Single cell tutorial

Graph Edges (must be uploaded): A file containing the interactions between nodes.

Graph Nodes (must be uploaded): A file containing node attributes.

Node Group: A file containing node groups for single or multiple network visualizations.

Data 1: A file containing continuous values for the outermost ring.

Data 2: A file containing continuous values for the second ring.

Data 3: A file containing integer values for the third ring.

Data 4: A file containing integer values for the innermost ring.

Sample Group: A file containing group information for individual bars in the ring (e.g., genes in a patient similarity network or patients in a gene-gene interaction network).

1. Overview

The Single Cell interaction network is designed to model gene–gene interactions across different cell groups derived from single-cell data.
In this framework, interactions are defined not only by genes, but also by the cell groups in which those genes are expressed.

The Single Cell template should be used when analyzing single-cell or cell-group–level data.

The required input files include:

- singlecell_edges.csv

- singlecell_nodes.csv

- singlecell_megList.csv

- singlecell_expression_matrix.csv

- singlecell_methylation_matrix.csv

- singlecell_cnv.csv

- singlecell_snv.csv

2. Input File Descriptions

A. singlecell_edges.csv — Cell Group Interaction Edges

This file defines gene–gene interactions occurring between specific cell groups.

Each row represents one directed interaction edge, defined by a gene pair and a pair of cell groups.

Columns:

- **from_gene**
  The source gene involved in the interaction.

- **to_gene**
  The target gene involved in the interaction.

- **from**
  The source cell group in which the interaction originates.

- **to**
  The target cell group receiving the interaction.

- **interact**
  A label describing the gene–gene interaction (e.g., ligand–receptor pair).
  This column is optional and used for visualization purposes.

- **weight**
  The interaction strength between the two cell groups.
  Higher values indicate stronger interactions.

Notes:

- The columns from, to, and weight is mandatory.

- The columns from_gene, to_gene, and interact are optional.

- If the interact column is provided, edges can be colored by interaction type using the *"color by interact_id"* option in directed graphs.

from_gene	to_gene	from	to	interact	weight
FGF7	FGFR1	APOE+ FIB	APOE+ FIB	FGF7_FGFR1	0.006276
FGF7	FGFR1	FBN1+ FIB	APOE+ FIB	FGF7_FGFR1	0.004855
FGF7	FGFR1	COL11A1+ FIB	APOE+ FIB	FGF7_FGFR1	0.003576
FGF7	FGFR1	APOE+ FIB	FBN1+ FIB	FGF7_FGFR1	0.009363
FGF7	FGFR1	FBN1+ FIB	FBN1+ FIB	FGF7_FGFR1	0.007247
FGF7	FGFR1	COL11A1+ FIB	FBN1+ FIB	FGF7_FGFR1	0.005341
FGF7	FGFR1	APOE+ FIB	COL11A1+ FIB	FGF7_FGFR1	0.007386
FGF7	FGFR1	FBN1+ FIB	COL11A1+ FIB	FGF7_FGFR1	0.005715

B. singlecell_nodes.csv — Gene–Cell Group Nodes

This file defines the nodes of the network, where each node corresponds to a gene within a specific cell group.

Each row represents one (gene, cell group) combination.

Columns:

- **name**
  Gene symbol.

- **cellgroup**
  The cell group in which the gene is expressed.

The same gene may appear multiple times if it is present in multiple cell groups.

name	cellgroup
FGF7	APOE+ FIB
FGF7	FBN1+ FIB
FGF7	COL11A1+ FIB
VEGFA	LC
CCL19	Inflam. FIB
CXCL12	APOE+ FIB
CXCL12	FBN1+ FIB
CXCL12	Inflam. FIB

C. singlecell_megList.csv — Gene–Cell Group Community Assignment

This file assigns each gene–cell group pair to a functional community.

Each row represents one gene in one cell group.

Columns:

- **gene**
  Gene symbol.

- **cellgroup**
  Cell group name.

- **community**
  Community identifier (integer).

If no predefined community structure is available, users may assign arbitrary integer values as placeholders. But if all the gene names come from one network without groups separation, please just assign one arbitrary integer.

gene	cellgroup	community
FGF7	APOE+ FIB	1
FGF7	FBN1+ FIB	1
FGF7	COL11A1+ FIB	1
VEGFA	LC	1
CCL19	Inflam. FIB	1
CXCL12	APOE+ FIB	1
CXCL12	FBN1+ FIB	1
CXCL12	Inflam. FIB	1
MIF	APOE+ FIB	1
MIF	FBN1+ FIB	1

D. singlecell_expression_matrix.csv — Gene Expression Matrix

This file provides gene expression levels aggregated at the cell-group level.

Format requirements:

- A column named cellgroup is mandatory.

- Each row represents one cell group.

- Each column (except cellgroup) represents a gene.

- Values represent normalized gene expression levels.

The presence of the cellgroup column allows the system to automatically recognize the data as single-cell–based input.

cellgroup	ANGPTL1	ANGPTL2	ANGPTL4	ANXA1	APCDD1
APOE+ FIB	0	0	0	2.078231	0
FBN1+ FIB	0.472447	0.399898	0	2.441575	0
COL11A1+ FIB	0	0	0	0.62687	0.683742
Inflam. FIB	0	0	0	1.966858	1.618042
cDC1	0	0	0	2.481764	0
cDC2	0	0	0	2.730448	0
LC	0	0	0	2.232209	0
Inflam. DC	0	0	0	0.391897	0
TC	0	0	0	2.466237	0
Inflam. TC	0	0	0	1.898375	0
CD40LG+ TC	0	0	0	2.574463	0
NKT	0	0	0	2.444885	0

E. singlecell_methylation_matrix.csv — DNA Methylation Matrix

This file contains gene-level DNA methylation data for each cell group.

The format is identical to the expression matrix:

- Rows: Cell groups

- Columns: Gene symbols

- Values: Normalized methylation levels

cellgroup	ACKR1	ACKR2	ACKR3	ACKR4	ACVR1	ACVR1B
APOE+ FIB	1	0	0	1	1	1
FBN1+ FIB	1	1	1	0	0	0
COL11A1+ FIB	1	0	1	0	1	1
Inflam. FIB	0	1	0	0	1	1
cDC1	1	1	1	1	1	1
cDC2	0	1	1	1	1	0
LC	0	1	1	1	0	0
Inflam. DC	1	1	1	1	1	1
TC	1	1	0	0	1	1

F. singlecell_cnv.csv — Copy Number Variation (CNV)

This file describes **copy number variation states of genes across cell groups**.

- **Rows:** Cell groups
- **Columns:** Gene symbols

Values:

- 0 : Copy-number neutral
- 1 : Copy-number gain
- -1: Copy-number loss

Each row represents CNV profiles for one cell group.

cellgroup	ACKR1	ACKR2	ACKR3	ACKR4	ACVR1	ACVR1B
APOE+ FIB	1	0	0	0	0	0
FBN1+ FIB	1	1	0	1	0	1
COL11A1+ FIB	1	1	1	0	1	0
Inflam. FIB	1	0	0	0	0	0
cDC1	0	0	1	1	0	1
cDC2	0	0	0	0	1	0
LC	0	0	1	0	1	0

G. singlecell_snv.csv — Single Nucleotide Variations (SNV)

This file records **mutation information for genes in each cell group**.

The format is the same as the CNV file:

- **Rows:** Cell groups
- **Columns:** Gene symbols

Values:

- 0 : No mutation
- 1 : One mutation
- 2 : Two mutations

In downstream analysis, any value greater than 0 is treated as **mutation present**, and the gene is labeled as a mutation gene.