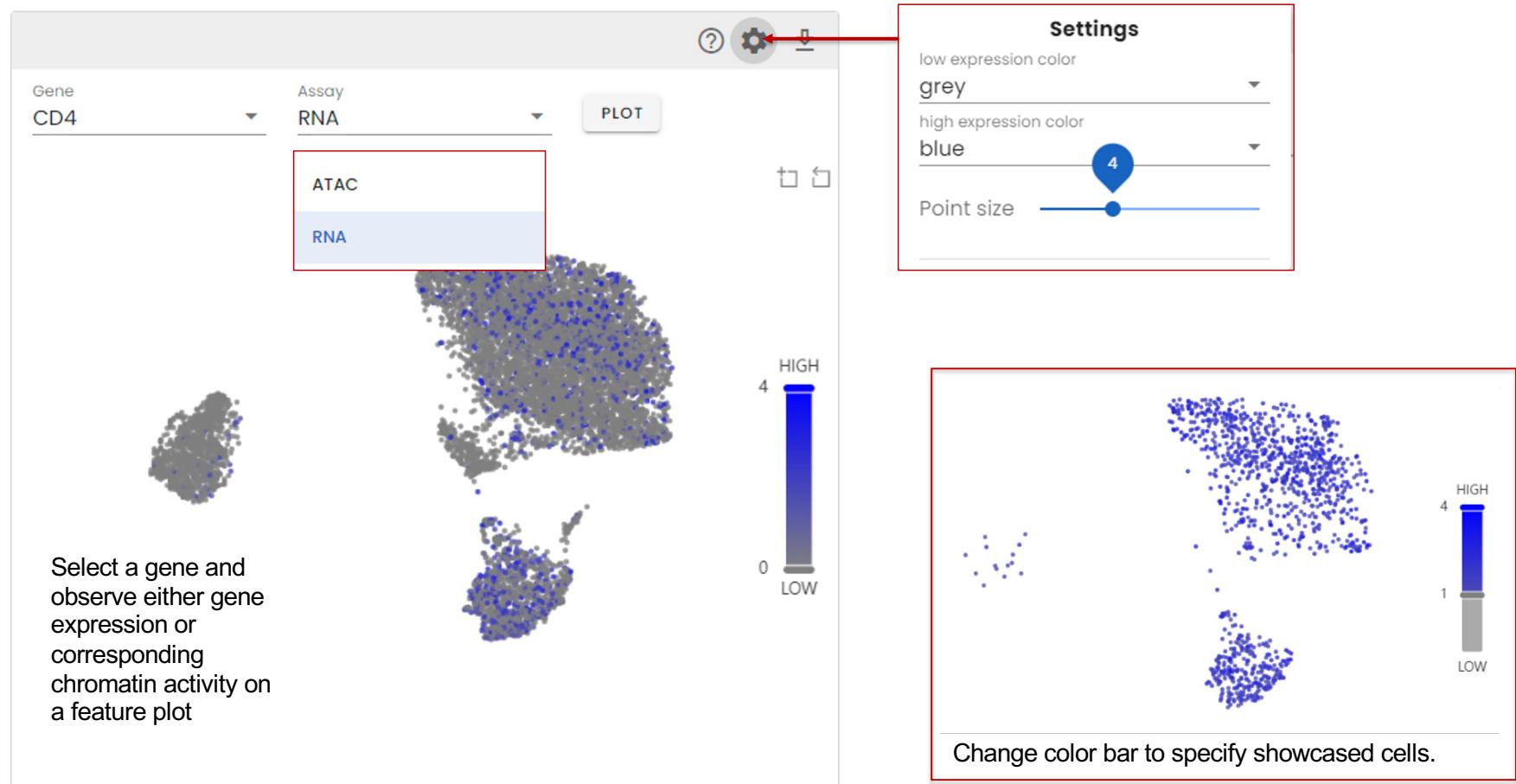
Cell identity

Active cell identity

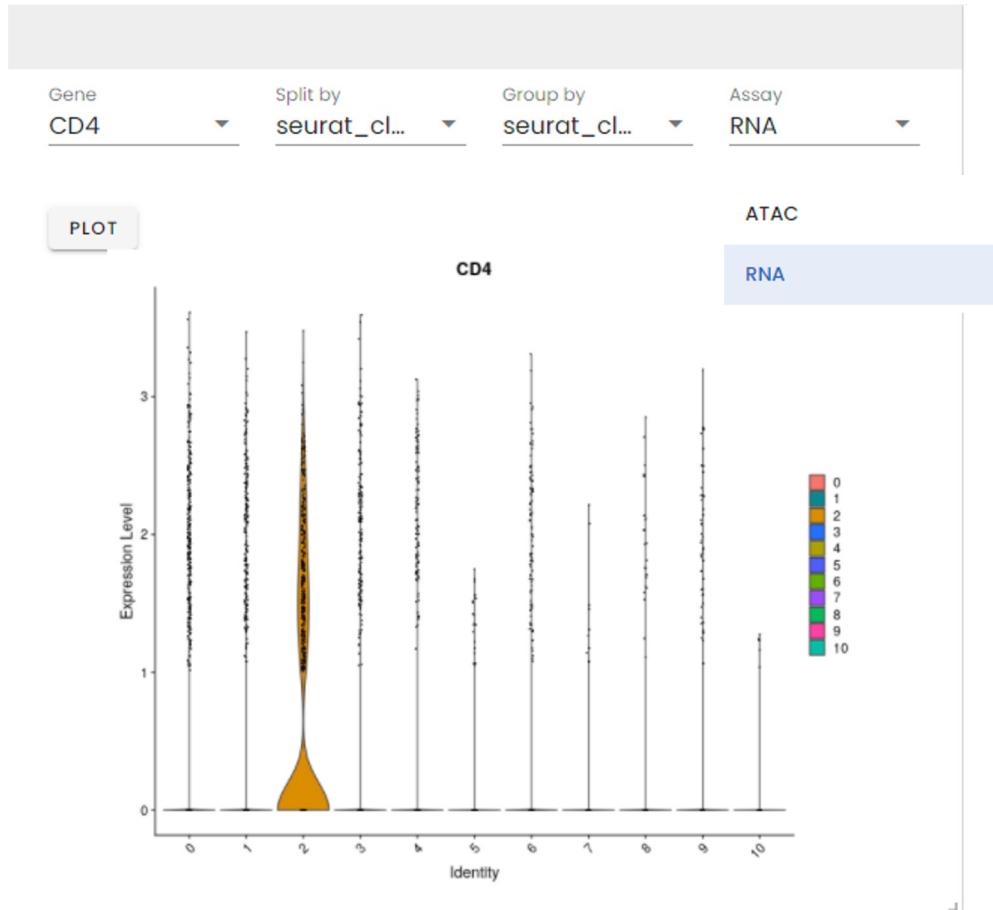
Select identity
hgt_cluster

Rows per page: 10 1-10 of 863 < >

3.2.8 Cell clustering – Gene feature plot



3.2.9 Cell clustering – Violin plot



View gene violin plot. If you have multiple metadata, you can choose to split visualization by one type. We follow the same logic as used in Seurat.

3.2.10 Cell clustering – Functional enrichment

Gene set enrichment analysis

Tool: GSEA Direction: all **CALCULATE**

pathway	Adjusted p-value	NES ↓	si
DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN	0.7061	2.8736	5
GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_UP	0.5972	2.4825	13
LEE_DIFFERENTIATING_T_LYMPHOCYTE	0.7113	2.4601	5
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	0.5972	2.3336	12
PUJANA_BRCA2_PCC_NETWORK	0.6096	2.1762	3
BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_UP	0.6096	2.1026	8
KANG_DOXORUBICIN_RESISTANCE_UP	0.5972	2.0821	9
GRAHAM_CML QUIESCENT_VS_NORMAL QUIESCENT_UP	0.6096	2.0709	7
FUJII_YBX1_TARGETS_DN	0.6316	2.0455	19

Rows per page: 10 1-10 of 4918

Hallmark gene sets (H)

Positional gene sets (C1)

Curated gene sets (C2)

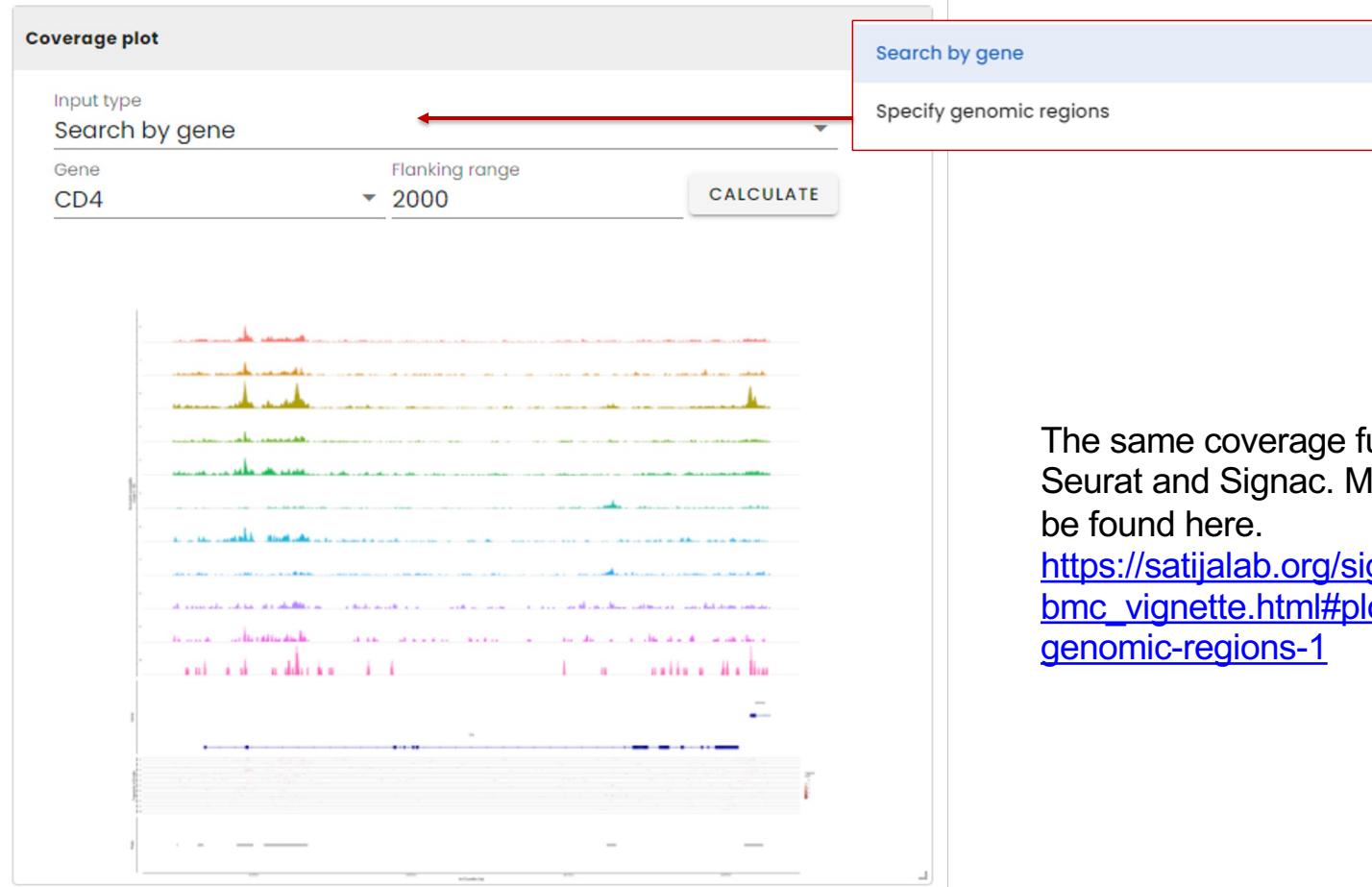
Regulatory target gene sets (C3)

Computational gene sets (C4)

Ontology gene sets (C5)

Oncogenic signature gene sets (C6)

3.2.11 Cell clustering – Coverage plot



The same coverage function used in Seurat and Signac. More details can be found here.

https://satijalab.org/signac/articles/pbmc_vignette.html#plotting-genomic-regions-1

3.3 Network construction

Gene Regulatory Network

CALCULATE

1. Select cell cluster
0

Plot regulons network:

2. Select regulons
SRF (+4 others)

Add top N by centrality

Add top N by logFC

Selections applied:

TF	Centrality	logFC	Remove
SRF	0.1168	0.2796	
NR3C1	0.1303	0.1832	
SREBF1	0.1284	0.1045	
NFIA	0.1448	0.0965	
JUND	0.1249	0.0917	

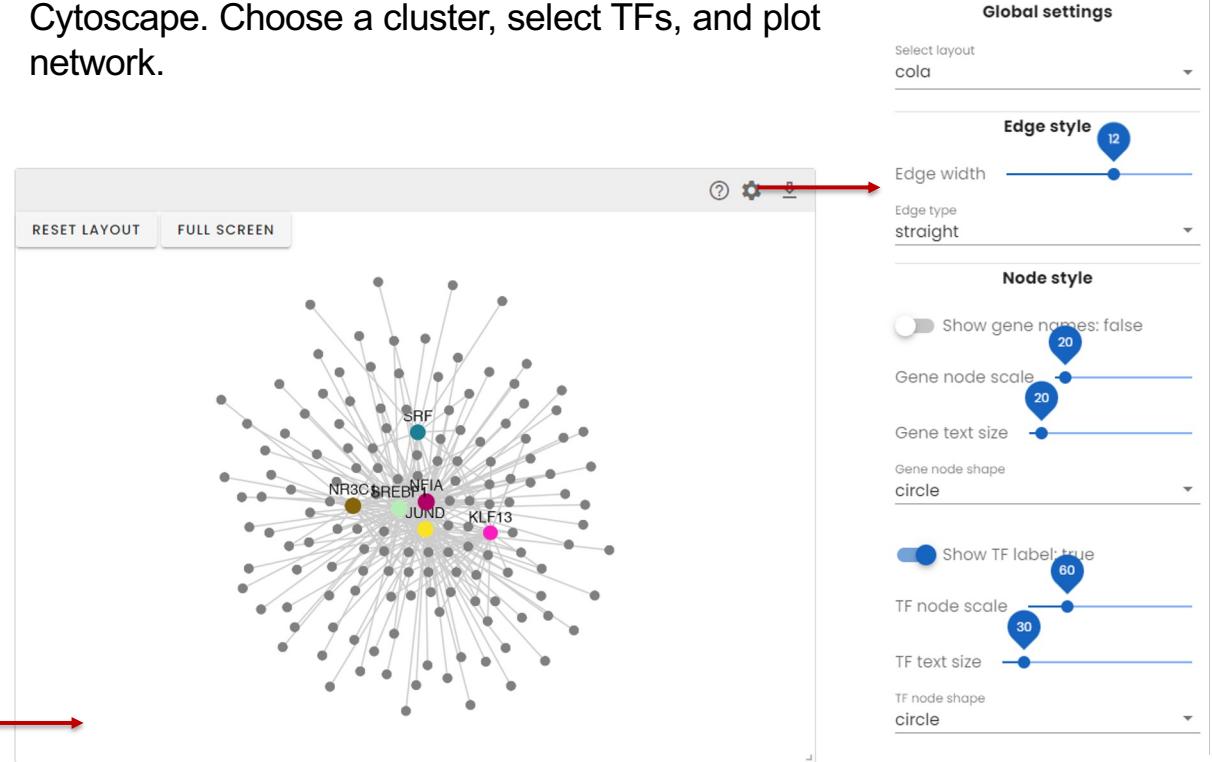
Rows per page: 10 1-5 of 5 < >

PLOT **REMOVE ALL**

Search TF/genes of interest

TF Target genes

DeepMAPS provides network construction via Cytoscape. Choose a cluster, select TFs, and plot network.



3.3 Network construction

Regulons						
TF	Centrality	# genes	RAS	logFC ↓	adj.p-value	Details
SRF	0.1168	13	0.1331	0.2796	0.1036	<button>Show</button>
NR3C1	0.1303	18	0.1072	0.1832	1	<button>Show</button>
SREBF1	0.1284	45	0.0598	0.1045	1	<button>Show</button>
NFIA	0.1448	69	0.1112	0.0965	0.0027	<button>Show</button>
JUND	0.1249	51	0.0743	0.0917	1	<button>Show</button>
SOX2	0.1206	47	0.0985	0.0829	1	<button>Show</button>
MAFK	0.1376	53	0.0583	0.0687	1	<button>Show</button>
MYB	0.1485	54	0.0946	0.0643	1	<button>Show</button>
MEF2B	0.3114	67	0.1194	0.0509	1	<button>Show</button>
CDX2	0.2179	92	0.2048	0.0454	1	<button>Show</button>

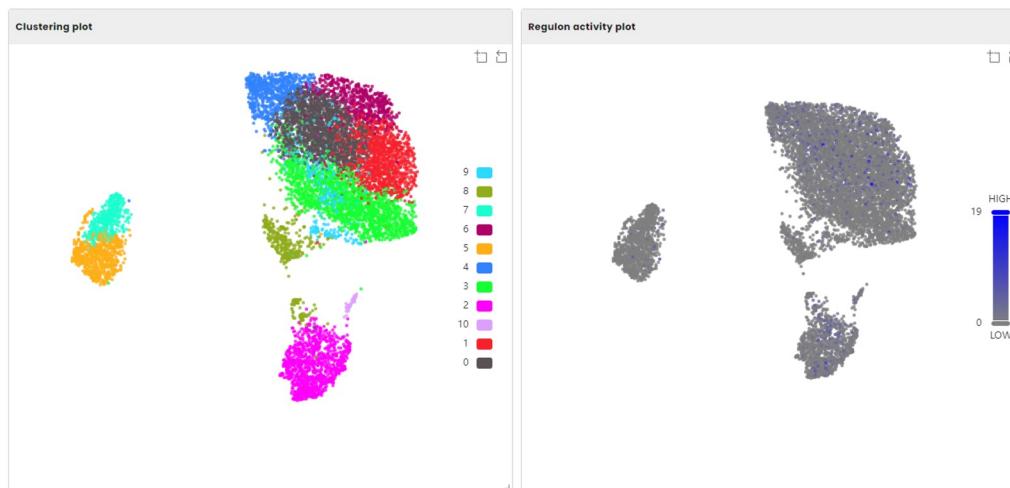
Rows per page: 10 < >

For each cell cluster, we provide a full regulon list named by TFs. For more details of how centrality, RAS, and logFC is calculated, please check DeepMAPS manuscript.

3.3 Network construction

TF	Centrality	# genes	RAS	logFC ↓	adj.p-value	Details
SRF	0.1168	13	0.1331	0.2796	0.1036	HIDE
NR3C1	0.1303	18	0.1072	0.1832	1	SHOW

We can also check all regulated genes in a TF-regulon and regulon activity UMAP.



Regulon genes		
Number of genes: 13		
BATF	UNIPROT	GENECARDS
TPM4	UNIPROT	GENECARDS
RNF149	UNIPROT	GENECARDS
TOX	UNIPROT	GENECARDS
STIM1	UNIPROT	GENECARDS
PSTPIP1	UNIPROT	GENECARDS
TRAF3	UNIPROT	GENECARDS
LYST	UNIPROT	GENECARDS
EVL	UNIPROT	GENECARDS
ARID5A	UNIPROT	GENECARDS
CFL1	UNIPROT	GENECARDS
IGF2R	UNIPROT	GENECARDS

CITE-seq and multiple scRNA-seq integrative analysis examples are similar to the scRNA-seq and scATAC-seq, with minor differences. We will add more functions in the future updates.

(Network construction currently is only provided for scRNA-seq and scATAC-seq analysis)

4. User workspace

Once you register and login your account, you will see a workspace that record all history jobs.

Profile



Email: flykun0620@gmail.com
Name: Cankun Wang

Projects

Job ID	Title	description	Created at	Type	Action
1642388187073	TEST PROJECT 1	TEST	2022-01-17	multiple-rna	OPEN
1642398270344	TEST PROJECT 2		2022-01-17	multiome	OPEN
lymphoma_14k	10X Human lymphoma 14k cells		2022-01-17	multiome	OPEN



THANK YOU

Acknowledgement

Please cite:

Ma, A., Wang, X., Li, J. et al. Single-cell biological network inference using a heterogeneous graph transformer. *Nat Commun* 14, 964 (2023). <https://doi.org/10.1038/s41467-023-36559-0>

Funding:

R01-GM131399, R35-GM126985, and U54AG075931 from the National Institute of General Medical Sciences of the National Institutes of Health.
NSF1945971 from the National Science Foundation.