33rd CONFERENCE ON
Intelligent Systems for Molecular Biology

AND THE 24th
European Conference on Computational Biology

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DATES: July 20 – 24

Computational approaches for deciphering cell-cell communication from single-cell transcriptomics and spatial transcriptomics data

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July 15th 2025

UNIVERSITÀ DEGLI STUDI DI PADOVA

DIPARTIMENTO DI INGEGNERIA DELL'INFORMAZIONE

Institute for Computational Genomics

RWTH AACHEN UNIVERSITY

Who we are

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PostDoc Researcher

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Assistant Professor

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Behind the scene

Matteo Baldan
PhD Student

Gaia Tussardi
PhD Student

Thiago Maié
PostDoc Researcher

Kai Peng
PhD Student

Outline

TIME	CONTENT
09:00-09:30	**Introduction to computational inference of intercellular and intracellular cell-cell communication** Overview of cell-cell communication inference, assumptions and challenges, a priori biological knowledge, current approaches for intercellular and intracellular signaling *Barbara Di Camillo, Giacomo Baruzzo*
09:30-10:30	**Hands-on analysis of Myocardial Infarction scRNA-seq** Presentation of case study: human myocardial infarction, tutorial on cell-cell communication analysis from single cell transcriptomics data *Giulia Cesaro (Helpers: Baldan Matteo and Tussardi Gaia)*
10:30-10:45	**Coffee Break**

Outline

10:45-11:15	**Introduction to comparative analysis of cell-cell communication and spatial analysis** Overview of cell-cell communication comparative analysis and computational approaches, spatial transcriptomics technologies and platforms: pro and cons *Ivan Costa*
11:15-11:45	**Hands on analysis of Myocardial Infarction ST and scRNA-seq (part 1)** Tutorial on comparative analysis from single-cell transcriptomics and spatial transcriptomics data using myocardial infarction case study *James Nagai, Mayra Ruiz (Helpers: Thiago Maié and Kai Peng)*
11:45-12:00	**Coffee Break**
12:00-12:45	**Hands on analysis of Myocardial Infarction ST and scRNA-seq (part 2)** Tutorial on comparative analysis from single-cell transcriptomics and spatial transcriptomics data using myocardial infarction case study *James Nagai, Mayra Ruiz (Helpers: Thiago Maié and Kai Peng)*
12:45-13:00	**Q&A Conclusion**

Learning objectives

- Understanding and identifying the **key theoretical concepts** of cell-cell communication analysis
- Lay the **foundations** of **main computational approache**s for cell-cell communication inference
- Develop **critical thinking** skills to choose and apply the most **appropriate tools** tailored to the specific research questions and analysis contents
- Gain **hands-on experience** in applying these computational methods to **real-world data**
- Learn how to **interpret** and **evaluate** the **results** in the context of biological systems

Introduction to computational inference of intercellular and intracellular cell-cell communication

Barbara Di Camillo & Giacomo Baruzzo
University of Padova, Italy

July 15th 2025

Multi-cells systems

Tissues and organs are **complex multi-cells systems made of multiple subpopulation of cells**

Tissues and organs are built up by **single, autonomous cells**, **without a full global view** of the system, and **no designated controlling cell**

Cells are **spatially and temporally organized** and able to **communicate and interact** with each other to orchestrate **self-assembly and response to stimuli as a whole**.

New technologies, new questions

- How is information processed within the single cell?

- How do cells communicate among them and with the environment?

- How do cells cooperate?

- How do tissues / organs manifest self-organization and renewal ?

- What new properties may result from collective cell behavior?

Cells processing information and exchanging information might be a central aspect to answer these questions
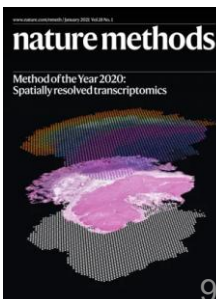
"scRNA-seq on cell development"
Breakthrough of the Year 2018
Science

"Single-cell multimodal omics"
Methods of the Year 2019
Nature Methods

"Single-cell spatial transcriptomics"
Methods of the Year 2020
Nature Methods

A naïve but hopefully inspiring example:

*Analysis of a minimal
gene regulatory network
of cell differentiation*

A two-stage differentiation process

Neuron   Glia
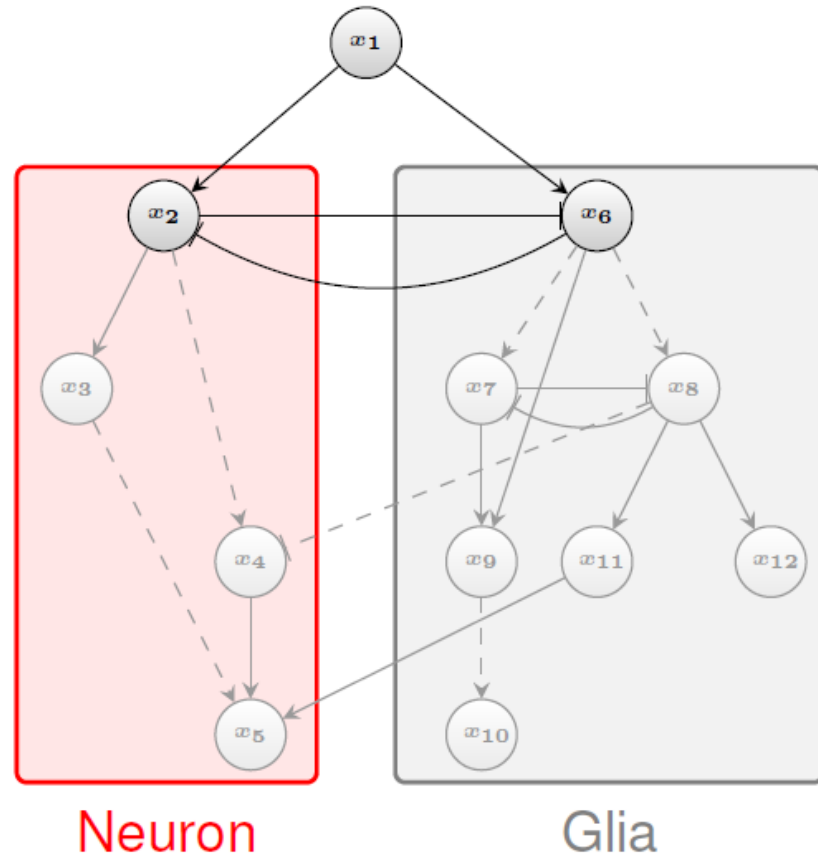
First step switch

$$Pax\ 6:\ \dot{x}_1 = \gamma x_1(t) + \xi_1(t)$$

$$Mash\ 1:\ \dot{x}_2 = a\frac{x_1^n}{1 + x_1^n + x_6^n} - kx_2 + \xi_2(t)$$

$$Hes\ 5:\ \dot{x}_6 = a\frac{x_1^n}{1 + x_1^n + x_2^n} - kx_6 + \xi_6(t)$$

From Understanding the Development Landscape of the Canonical Fate-Switch Pair to Constructing a Dynamic Landscape for Two-Step Neural Differentiation
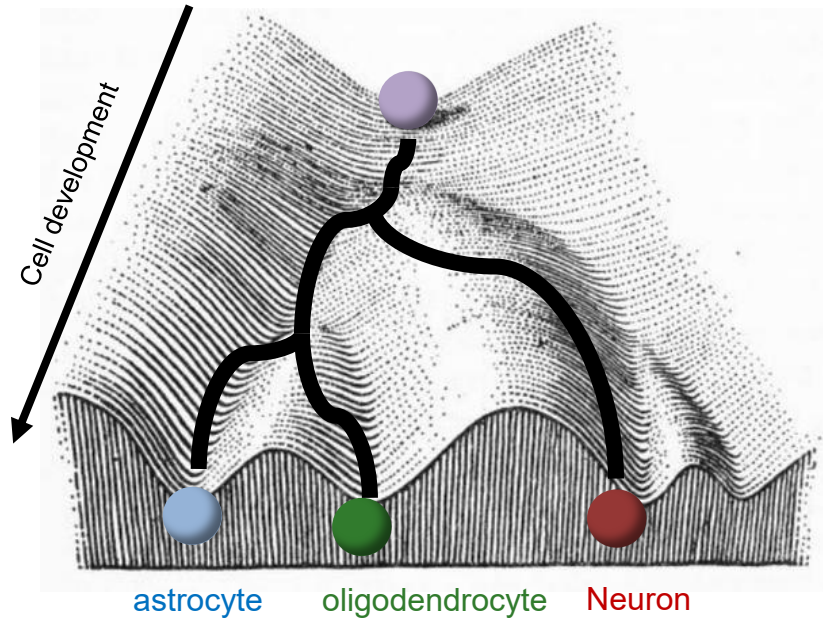
Xiaojie Qiu[9], Shanshan Ding[9], Tieliu Shi*

Center for Bioinformatics and Computational Biology, and The Institute of Biomedical Sciences, School of Life Sciences, East China Normal University, Shanghai, China
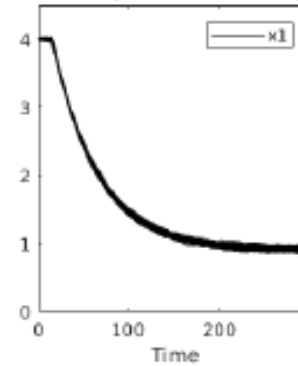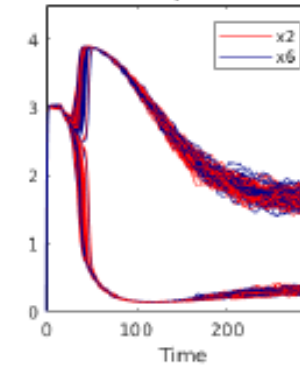
A two-stage differentiation process

Second step switch

$$Hes\ 5:\ \dot{x}_6 = a\frac{x_1^n}{1 + x_1^n + x_2^n} - kx_6 + \xi_6(t)$$

$$Scl:\ \dot{x}_7 = a_e\frac{x_6^n}{1 + x_6^n + x_8^n} - kx_7 + \xi_7(t)$$

$$Olig\ 2:\ \dot{x}_8 = a_e\frac{x_6^n}{1 + x_6^n + x_7^n} - kx_8 + \xi_8(t)$$

Oligodendrocyte

Astrocyte

Xiaojie Qiu, Shanshan Ding, Tieliu Shi*

Center for Bioinformatics and Computational Biology, and The Institute of Biomedical Sciences, School of Life Sciences, East China Normal University, Shanghai, China

Waddington's landscape

Cell development

astrocyte   oligodendrocyte   Neuron

Pax 6 (100 simulations)

1st step switch

2nd step switch

Neuron

Astrocyte

Oligodendrocyte

Multiple simulations, with fixed parameters and initial conditions, result in precursor cells differentiating to nervous cells of different types.
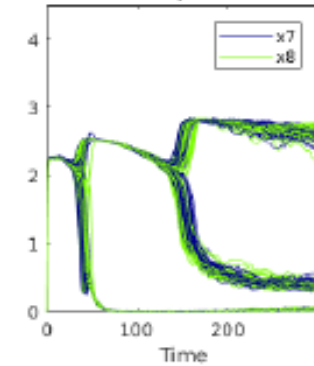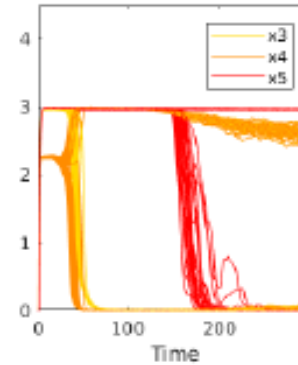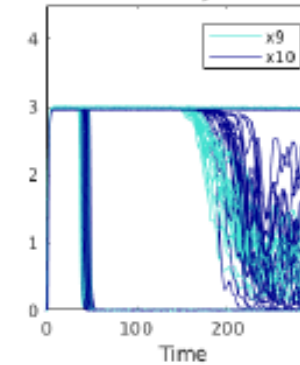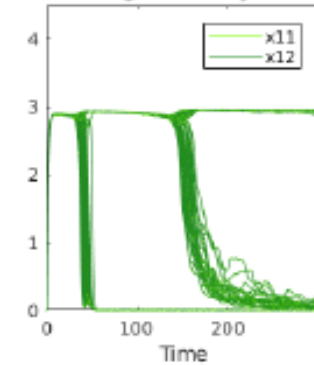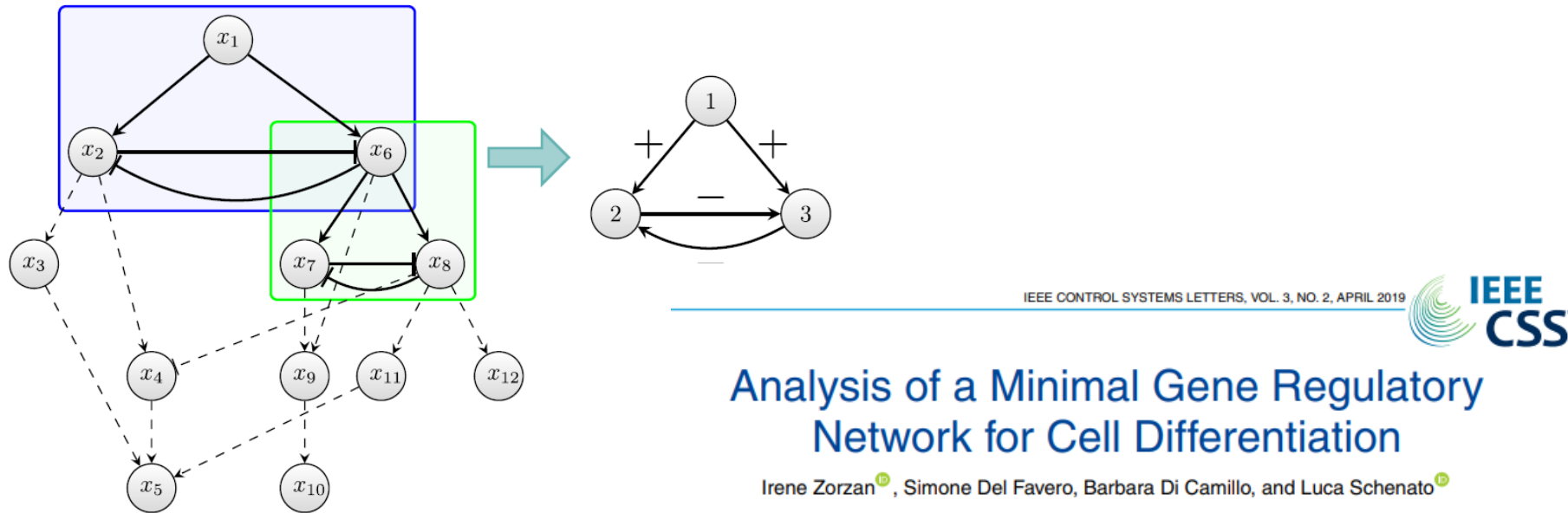
13

A minimal cell regulatory module for cell differentiation

Analysis of a Minimal Gene Regulatory Network for Cell Differentiation

Irene Zorzan[iD], Simone Del Favero, Barbara Di Camillo, and Luca Schenato[iD]

A key role is played by the expression level of Gene 1
- If it is sufficiently low or sufficiently high, the cell belongs to an undifferentiated stage where Gene 2 and Gene 3 are equally expressed
- If it is within a specific range of values (that depend on the system parameters), then Gene2 is over-expressed wrt to Gene3 or vice-versa (differentiated stage)

Simulation of the 1ˢᵗ step on a 2D lattice

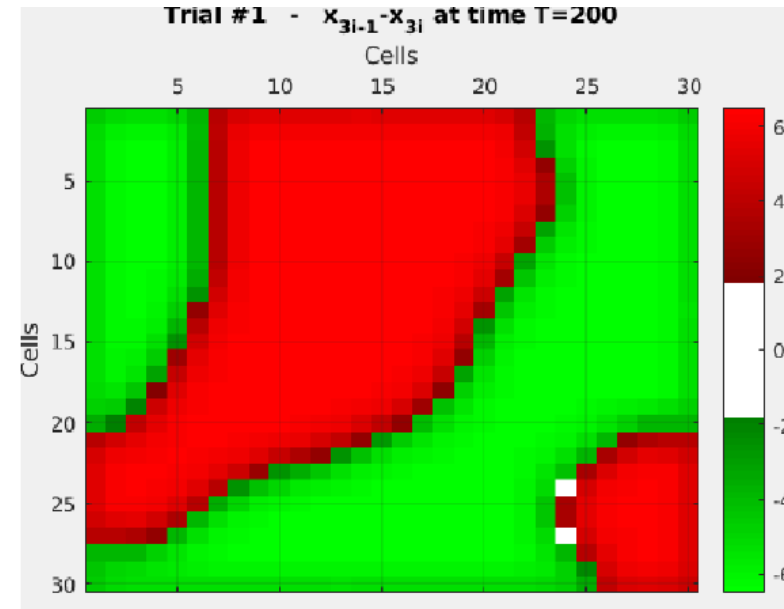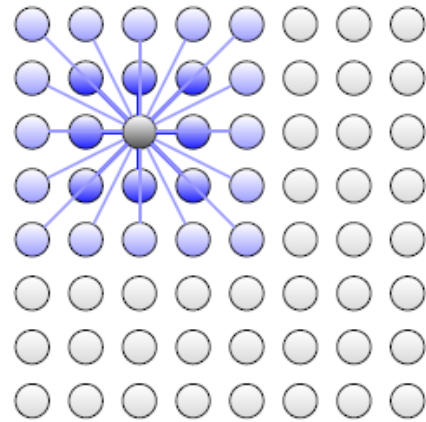Let's depict the fate of different cells in space
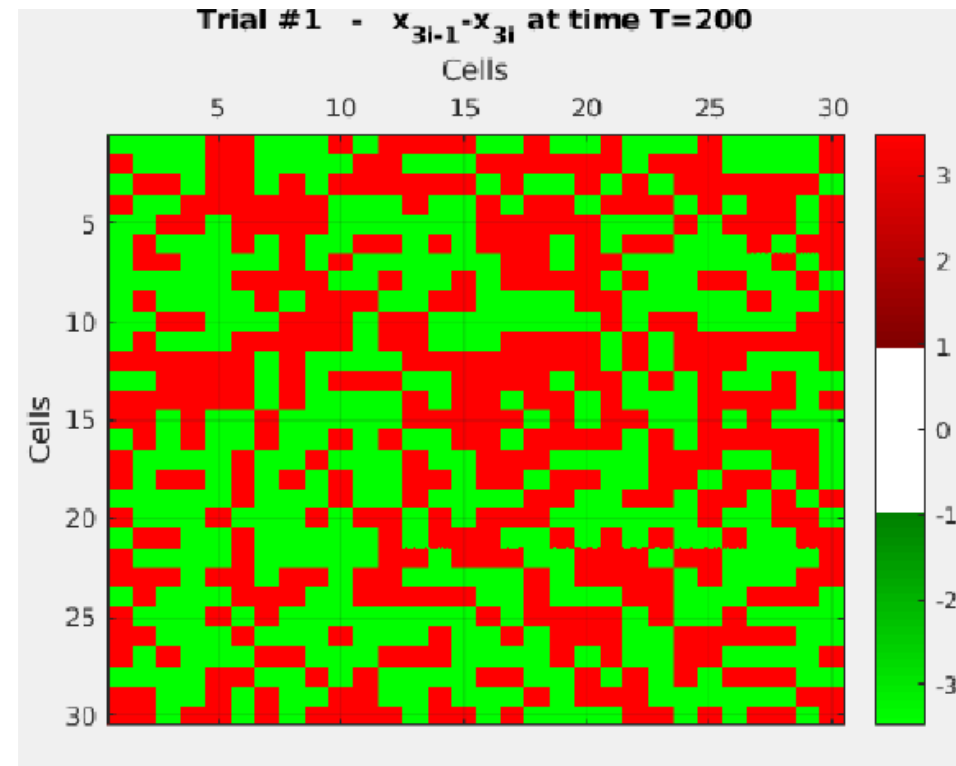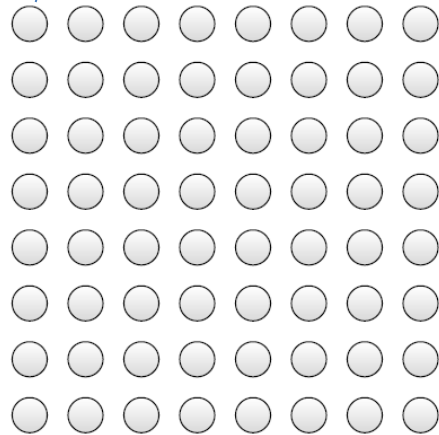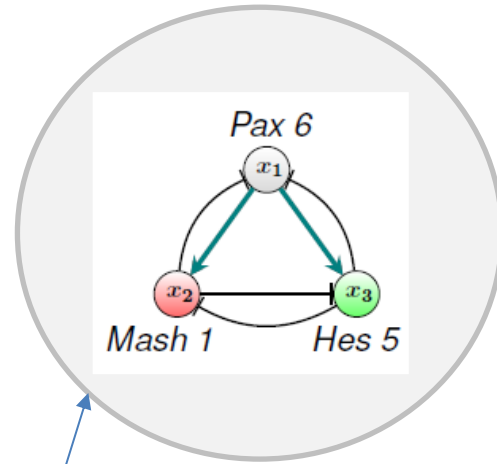
Simulating cell-cell interaction

We might think about an additional mechanism that allows driving the differentiation in a specific direction

Imagine cells sensing their neighbours:
- Positive feedback among type-specific genes of the same type
- Negative feedback among type-specific genes of different type

Simulating cell-cell and environment interaction

Cells sensing their neighbours and the environment:
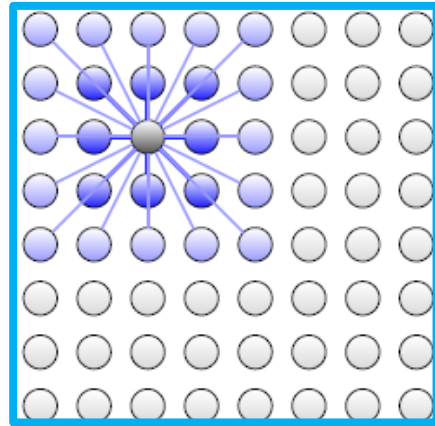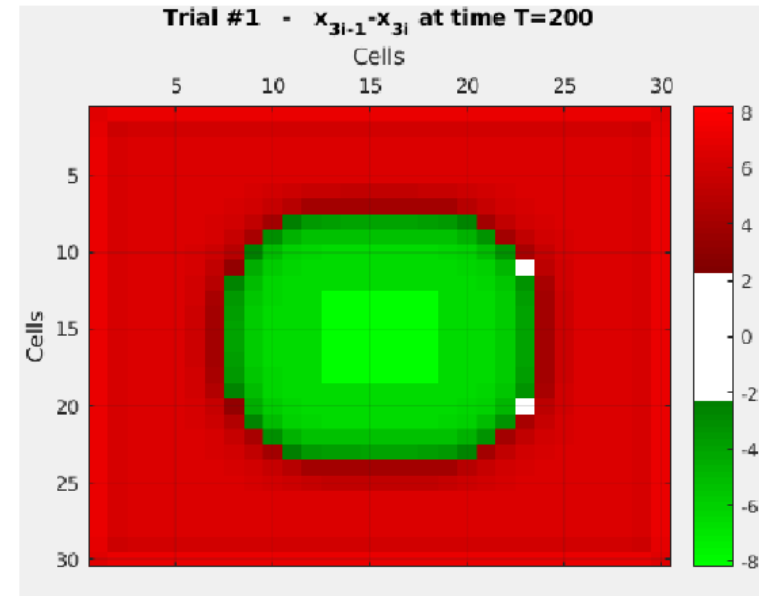- Positive feedback among type-specific genes of the same time
- Negative feedback among type-specific genes of different type
- Signal from the border of the lattice

Adding border effect…

How do we model cell communication

Single cells exchanging information

A widely used mechanism of cellular communication is based on ligand–receptor interactions:

- A sender cell secretes a signaling protein, i.e. a ligand
- The ligand binds the receptor, of another cell (receiver cell).
- As a response the receptor activates a signaling cascade inside the cell that triggers a modification and in turns, might lead to transcriptional activation/inhibition of specific genes.

Ligand (protein)

Receptor (protein)

Biological signaling

Target proteins
(some are TF)

Transcription (effect
of communication)

INTERcellular communication

Intercellular signaling

Ligand   Receptor

Sender cell   Receiver cell
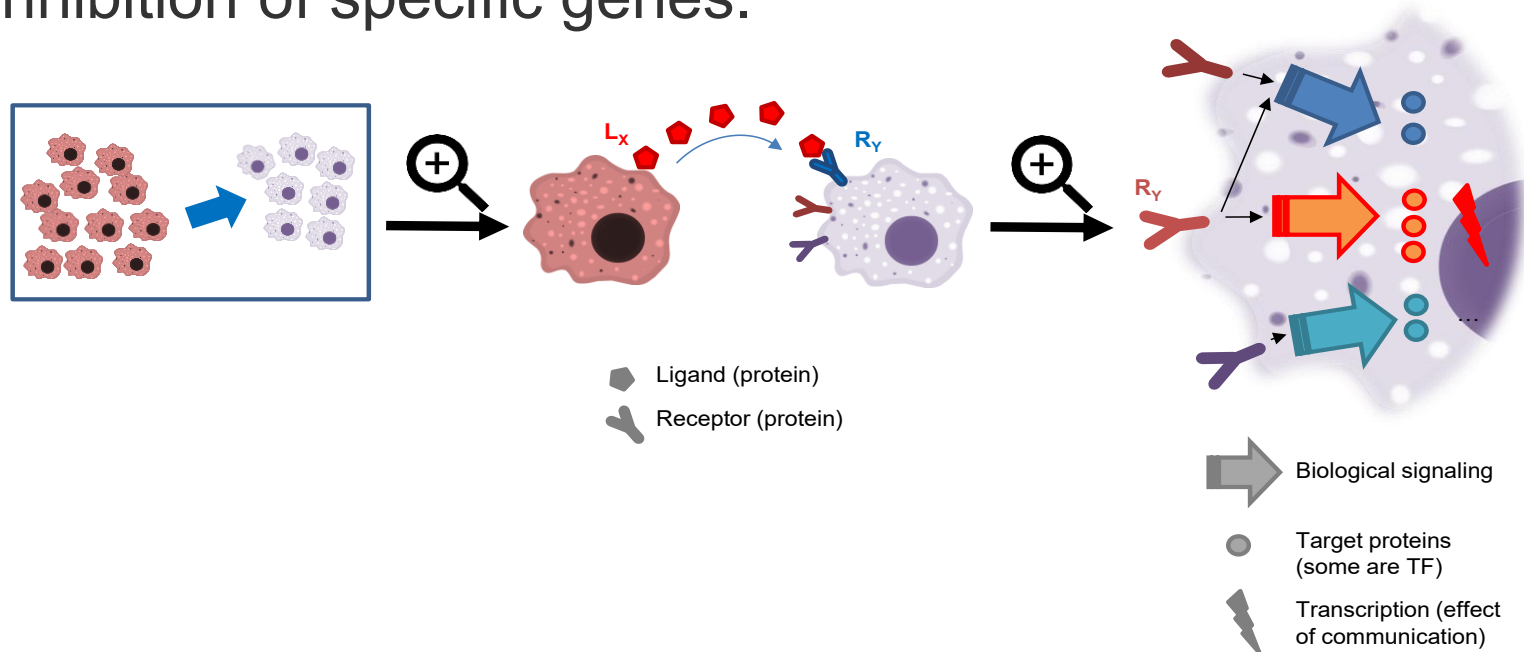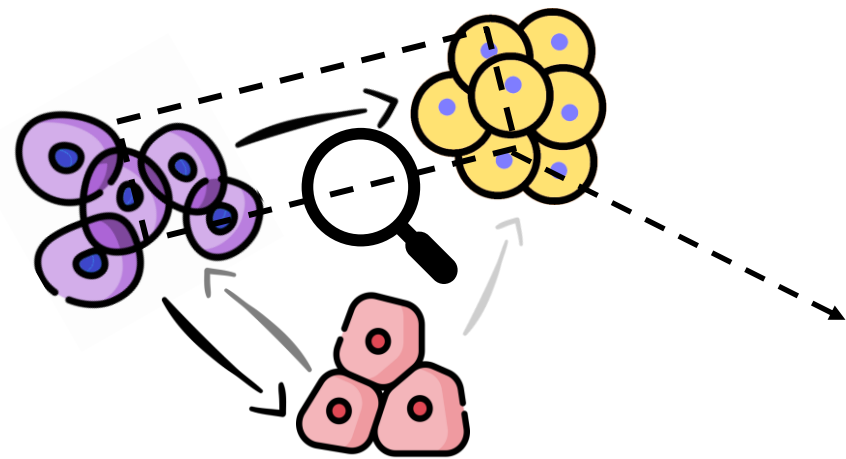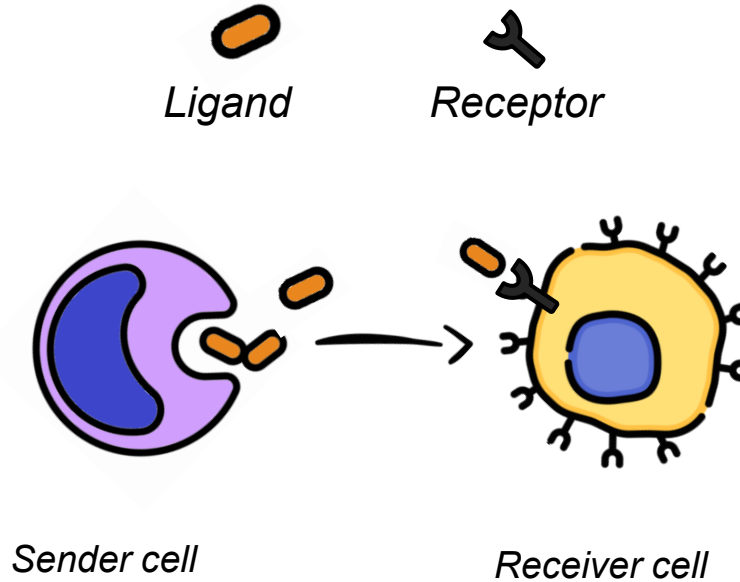
RNA expression as proxy for protein activity

- Cell communication is primarily mediated by proteins: ligands and receptors
- Direct measurement of proteins at single-cell resolution is technically challenging and resource-intensive.
- We assume mRNA expression reflects the presence and activity of signaling proteins

Single-cell RNA sequencing

Single-cell RNA-seq data

Ligand
Receptor
...
Target genes
...
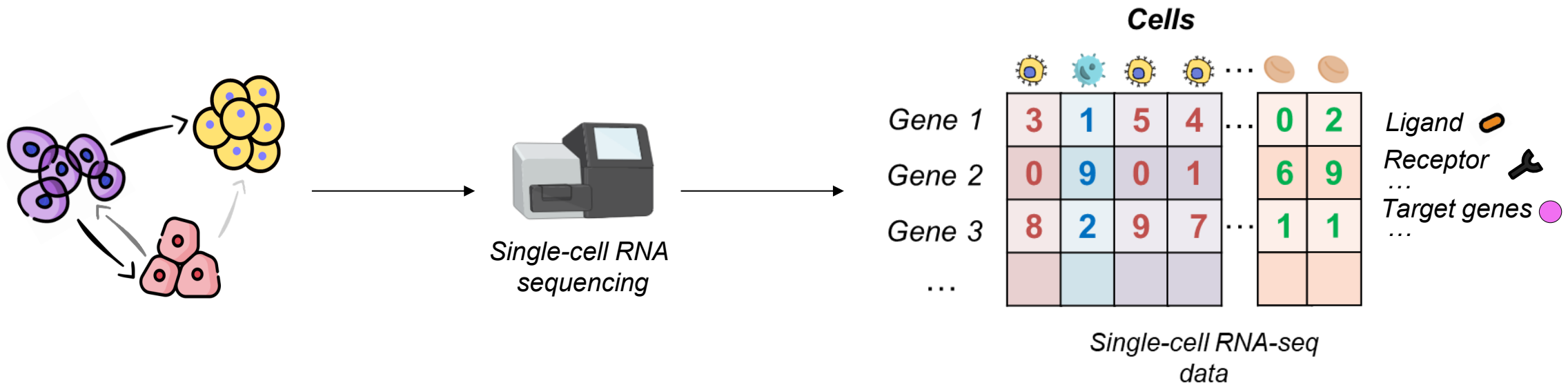
The added value of spatial transcriptomics
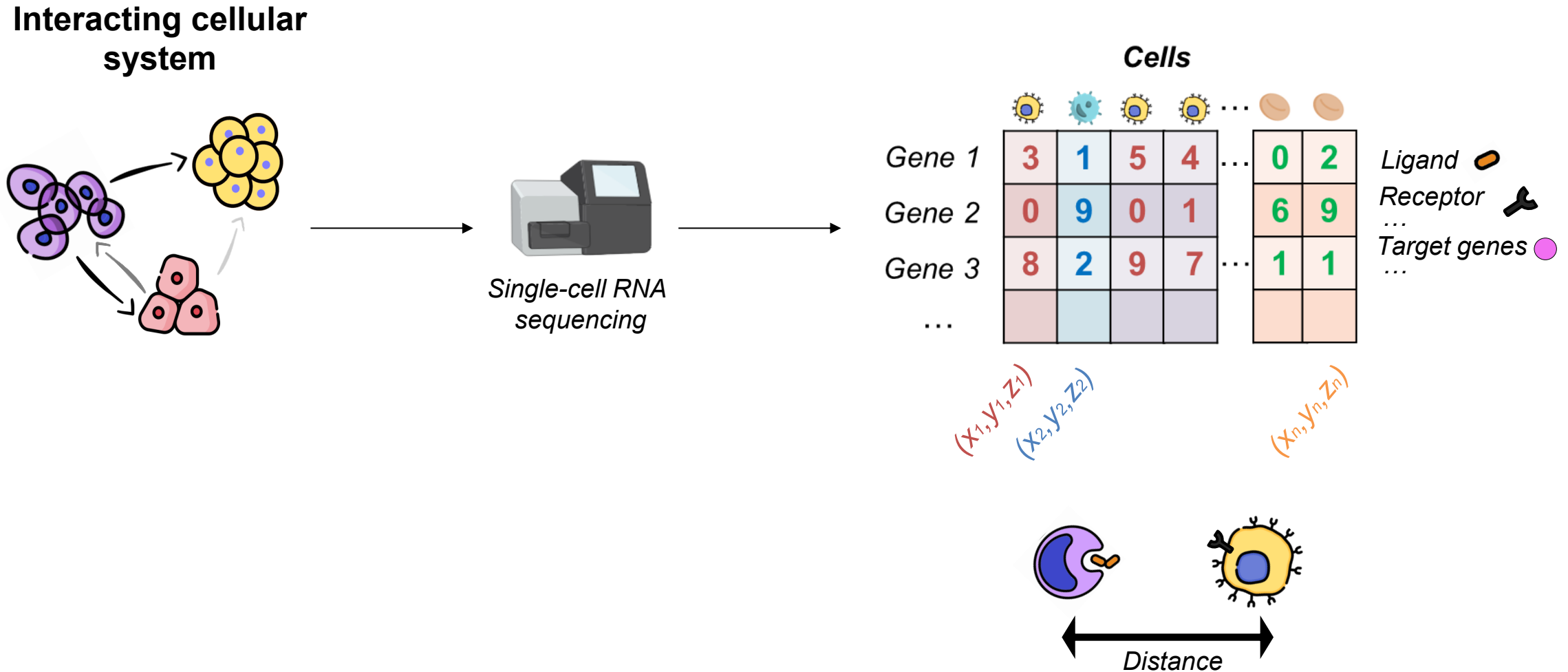
INTRAcellular communication
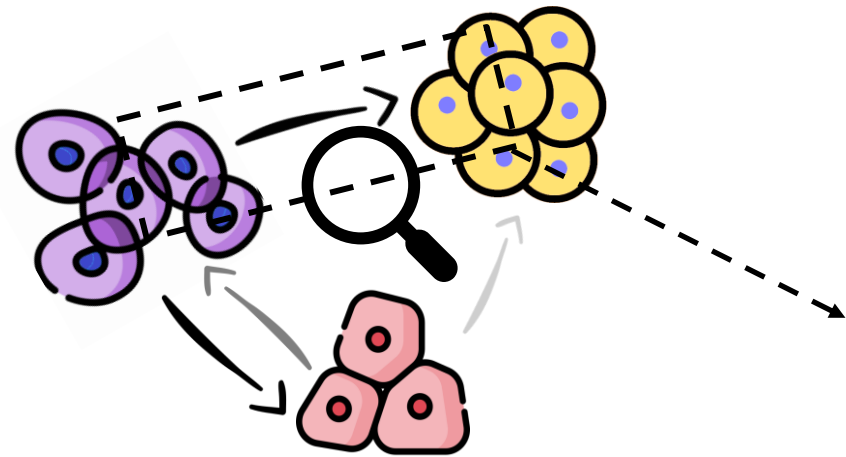
Intercellular signaling + **Intracellular signaling**

Ligand

Receptor

Transcription factor

Target genes

Cellular response

Sender cell

Receiver cell
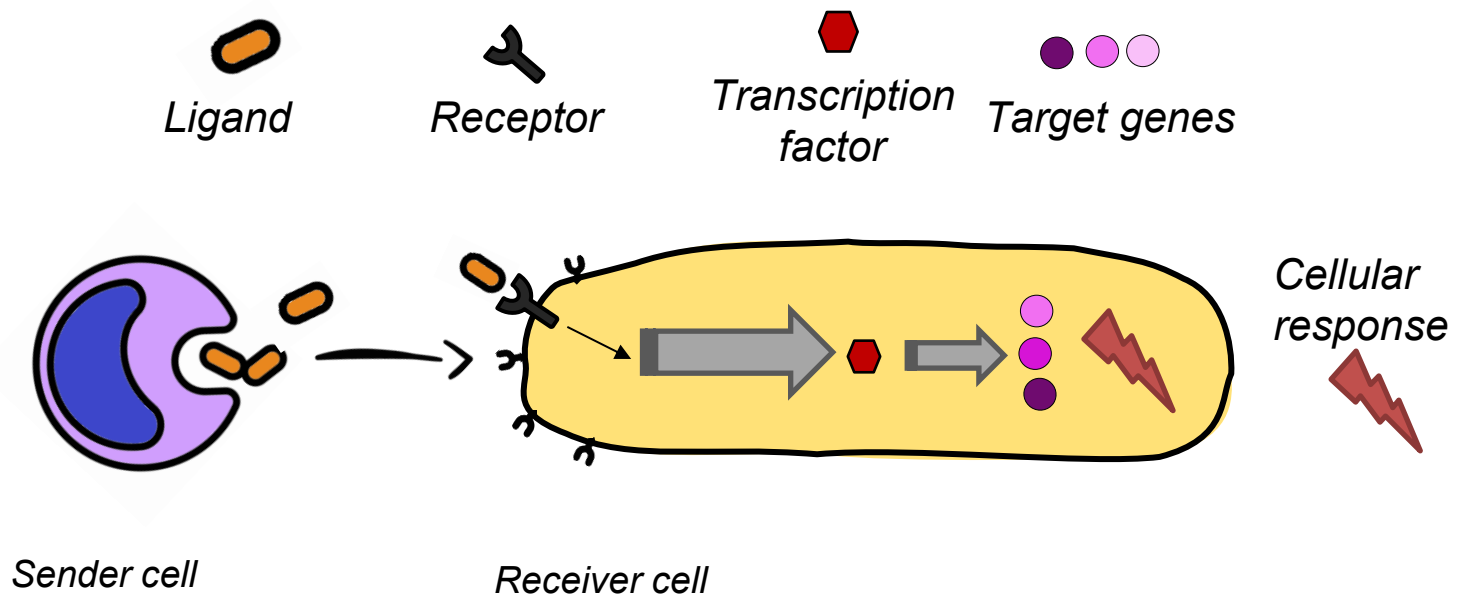
Zooming In: Intracellular Communication

- Once a ligand binds to its receptor, the signal is transmitted inside the cell through a cascade of signaling proteins.
- This intracellular signaling ultimately regulates target gene expression in the nucleus.
- By analyzing the expression of downstream target genes, we can infer the activation state of specific pathways.
- This also helps us model how extracellular signals shape cellular behavior.

Receptor *r*

Gene graph
p

Transcription factor
t

Target genes

Signaling pathways

Transcriptional regulatory network

node ☐ = Biological entity

edge ↗ = chemical reaction
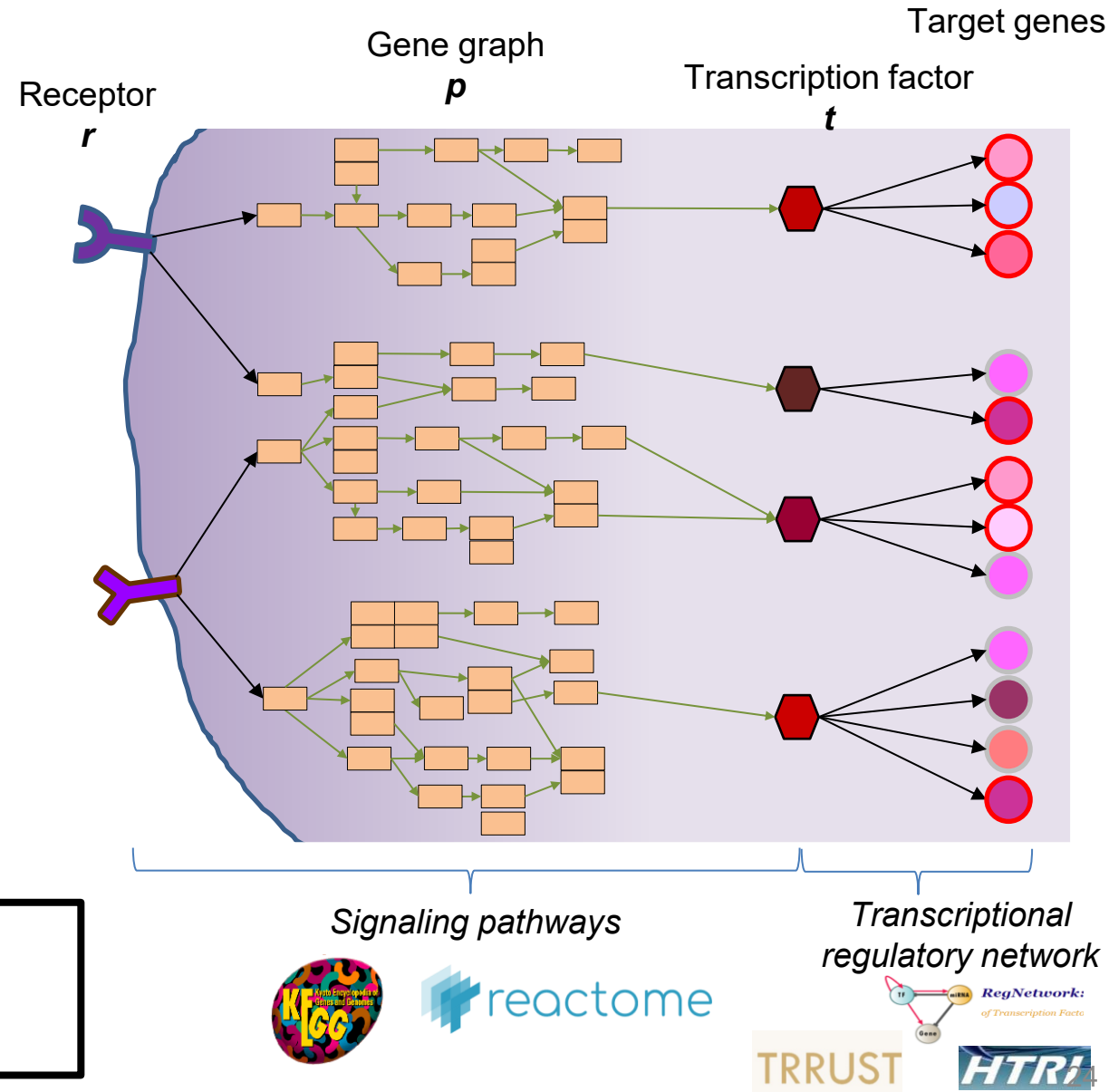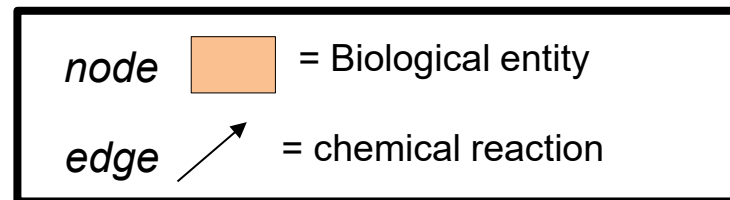
Bioinformatics analysis
of cell communication
from transcriptomics data

Bioinformatics analysis of CCC

transcriptomics data

CCC DB

scRNA-seq

spatial transcriptomics

Known INTERcellular interactions

Ligand-receptor pairs

Known cell clusters/types

CCC Tool

INTERcellular signaling inference
- What is measured?
- How is measured?
- What are the assumptions?

- INTRAcellular signaling?
- Multi-condition analysis?
- Output?

Ligand	Receptor	Sender	Receiver	Score
WNT5A	FZD5	B cell	T cell	0.95
TGFB1	TGFBR1; TGFBR2	Neurons	Microglia	0.1
…	…	…	…	…

CCC DB

Standard (mandatory) part

Optional part

Typically, a ligand

Typically, a receptor

For multi-species DB

Supporting information

Intracellular information

Validation? Secreted? Location? Other…

Target	Source
WNT5A	FZD5
TGFB1	TGFBR1;TGFBR2
TGFB2	TGFBR1;TGFBR2

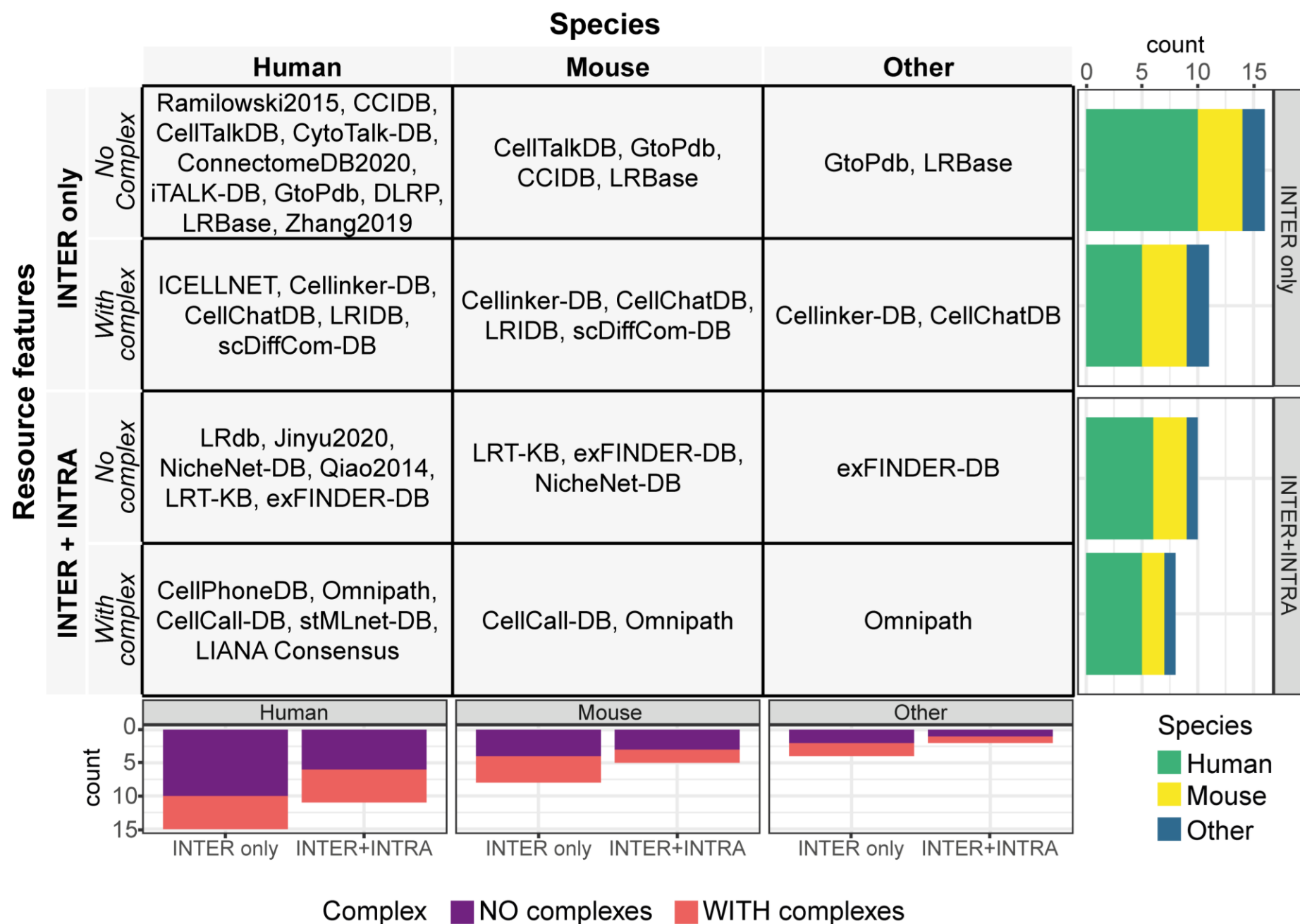| Species	Literature	Source	Pathways	Downstream genes	…
Human	…	KEGG	ncWNT	TCF, …	
Human	…	KEGG	TGFb	Smad4, …	
Human	…	KEGG	TGFb	Smad4, …	

Multi-subunit receptor

CCC DB

~ 50 CCC DBs, half of them include intercellular signaling on Human data

DBs differ in terms of:
- Species: Human, Mouse, Rat, Zebrafish, etc.
- Scope: generalist vs specific (e.g. tissue, disease)
- Sources: other DBs, literature, mining, etc.
- Num. LR pairs: from hundreds to thousands
- Information about protein complexes (multi-subunit): included or omitted
- Annotated signaling: INTER only (i.e. ligand-receptor) or INTER+INTRA
- …

Image taken from: Cesaro et al. (2025) "Advances and Challenges in Cell-Cell Communication Inference: A Comprehensive Review of Tools, Resources, and Future Directions", Briefings in Bioinformatics

CCC - Catalog

- Web resources containing CCC DBs and CCC tools

- Detailed catalog of 26 CCC DBs

- Interactive filtering and statistics

https://sysbiobig.gitlab.io/ccc-catalog/resources.html

Review/comparison of available CCC DBs

- Ma et al. (2021) "Applications and analytical tools of cell communication based on ligand-receptor interactions at single cell level", Cell & Bioscience [Link]

- Armingol et al. (2021) "Deciphering cell-cell interactions and communication from gene expression", Nature Reviews Genetics [Link]

- Peng et al. (2022) "Cell–cell communication inference and analysis in the tumour microenvironments from single-cell transcriptomics: data resources and computational strategies", Briefings in Bioinformatics [Link]

- Dimitrov et al. (2022) "Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data", Nature Communications [Link]

- Wang et al. (2022) "A systematic evaluation of the computational tools for ligand-receptor-based cell–cell interaction inference", Briefings in Functional Genomics [Link]

- Cesaro et al. (2025) "Advances and Challenges in Cell-Cell Communication Inference: A Comprehensive Review of Tools, Resources, and Future Directions", Briefings in Bioinformatics [Link]

CCC DBs used in this tutorial

Database	Species	Number of annotated LR pairs (Human only)	Protein complex (multi-subunit)	Intracellular signaling	URL	Sources
CellChatDB	Human; Mouse; Zebrafish	3233	Yes	No	Link	KEGG; CellPhoneDB; NeuronChatDB; Other literature
CellPhoneDB	Human	2912	Yes	Yes	Link	Uniprot; RCSB protein bank data; Reactome; HMPR; Other literature
ConnectomeDB	Human	2293	No	No	Link	Ramilowski2015; CellPhoneDB[v2]; STRING; Baccin2020; LRdb; ICELLNET; Other Literature
Liana Consensus	Human	4624	Yes	Yes	Link	Cellinker-DB; CellTalkDB; ConnectomeDB2020; iTALK-DB; Ramilowski2015; Kirouac2010; Baccin2020; CellPhoneDB; CellChatDB; EMBRACE; CellCall-DB; ICELLNET; GtoPdb; HPMR; OmniPath; KEGG; Reactome

CCC tools

- More than 100 CCC tools!
- Almost half of them
  - support scRNA-seq or spatial transcriptomics (ST)
  - are "general purpose" tools
- Each tools has its own characteristics, pros and cons
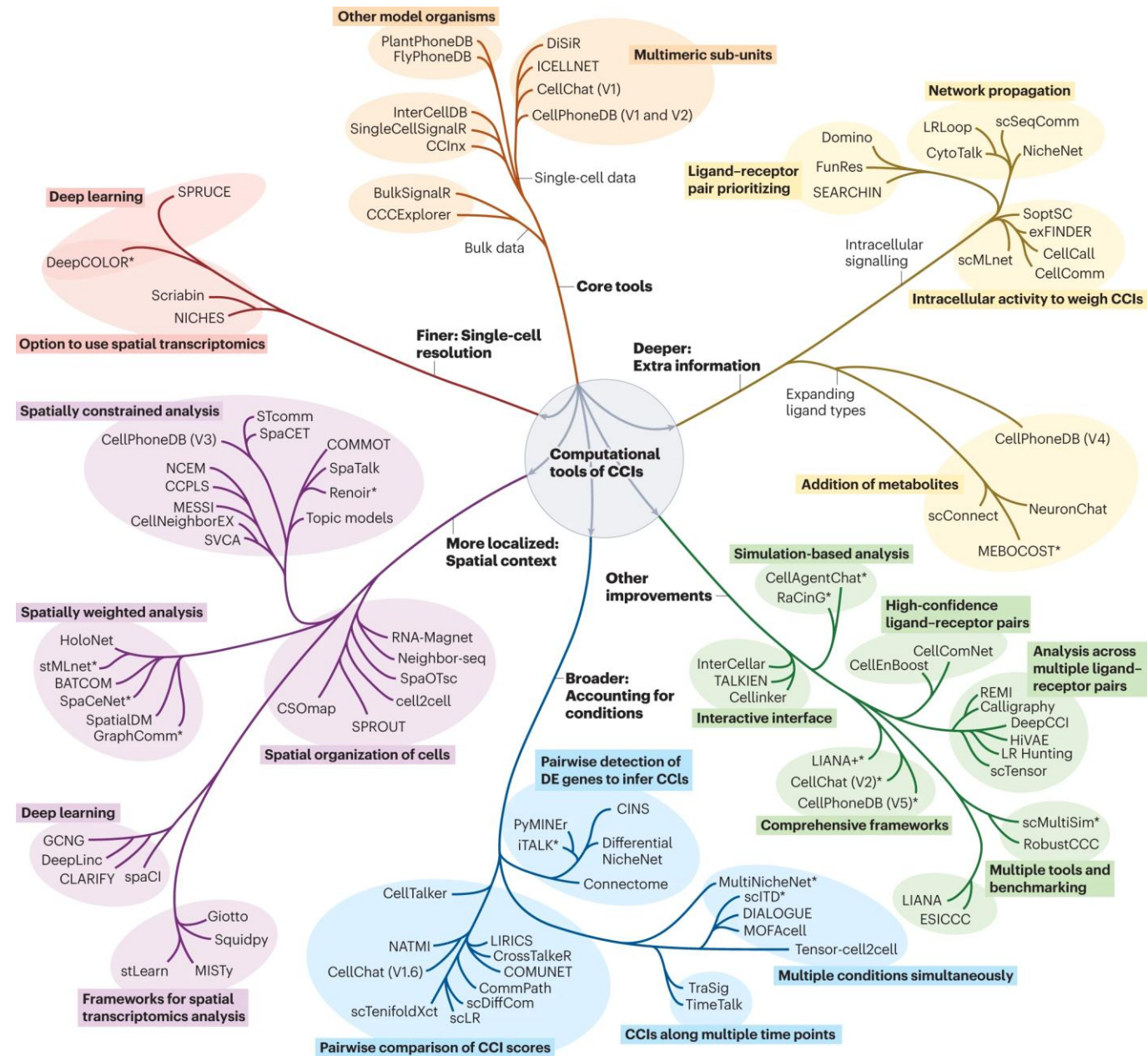
CCC tools

CCC tools mainly differ in terms of:

- <u>Input</u>
  - What type of transcriptomics data?
  - What CCC DBs?
- <u>Intercellular inference</u>
  - What they measure?
  - How they measure its?
  - What are the assumptions?
- <u>Advanced analyses/features</u>

transcriptomics data

CCC DB

CCC Tool

Ligand	Receptor	Sender	Receiver	Score
WNT5A	FZD5	B cell	T cell	0.95
TGFB1	TGFBR1; TGFBR2	Neurons	Microglia	0.1
…	…	…	…	…
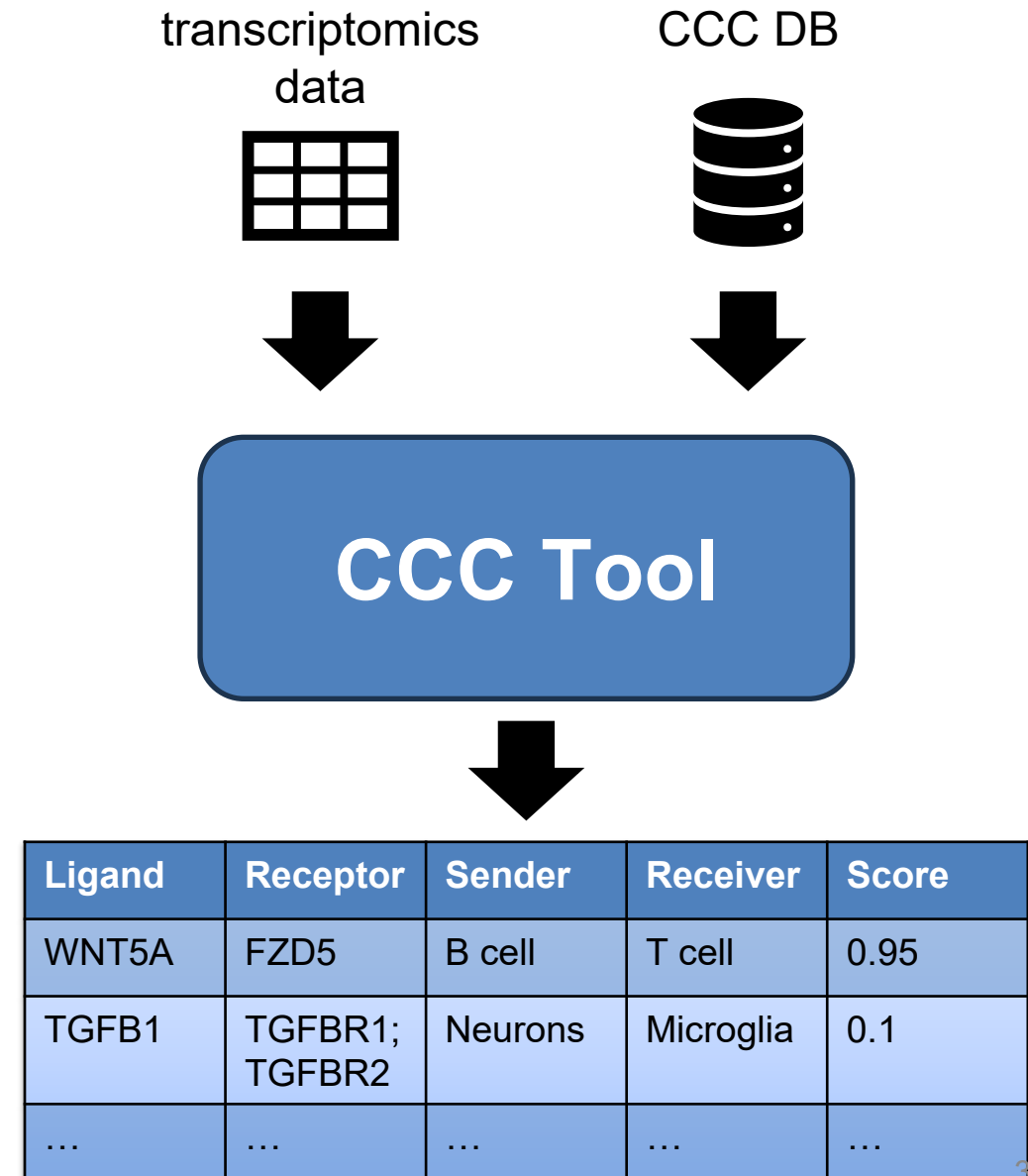
CCC tools - Input

CCC tools differ in terms of input:

- Transcriptomics data:
  - scRNA-seq
  - single cell ST (STsc)
  - spot-based ST (STspot)

- CCC DBs:
  - built-in, user-specified, none
  - INTER only, INTER+INTRA
  - protein complexes information

35
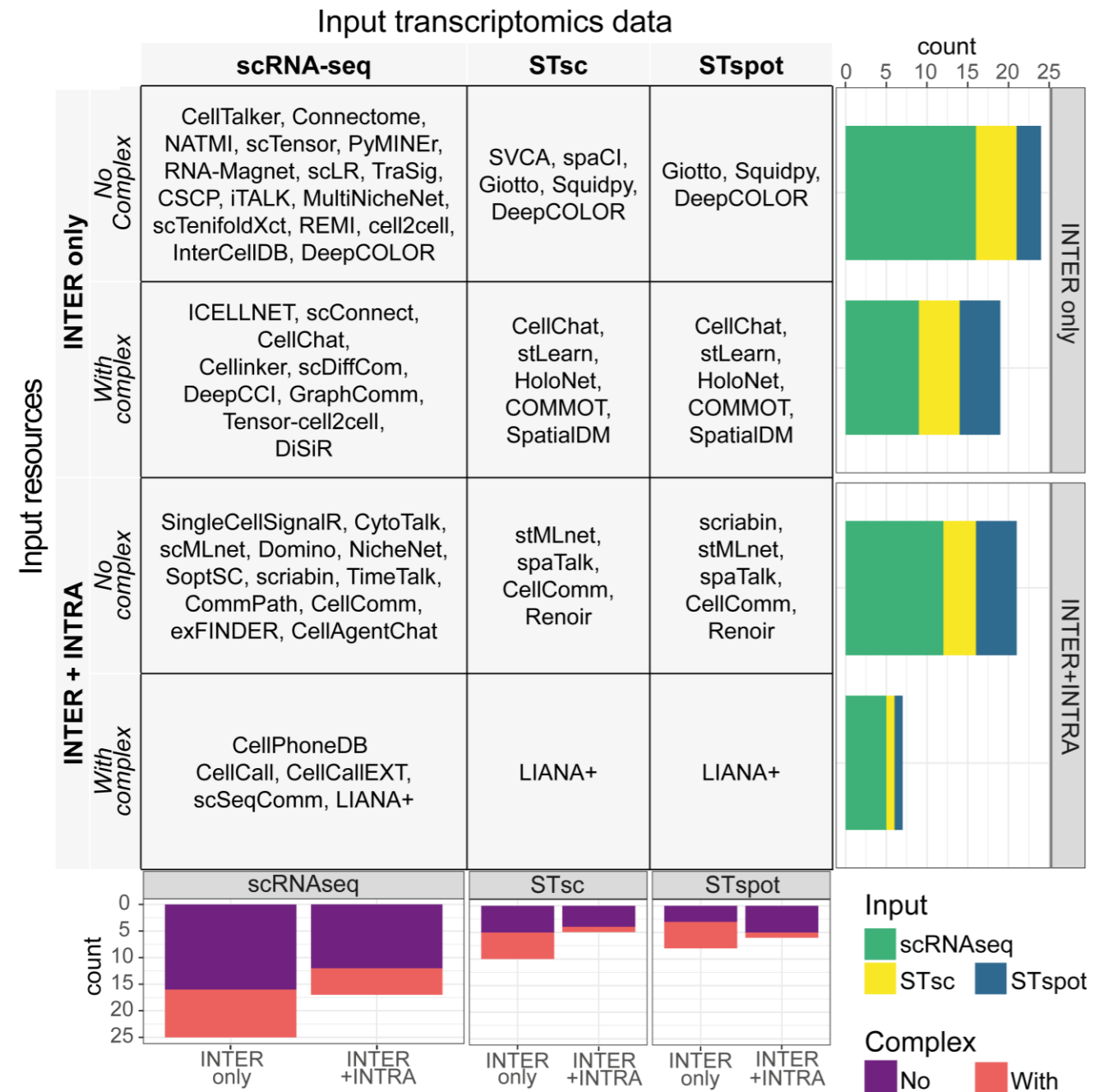
CCC tools – INTERcellular inference

CCC tools differ in how they infer intercellular signaling:

- Score value/range:
  - binary (yes/no) -> easy to understand, but no ranking
  - continuous -> allows results prioritization, but need a threshold
  - other
- Score meaning:
  - intensity -> emphasizes "strong" CCC interactions
  - specificity -> emphasizes unique or cell-type-specific CCC interactions
  - other
- Methodology: machine learning, correlation, network algorithms, etc.

CCC tools – Other features

CCC tools differ in additional features for end users:

- <u>Inference of INTRAcellular signaling</u>: yes | no
- <u>Support multi-condition analysis</u>: yes | no
- <u>Support time-series analysis</u>: yes | no
- <u>Built-in visualization</u>: circus plot, dot plot, etc.
- …

Why is important?
- Interpretability of results
- Level of details
- Handle complex design

And technical details:

- <u>Programming languages</u>: R, Python, etc.
- <u>Release format</u>: web app, R package, cmd line, etc.
- <u>Support to parallel execution</u>: yes | no
- <u>Quality of life</u>: tutorial, test dataset, container, etc.

Why is important?
- Integration with existing pipelines
- Usability
- Computational burden

CCC - Catalog

- Web resources containing CCC DBs and CCC tools

- Detailed catalog of 58 CCC tools

- Interactive filtering and statistics

CCC tools

Available bioinformatics tools for CCC analysis.

Column visibility ▾

10 ⌄ entries per page   Search: [   ]

Tool	LR DB - Source	INPUT - Type of data	INTER - Multisubunit	INTER - Score meaning	INTRA - Intracellular	OTHER - Visualization	SOFTWARE - Programming language	SOFTWARE - Code/ Software URL
cell2cell	built-in; user-specified	scRNAseq; bulk	No	Specificity, Intensity	No	Heatmap; CircosPlot; DotPlot	Python	Link
CellAgentChat	built-in; user-specified	scRNAseq	No	Specificity, Intensity	Yes	WebApp	R; Python	Link
CellCall	built-in	scRNAseq	Yes	Intensity	Yes	CircosPlot; Heatmap; SankeyPlot; SankeyPlot	R	Link
CellCallEXT	built-in	scRNAseq	Yes	Specificity, Intensity	Yes	DotPlot; SankeyPlot; CircosPlot; Heatmap	R	Link
CellChat	built-in; user-specified; built-in + user-specified	scRNAseq; STall	Yes	Specificity	No	NetworkPlot; CircosPlot; Heatmap; DotPlot; SankeyPlot; SpatialPlot; WebApp	R; C++	Link
CellComm	user-specified	scRNAseq; STall	No	Specificity, Intensity	Yes	DotPlot; NetworkPlot; BarPlot; Heatmap	R	Link
Cellinker	built-in	scRNAseq	Yes	Specificity, Intensity	No	WebApp	HTML; PHP	Link
CellPhoneDB (v4.1)	built-in; user-specified	scRNAseq	Yes	Specificity	Yes		Python	Link
CellTalker	built-in; user-specified	scRNAseq	No	Intensity	No	CircosPlot; ViolinBoxPlot	R	Link
COMMOT	user-specified	STall	Yes	Specificity, Intensity	No	NetworkPlot; Heatmap	Python	Link

https://sysbiobig.gitlab.io/ccc-catalog/tools.html

Literature about CCC tools

Review studies

Review studies focus on listing, classifying, and describing existing tools and resources. They do not typically involve extensive quantitative comparisons, agreement assessments, or tool rankings based on accuracy/robustness metrics derived from a ground truth.

- Shao et al. (2020) "New avenues for systematically inferring cell-cell communication: through single-cell transcriptomics data", Proteins & Cell [Link]
- Ma et al. (2021) "Applications and analytical tools of cell communication based on ligand-receptor interactions at single cell level", Cell & Bioscience [Link]
- Almet et al. (2021) "The landscape of cell-cell communication through single-cell transcriptomics", Current Opinion in Systems Biology [Link]
- Armingol et al. (2021) "Deciphering cell-cell interactions and communication from gene expression", Nature Reviews Genetics, 2021 [Link]
- Bridges et al. (2022) "Mapping and Validation of scRNA-Seq-Derived Cell-Cell Communication Networks in the Tumor Microenvironment", Frontiers in Immunology [Link]
- Jin et al. (2022) "Computational exploration of cellular communication in skin from emerging single-cell and spatial transcriptomic data", Biochemical Society Transaction [Link]
- Peng et al. (2022) "Cell-cell communication inference and analysis in the tumour microenvironments from single-cell transcriptomics: data resources and computational strategies", Briefings in Bioinformatics [Link]
- Wang et al. (2023) "The promising application of cell-cell interaction analysis in cancer from single-cell and spatial transcriptomics", Seminars in Cancer Biology [Link]
- Armingol et al. (2024) "The diversification of methods for studying cell-cell interactions and communication", Nature Review Genetics [Link]
- Cesaro et al. (2025) "Advances and Challenges in Cell-Cell Communication Inference: A Comprehensive Review of Tools, Resources, and Future Directions", Briefings in Bioinformatics [Link]

Literature about CCC tools

Comparison studies

Comparison studies mainly measure and quantify the agreement between CCC tools or CCC resources, often by comparing predictions and annotated interactions. These studies do not have the main goal of ranking tools/resources based on a ground truth.

- Dimitrov et al. (2022) "Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data", Nature Communications [Link]
- Wang et al. (2022) "A systematic evaluation of the computational tools for ligand-receptor-based cell-cell interaction inference", Briefings in Functional Genomics [Link]

Benchmarking studies

Benchmarking studies have the primary goal to rank CCC tools using quantitative metrics and a ground truth, assessing accuracy, robustness, or other performance aspects.

- Luo et al. (2023) "ESICCC as a systematic computational framework for evaluation, selection, and integration of cell-cell communication inference methods", Genome Research [Link]
- Liu et al. (2022) "Evaluation of cell-cell interaction methods by integrating single-cell RNA sequencing data with spatial information" Genome Biology [Link]
- Zhang et al. (2023) "RobustCCC: a robustness evaluation tool for cell-cell communication methods", Frontiers in Genetics [Link]
- Xie et al. (2023) "A Comparison of Cell-Cell Interaction Prediction Tools Based on scRNA-seq Data", Biomolecules [Link]
- Open Problems in Single cell (https://openproblems.bio)

CCC tools used in this tutorial

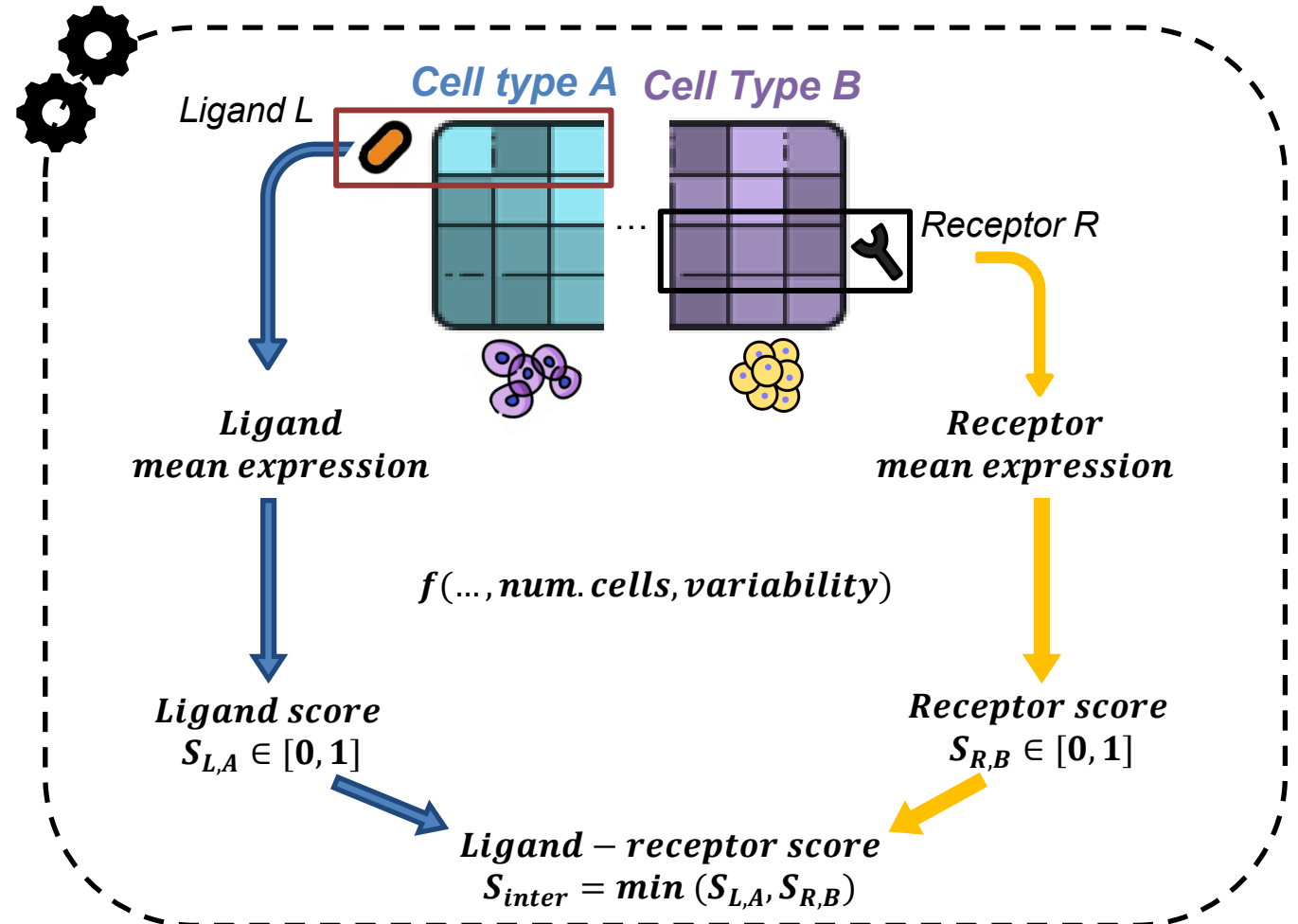| Tool	RNA-seq data	CCC DBs	INTER score meaning	INTRAcellular inference	Multi-condition analysis	Programming Language	URL
CellPhoneDB (4.1)	scRNAseq	built-in OR user-specified	Specificity	Yes	Yes	Python	[Link]()
scSeqComm	scRNAseq	built-in OR user-specified	Intensity	Yes	Yes	R	[Link]()
LIANA+	scRNAseq OR ST	built-in OR user-specified	Specificity, Intensity	Yes	Yes	Python	[Link]()
CellChat	scRNAseq OR ST	built-in OR user-specified	Specificity	No	Yes	R	[Link]()

scSeqComm - INTERcellular signaling

Quantify intercellular score

Strength/Intensity of Ligand-Receptor interaction across cell type A and B
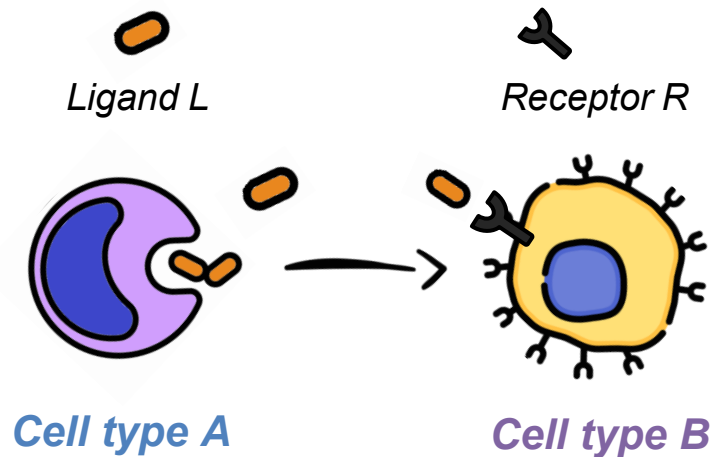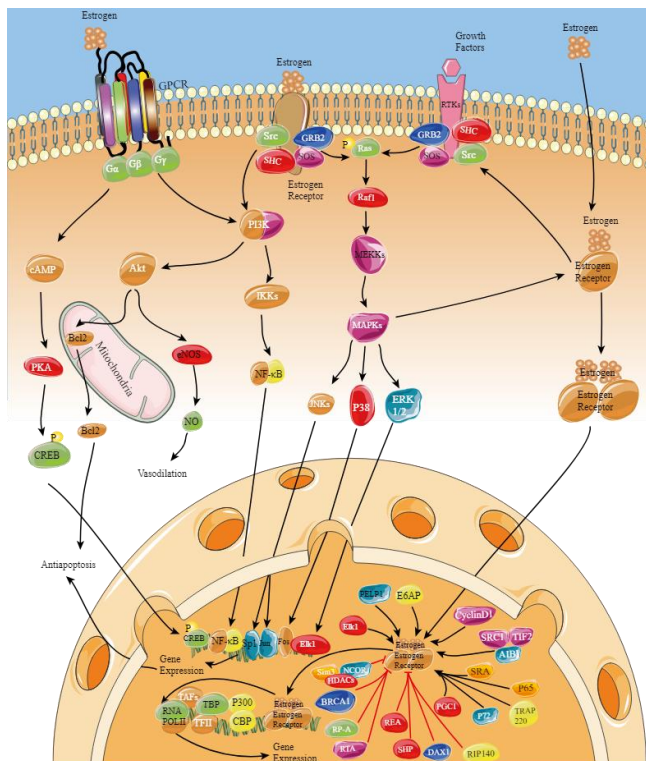

S_{inter} characteristics:
- Range [0,1]
- Minimum as fuzzy AND logical operator
- Measures intensity of intercellular signaling as
- functions of gene expression level…
- as well as the number of cells and cells variability

Ligand L

Receptor R

Cell type A

Cell type B

Cell type A   Cell Type B

Ligand L

Receptor R

Ligand mean expression

Receptor mean expression

$f(\dots, num.\,cells, variability)$

Ligand score $S_{L,A} \in [0,1]$

Receptor score $S_{R,B} \in [0,1]$

Ligand − receptor score $S_{inter} = min\,(S_{L,A}, S_{R,B})$

scSeqComm - INTRAcellular signaling

Example of intracellular signaling pathway

Receptor
r

Signaling pathway
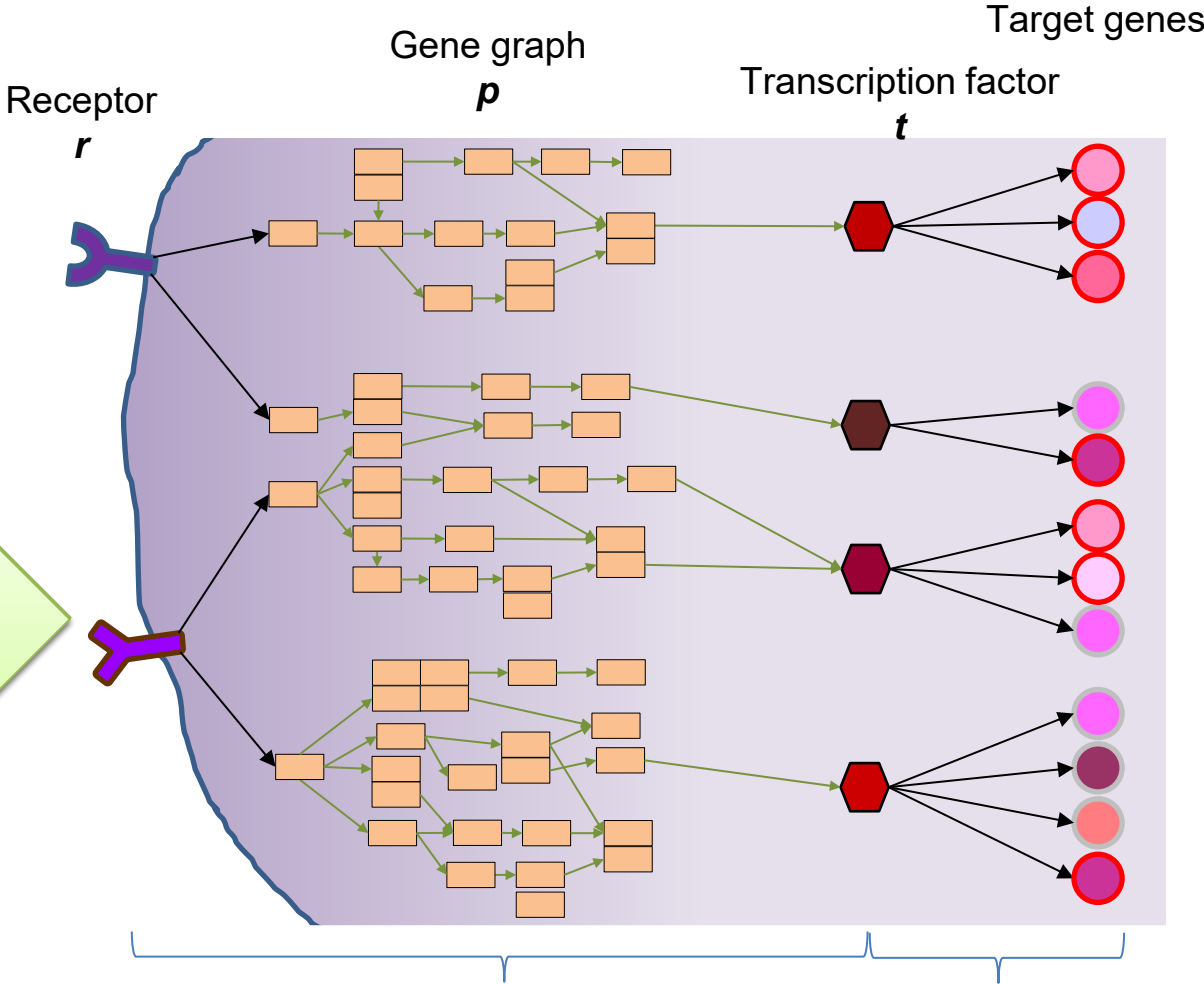
Transcription factor
t

Target genes
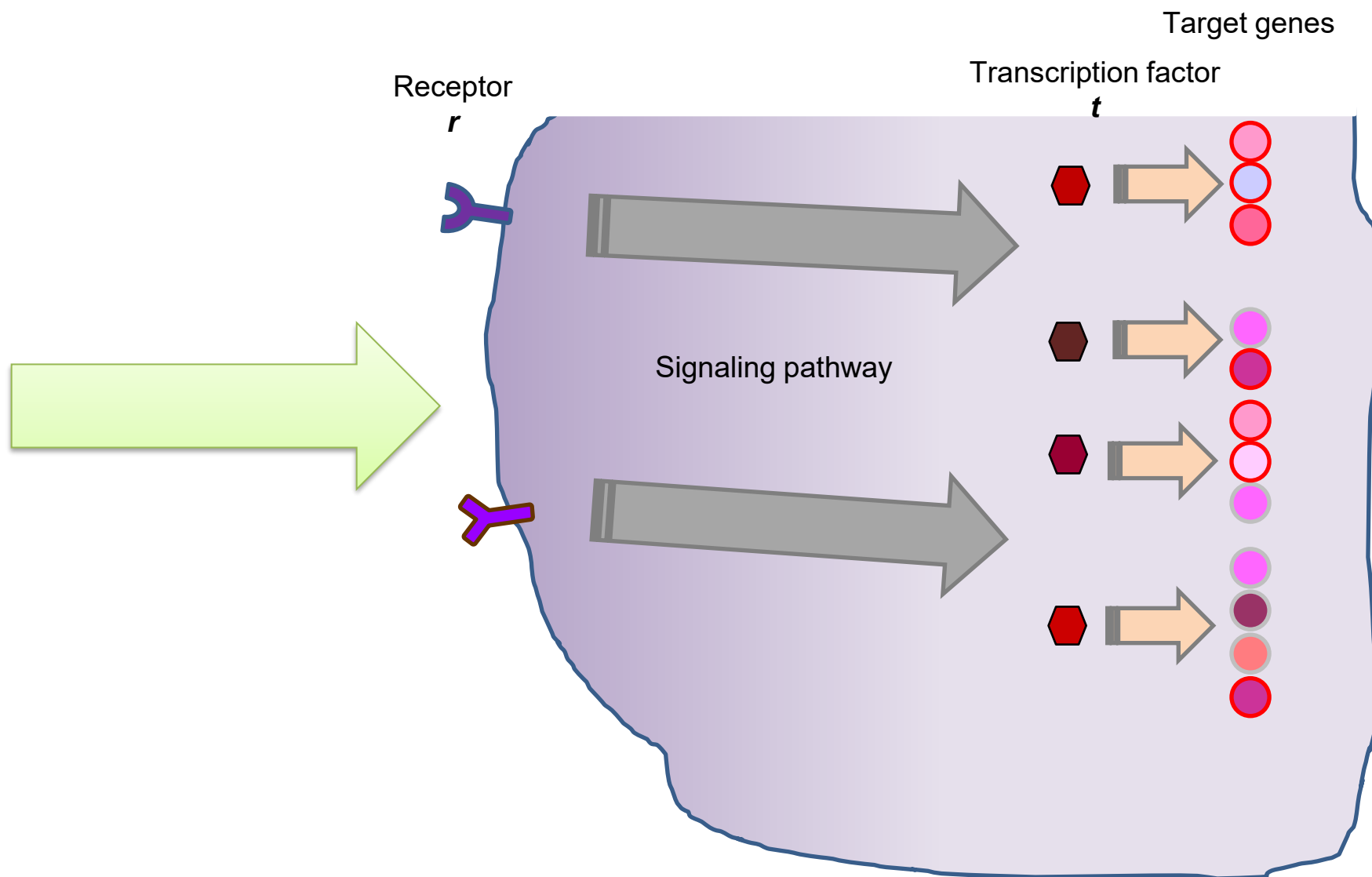
scSeqComm - INTRAcellular signaling

Conversion of biological knowledge in directed **gene graph**
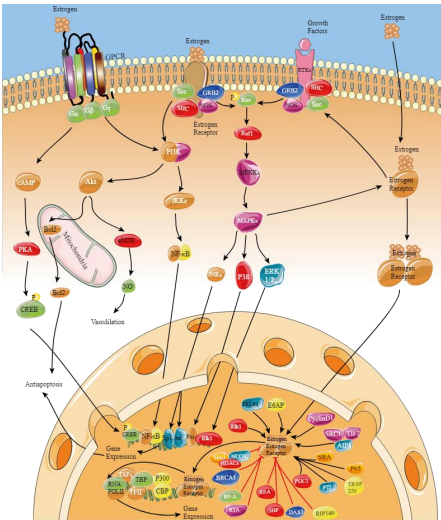
Example of intracellular signaling pathway

DEFINITION OF BIOLOGICAL-DRIVEN RULES

Target genes

Receptor
r

Gene graph
p

Transcription factor
t

Signaling pathways

Transcriptional regulatory network

node = Biological entity

edge = chemical reaction

scSeqComm - INTRAcellular signaling

S_{intra} characteristics:
- Range [0,1]
- Function of **gene graph topology** (Personalized Page rank)…
- …and **transcription factor / target gene activity** (statistical test on gene expression)

Receptor r

Gene graph p

Transcription factor t

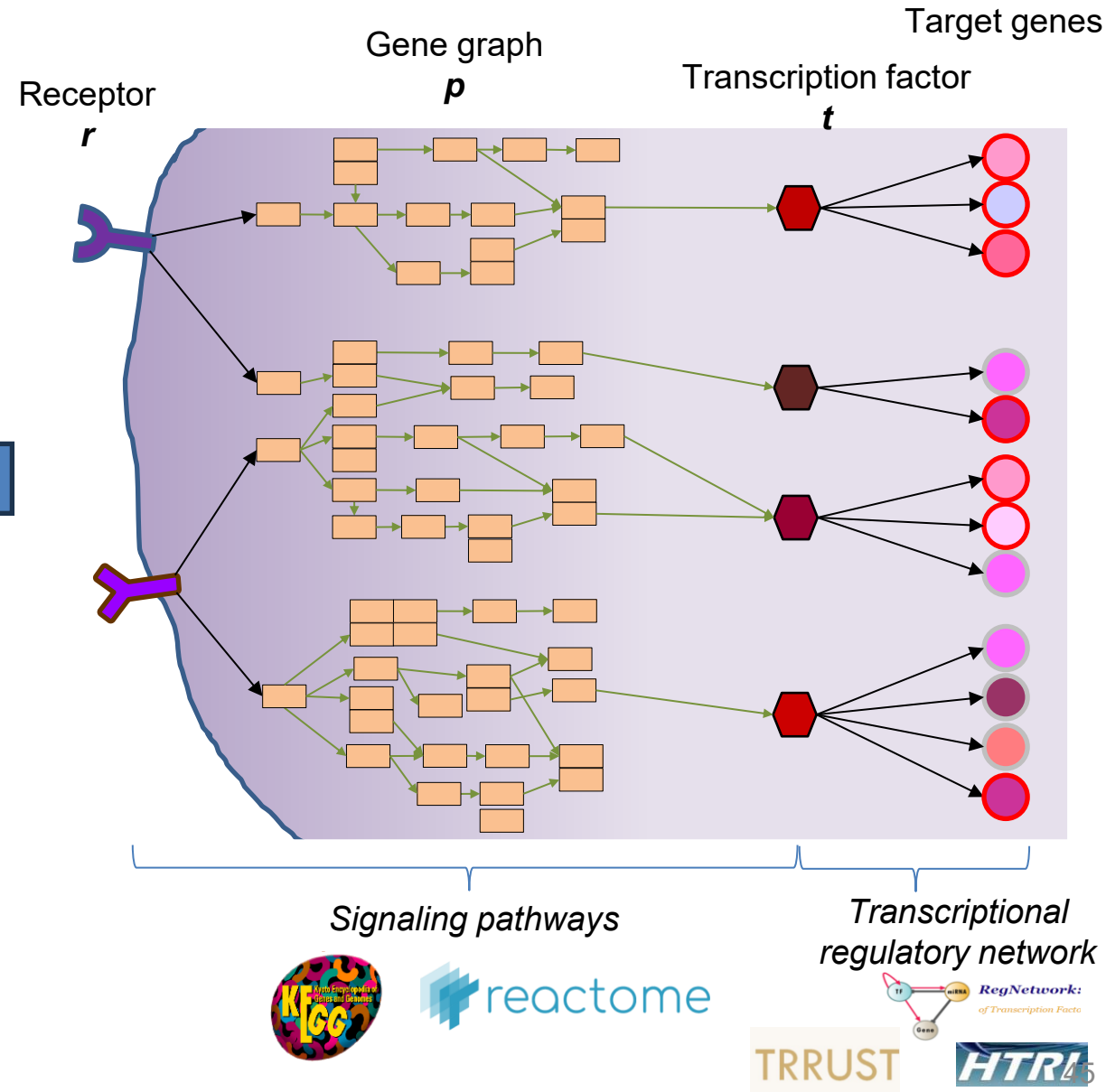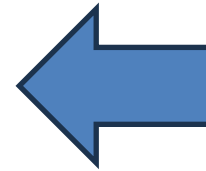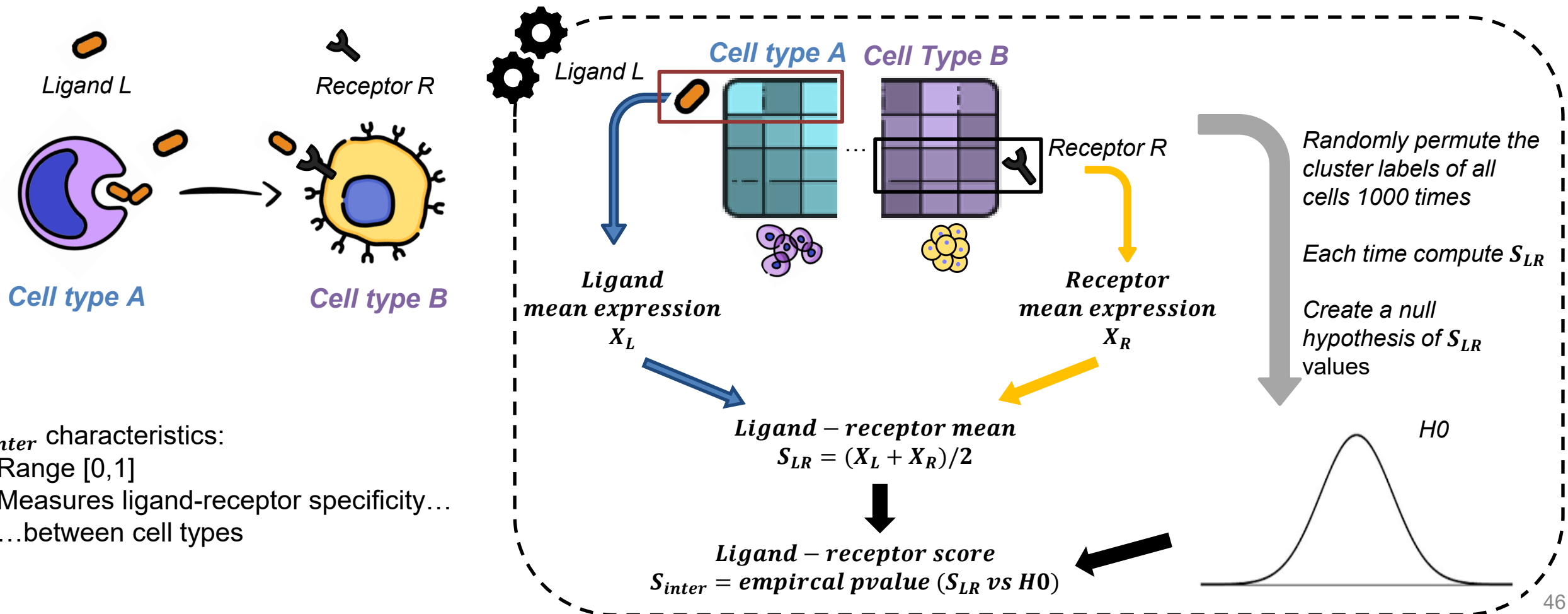Target genes

Signaling pathways

Transcriptional regulatory network

CellPhoneDB - INTERcellular signaling

Quantify intercellular score
<u>Specificity</u> of Ligand-Receptor interaction across cell type A and B

S_{inter} characteristics:
- Range [0,1]
- Measures ligand-receptor specificity...
- ...between cell types

Ligand L

Receptor R

Cell type A

Cell type B

Ligand L

Cell type A   Cell Type B

Receptor R

Randomly permute the cluster labels of all cells 1000 times

Each time compute S_{LR}

Create a null hypothesis of S_{LR} values

$Ligand$ $mean$ $expression$ X_L

$Receptor$ $mean$ $expression$ X_R

$Ligand - receptor$ $mean$
$$S_{LR} = (X_L + X_R)/2$$

$Ligand - receptor$ $score$
$$S_{inter} = empircal\ pvalue\ (S_{LR}\ vs\ H0)$$

H0

Hands on analysis of Myocardial Infarction scRNA-seq
Cesaro

Case study: Human Myocardial Infarction

a **Study design** — Sampling region
Control ▼ n = 4
IZ ▼ n = 12
BZ ▼ n = 3
RZ ▼ n = 6
FZ ▼ n = 6
31 samples from 23 patients
Human myocardial infarction

b Sampling time point — Time after initial symptoms (in days)
Acute phase / Fibrogenesis

c Multi-omic atlas — Spatial GEX — Spatial GEX space
Nuclei
snRNA-seq — Single-cell GEX space
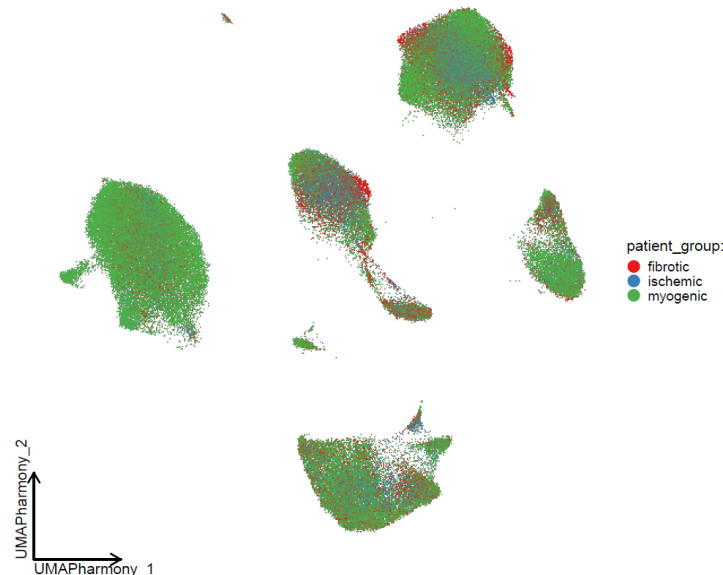snATAC-seq — Single-cell epigenomic space
FANS
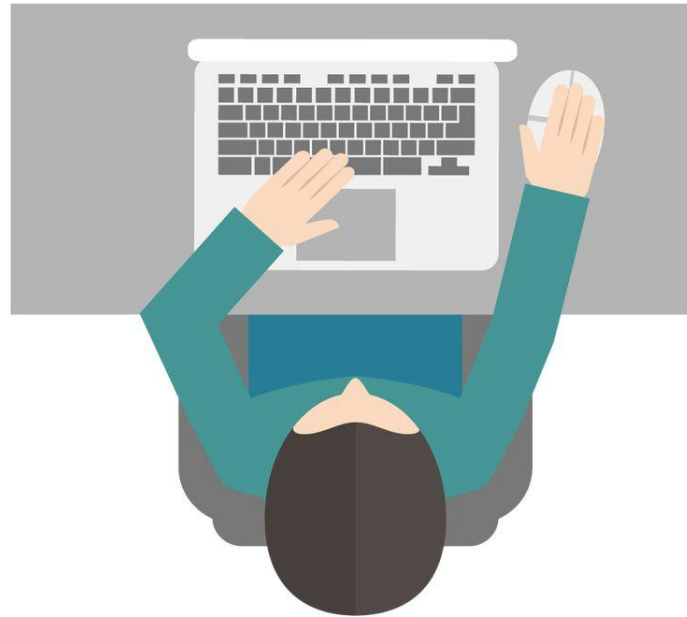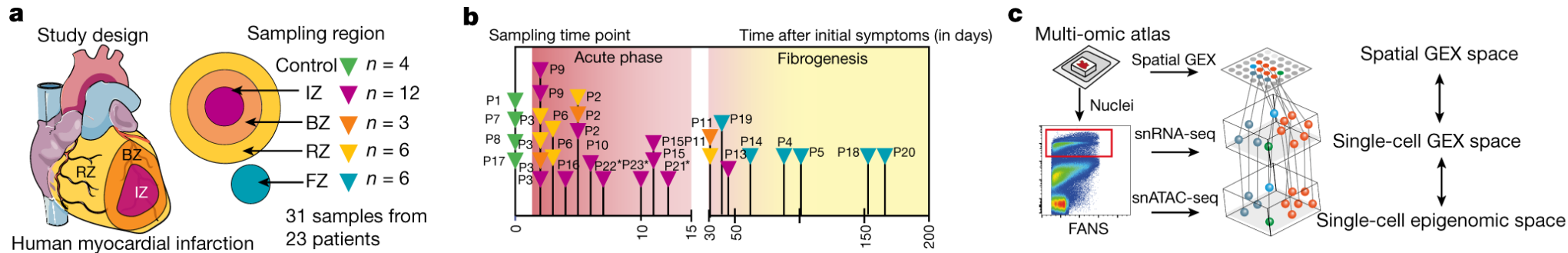
High-resolution map of human cardiac remodelling after myocardial infarction

- single-nucleus RNA sequencing (snRNA-seq)
- single-nucleus assay for transposase-accessible chromatin sequencing (scATAC-seq)
- spatial transcriptomics (ST)

23 samples
- Ischemic (n=5)
- Myogenic (n=13)
- Fibrotic (n=5)

patient_group:
- fibrotic
- ischemic
- myogenic

UMAPharmony_2
UMAPharmony_1

Christoph Kuppe, Ricardo O. Ramirez Flores, Zhijian Li, Sikander Hayat, Rebecca T. Levinson, Xian Liao, Monica T. Hannani, Jovan Tanevski, Florian Wünnemann, James S. Nagai, Maurice Halder, David Schumacher, Sylvia Menzel, Gideon Schäfer, Konrad Hoeft, Mingbo Cheng, Susanne Ziegler, Xiaoting Zhang, Fabian Peisker, Nadine Kaesler, Turgay Saritas, Yaoxian Xu, Astrid Kassner, Jan Gummert, … Rafael Kramann ✉   + Show authors

Case study: Human Myocardial Infarction

The dataset includes two levels of annotations:

- major cell type labels
- finer-grained cell type labels

Major cell types

cell_type:
- Adipo
- CM
- Endo
- Fib
- Lymphoid
- Mast
- Myeloid
- Neuronal
- PC
- vSMCs

Finer-grained cell types

cell_subtype2:
- Adipo
- Arterial_Endo
- CCL18_Macrophages
- CD_4
- CD_8
- Capillary_Endo
- Endocardial_Endo
- Fib1_SCARA5
- Fib2_Myofib
- Fib3_C7
- Fib4_COL15A1
- LYVE_FOLR_Macrophages
- LYVE_PLTP_Macrophages
- Lymphatic_Endo
- Mast
- Monocytes
- NK
- NK_T
- Neuronal
- Pericyte_1
- Pericyte_2
- Purkinje_fibers
- SPP1_Macrophages
- Venous_Endo
- damaged_CM
- healthy_CM
- intermediate_CM
- perivascular_fibroblasts
- vCM_3
- vCM_4
- vSMCs_1
- vSMCs_2

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