

# Graph representations and niche reconstruction

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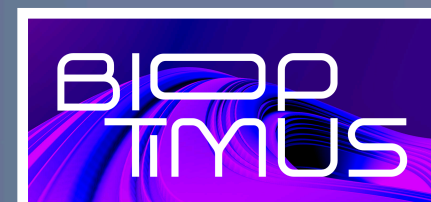
ELIXIR Spatial Omics Data Analysis

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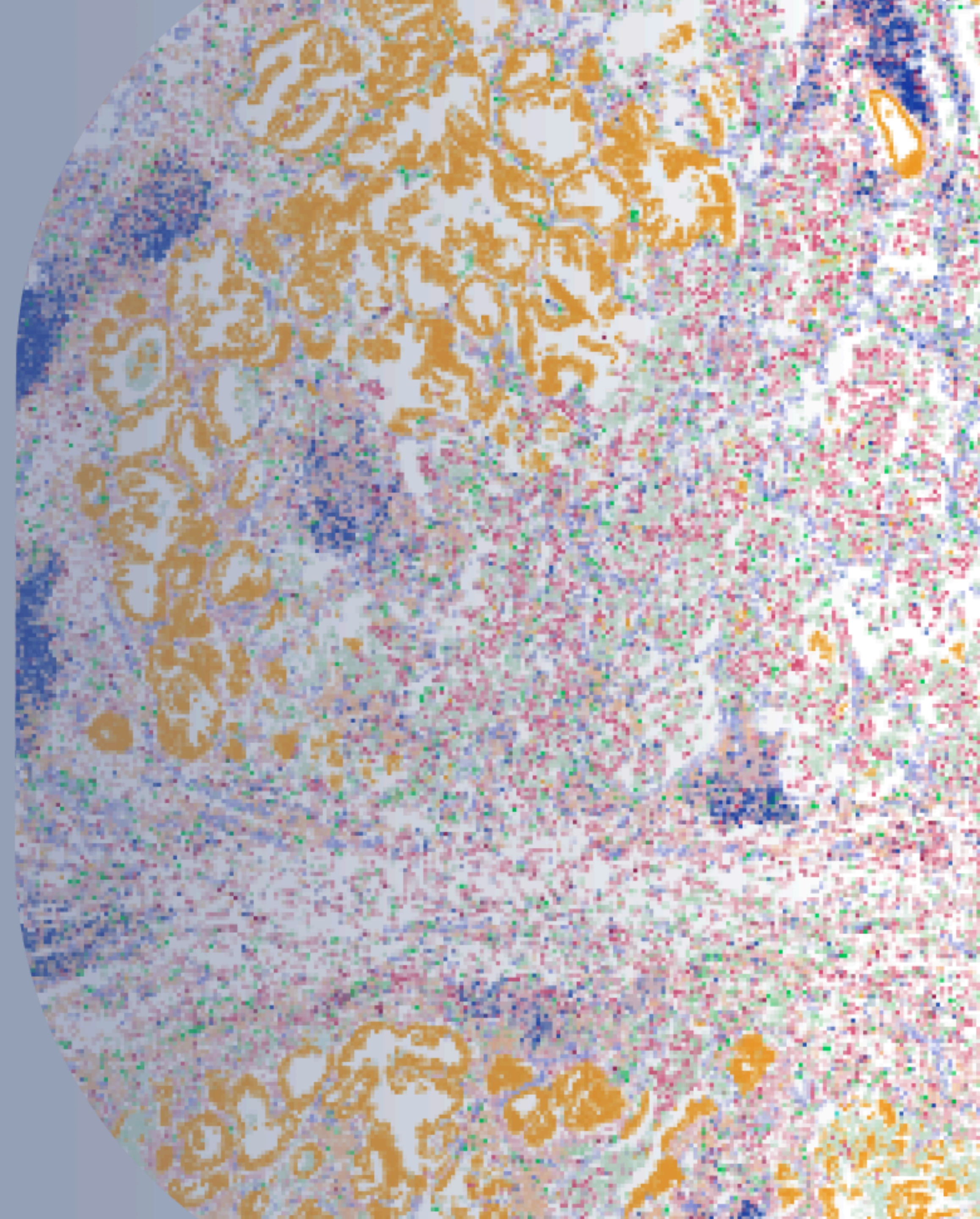
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# What are graphs and niches?

## Dictionary

Definitions from [Oxford Languages](#) · [Learn more](#)

 **graph**<sup>1</sup>  
/gra:f/

*noun*

a diagram showing the **relation** between variable quantities, typically of two variables, each measured along one of a pair of axes at right angles.

**Similar:** [chart](#) [diagram](#) [grid](#) [histogram](#) [bar chart](#) [pie chart](#) 

*verb*

plot or trace on a graph.

**Similar:** [plot](#) [trace](#) [draw up](#) [delineate](#)

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**Similar:** chart diagram grid histogram bar chart pie chart ⌵

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 **niche**  
/ni:ʃ,ntʃ/

*noun*

1. a comfortable or suitable position in life or employment.  
"he is now a partner at a leading law firm and feels he has found his niche"

**Similar:** ideal position calling vocation métier place function job ⌵

2. **a specialized segment** of the market for a particular kind of product or service.  
"he believes he has found a niche in the market"

*adjective*

denoting products, services, or interests that appeal to a small, specialized section of the population.

"other companies in this space had to adapt to being niche players"

*verb*

place (something) in a niche or recess.

"these elements were niched within the shadowy reaches"

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## Quantitative characterization of cell niches in spatial atlases

[Sebastian Birk](#), [Irene Bonafonte-Pardàs](#), [Adib Miraki Feriz](#), [Adam Boxall](#), [Eneritz Agirre](#), [Fani Memi](#), [Anna Maguza](#), [Rong Fan](#), [Gonçalo Castelo-Branco](#), [Fabian J. Theis](#), [Omer Ali Bayraktar](#),

» Identifying niches and quantifying their functions can help to **unravel important insights** into tissue architecture and **spatial biomarkers**, which can be harnessed to create novel diagnostic tools, identify new drug targets, and develop targeted therapies.

## Nicheformer: a foundation model for single-cell and spatial omics

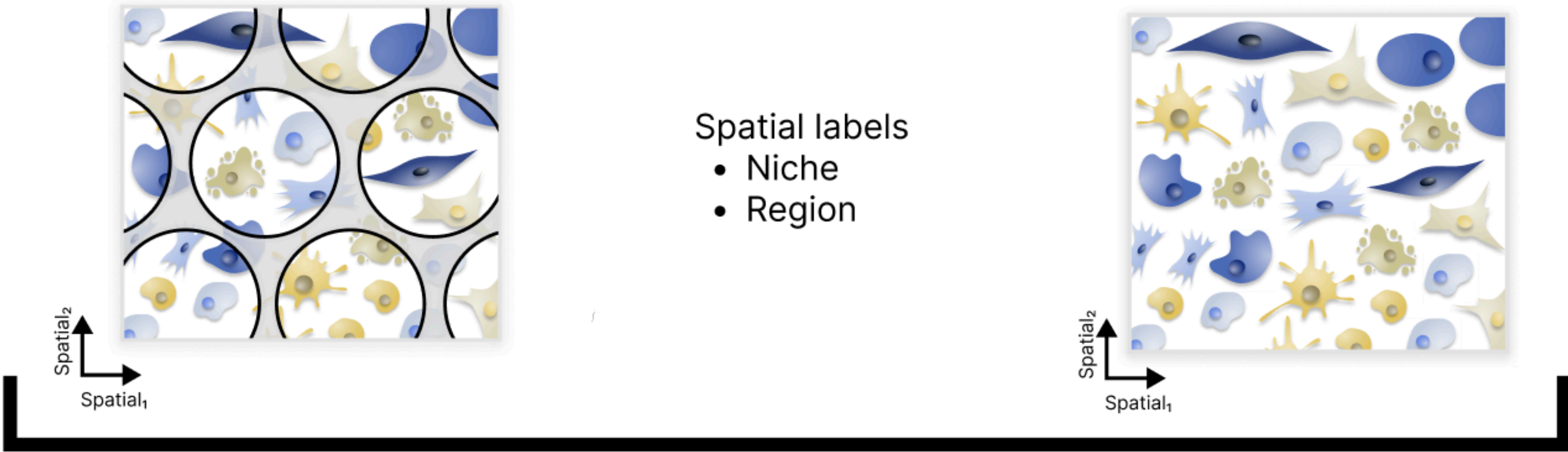
[Anna C. Schaar](#), [Alejandro Tejada-Lapuerta](#), [Giovanni Pallarès](#), [Mariia Minaeva](#), [Larsen Vornholz](#), [Leander Dony](#), [Francesca](#), [Fabian J. Theis](#)

doi: <https://doi.org/10.1101/2024.04.15.589472>

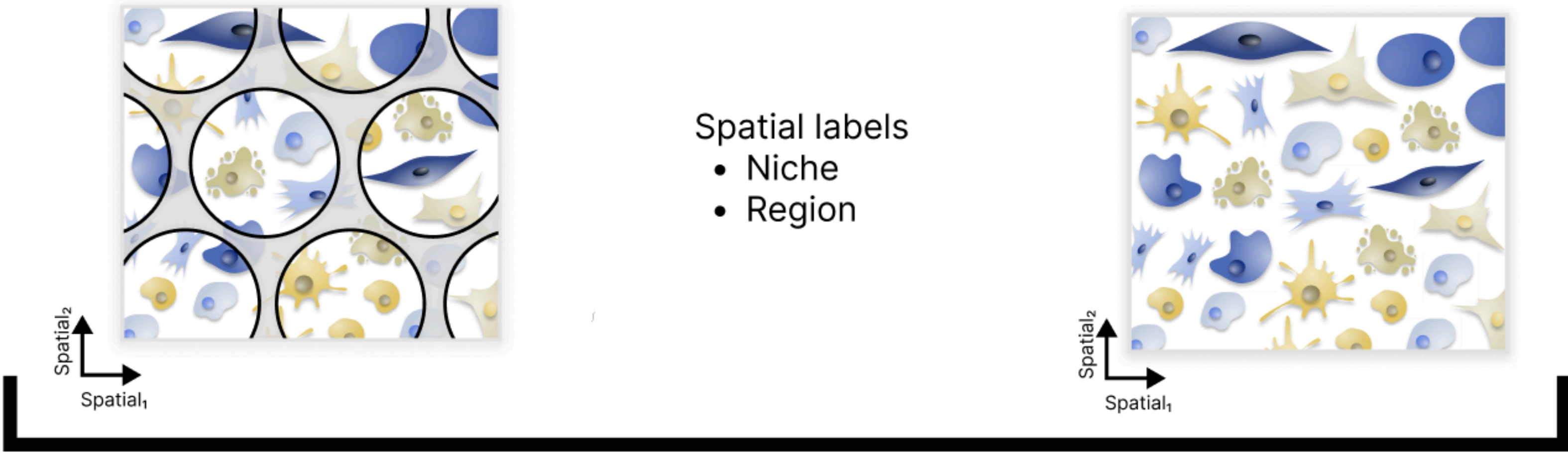
» In contrast to standard approaches to identifying cell types, **cellular niches** are defined by **spatially-dependent labels** obtained by combining **similarity in gene expression profiles** together with **spatial neighborhood structures, histological information or global structures in the tissue**. Cellular niches typically describe a local structure in a tissue, for example, a **tumor niche or immune niche**, which vary both in terms of gene expression, but also in terms of the cell type compositions. Similarly to niches, tissue regions can be defined as spatially consistent cellular states across a larger-than-a-niche tissue context. Importantly tissue regions are commonly composed of multiple different niches and therefore describe higher-level structures in a tissue.



# What are graphs and niches in the context of spatial omics?

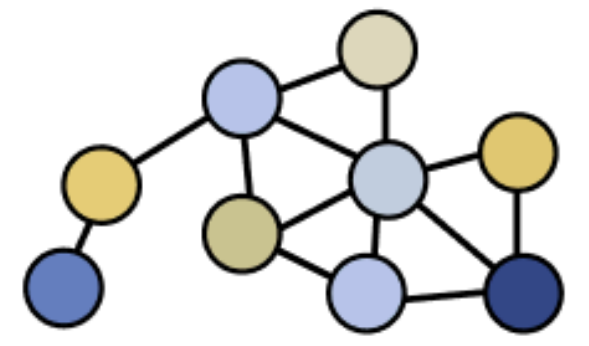


# What are graphs and niches in the context of spatial omics?



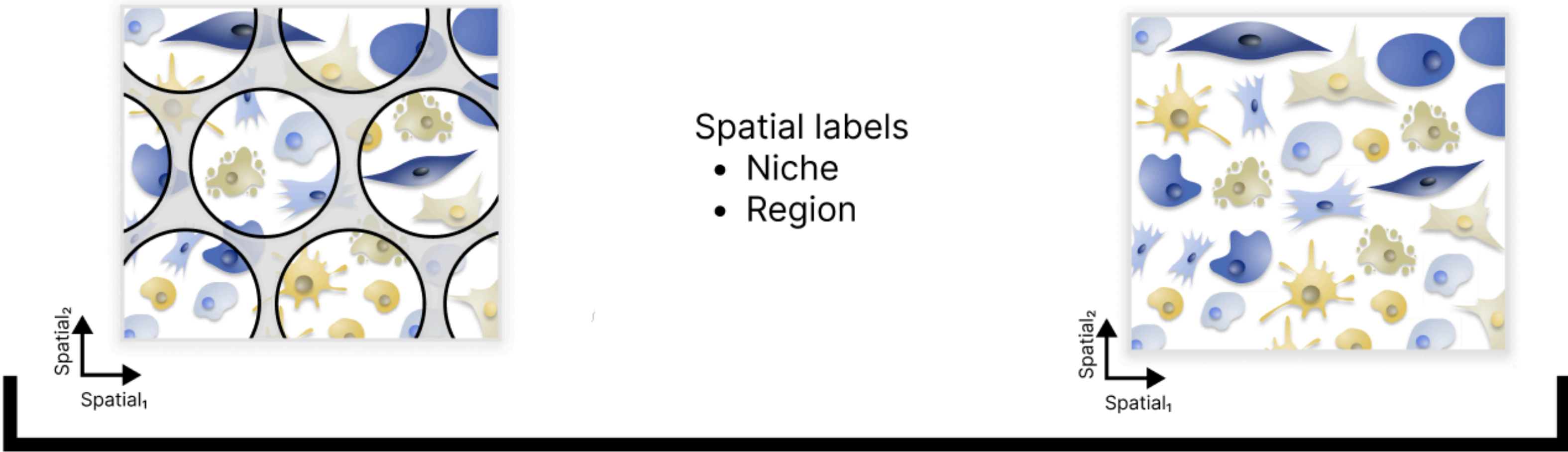
- Spatial labels
- Niche
  - Region

Spatial graph

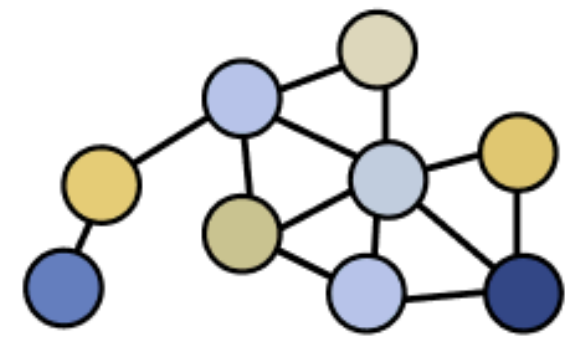


- Graph structure based on physical distances

# What are graphs and niches in the context of spatial omics?

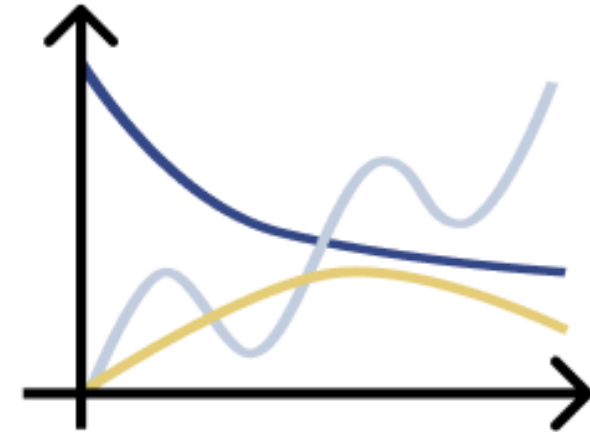


Spatial graph



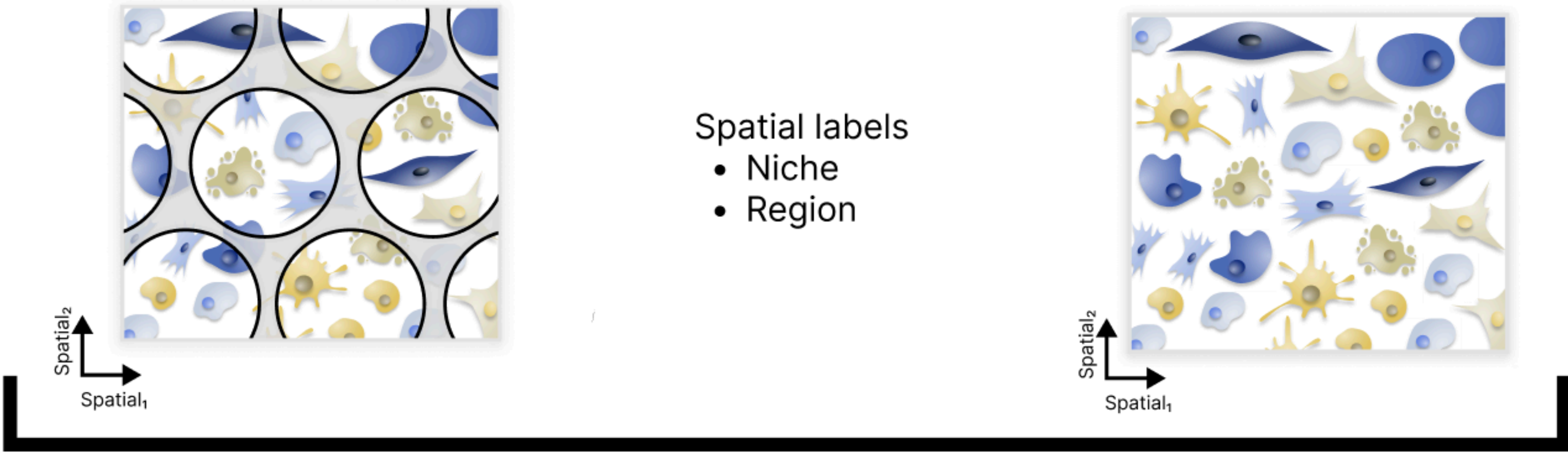
- Graph structure based on physical distances

Spatial metrics

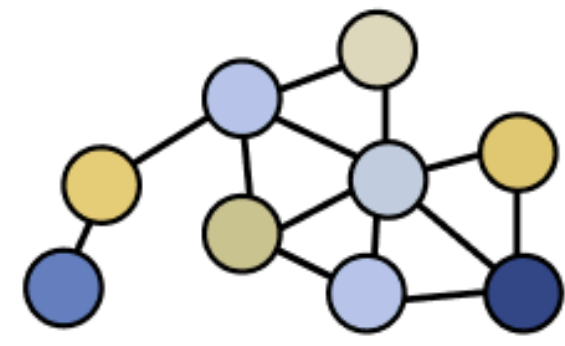


- GEX changes
- Spatially variable genes

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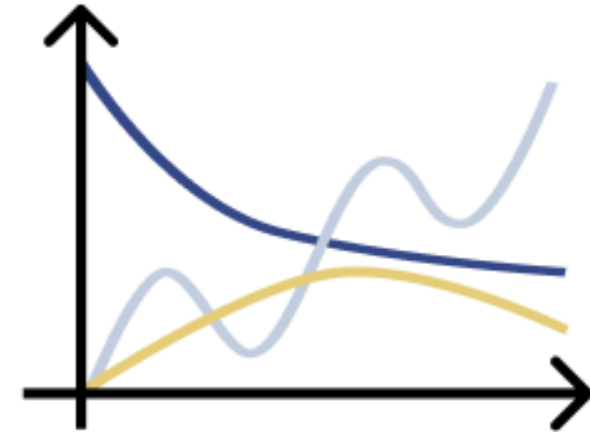


Spatial graph



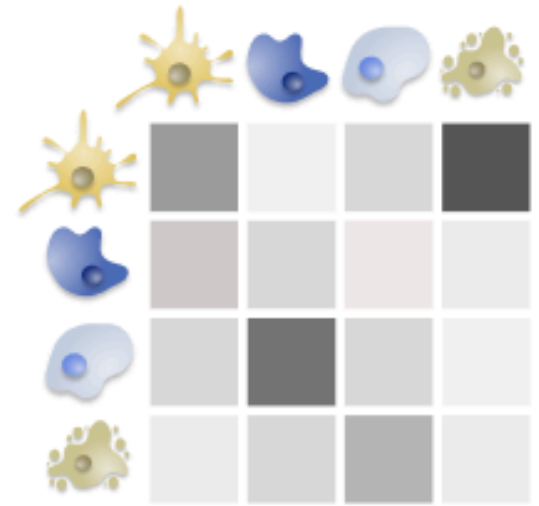
- Graph structure based on physical distances

Spatial metrics



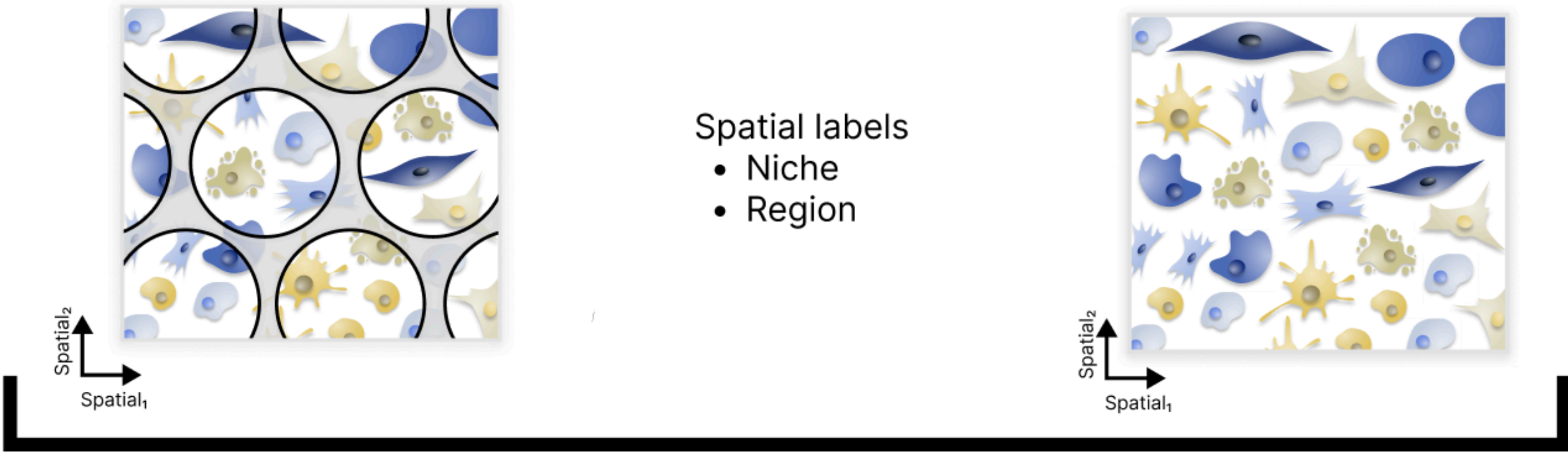
- GEX changes
- Spatially variable genes

Spatial composition

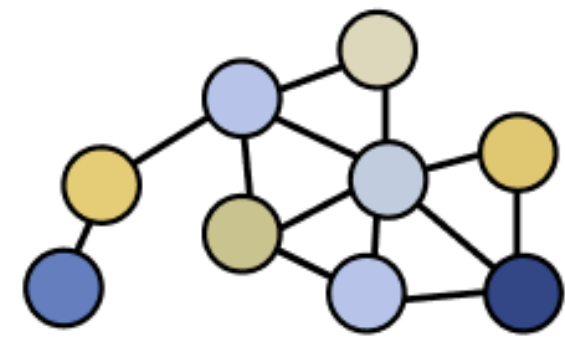


- Neighbourhood analysis
- Tumor micro-environments

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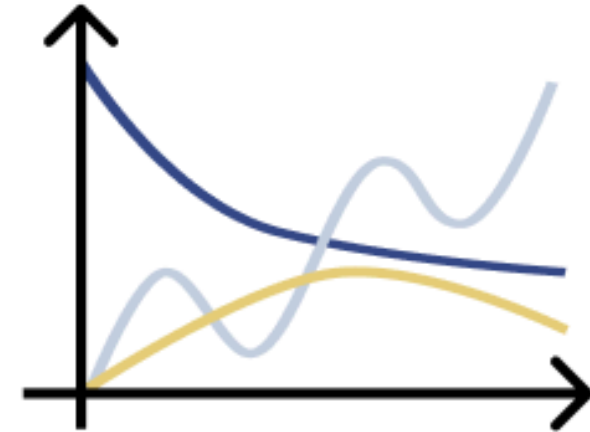


Spatial graph



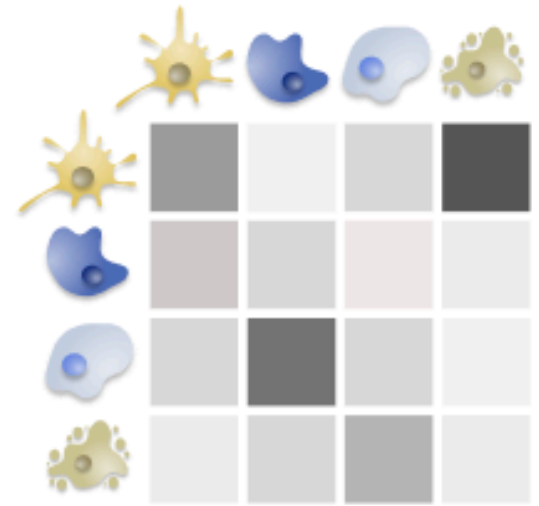
- Graph structure based on physical distances

Spatial metrics



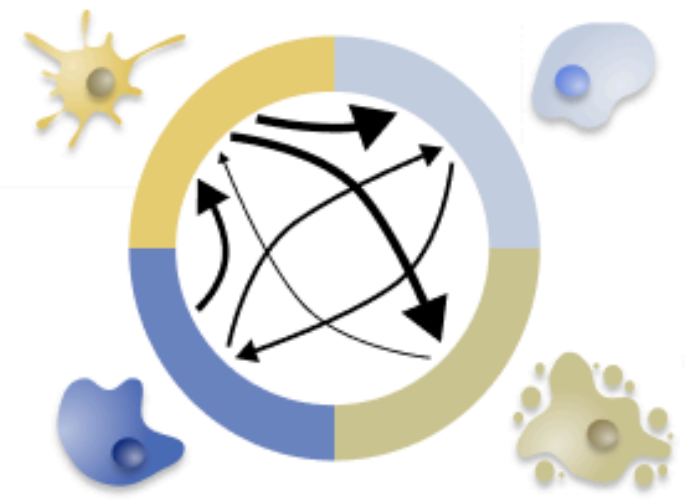
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Spatial composition



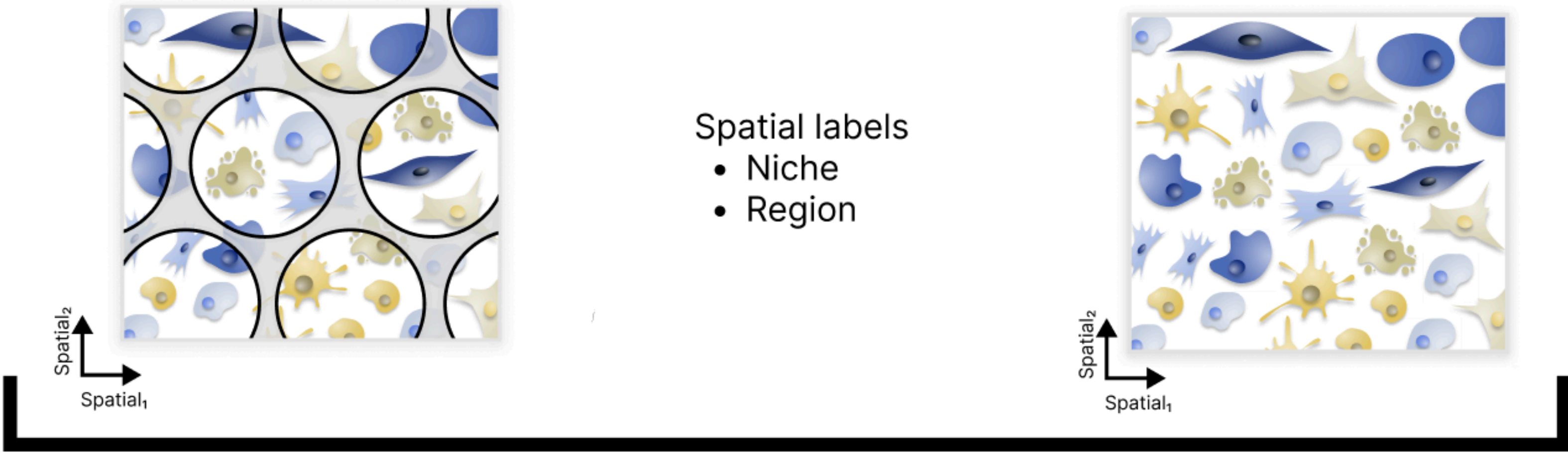
- Neighbourhood analysis
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Cell-cell communication



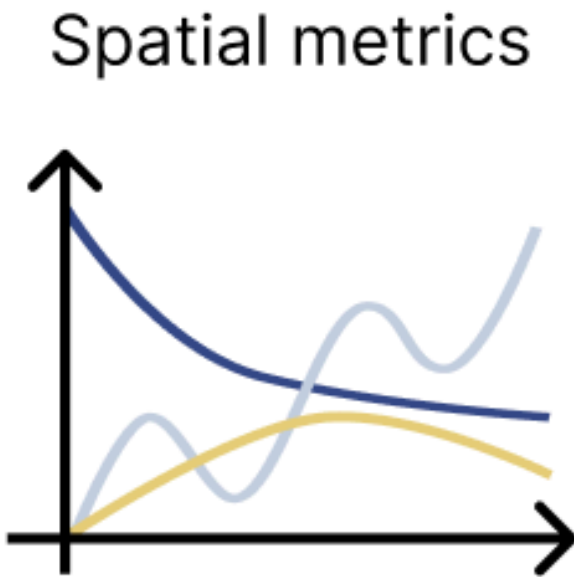
- Constraint cell-cell communication

# What are graphs and niches in the context of spatial omics?

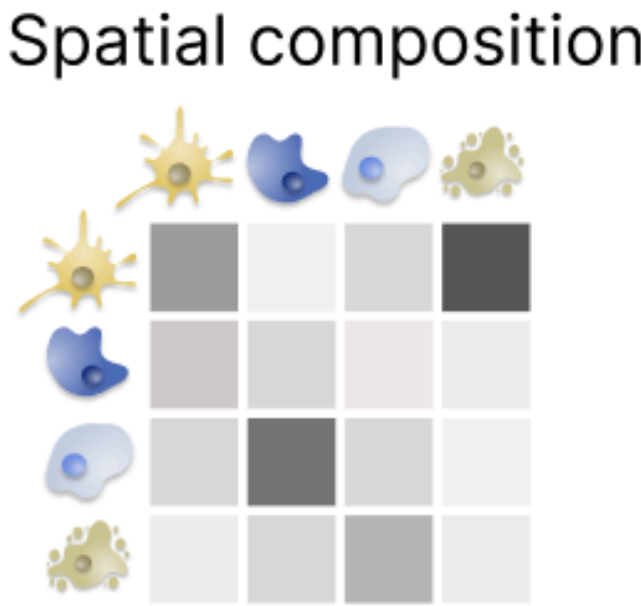


**Spatial graph**

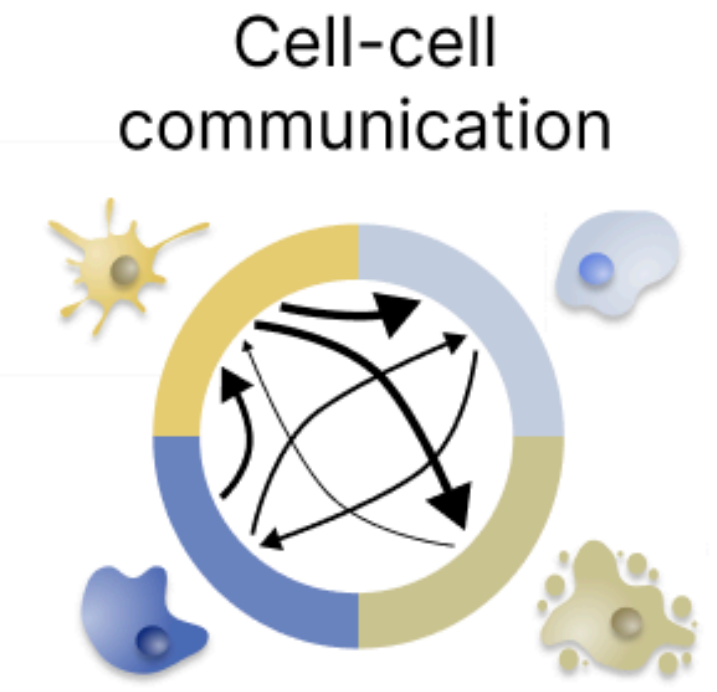
- Graph structure based on physical distances



- GEX changes
- Spatially variable genes

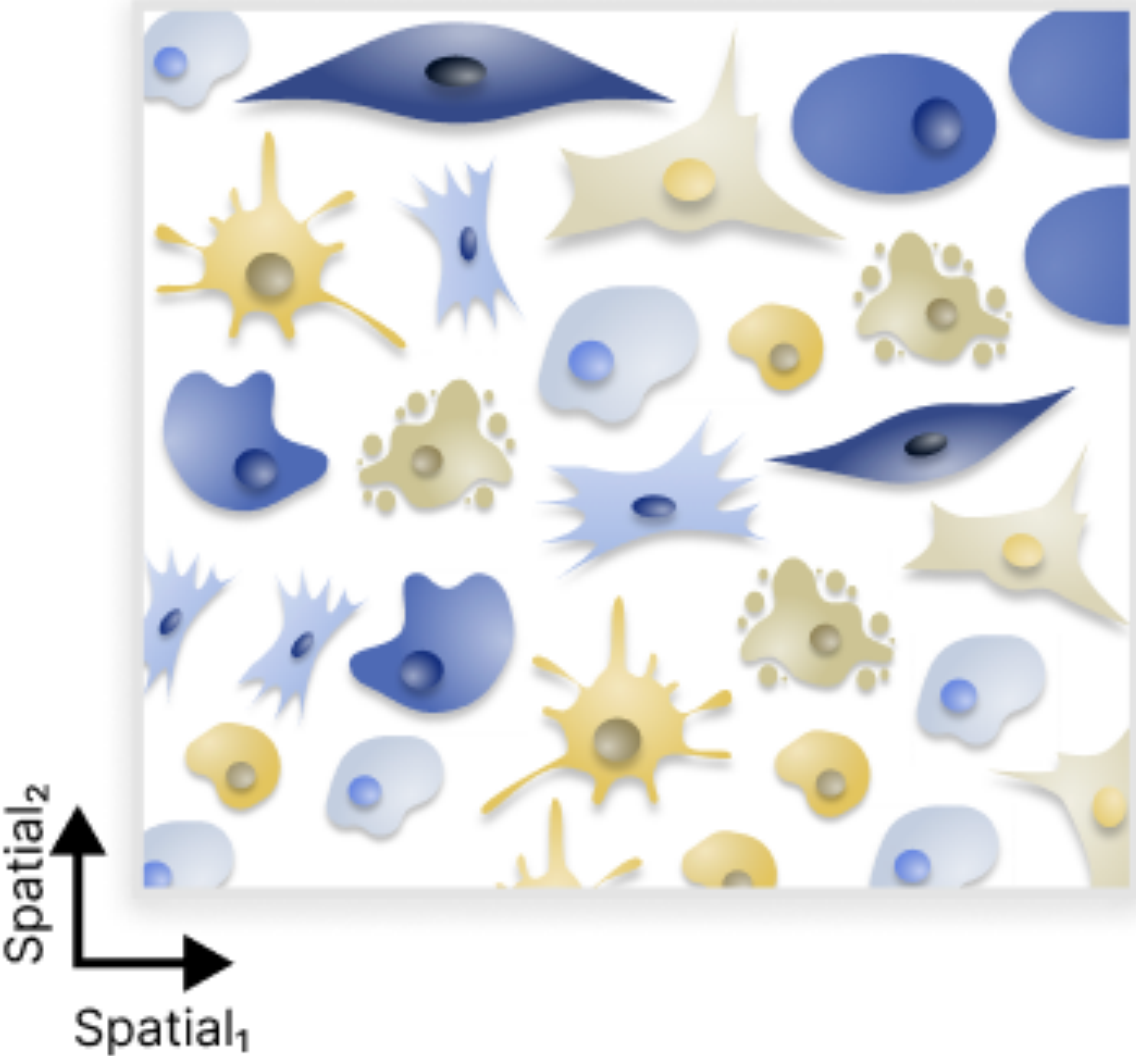


- Neighbourhood analysis
- Tumor micro-environments



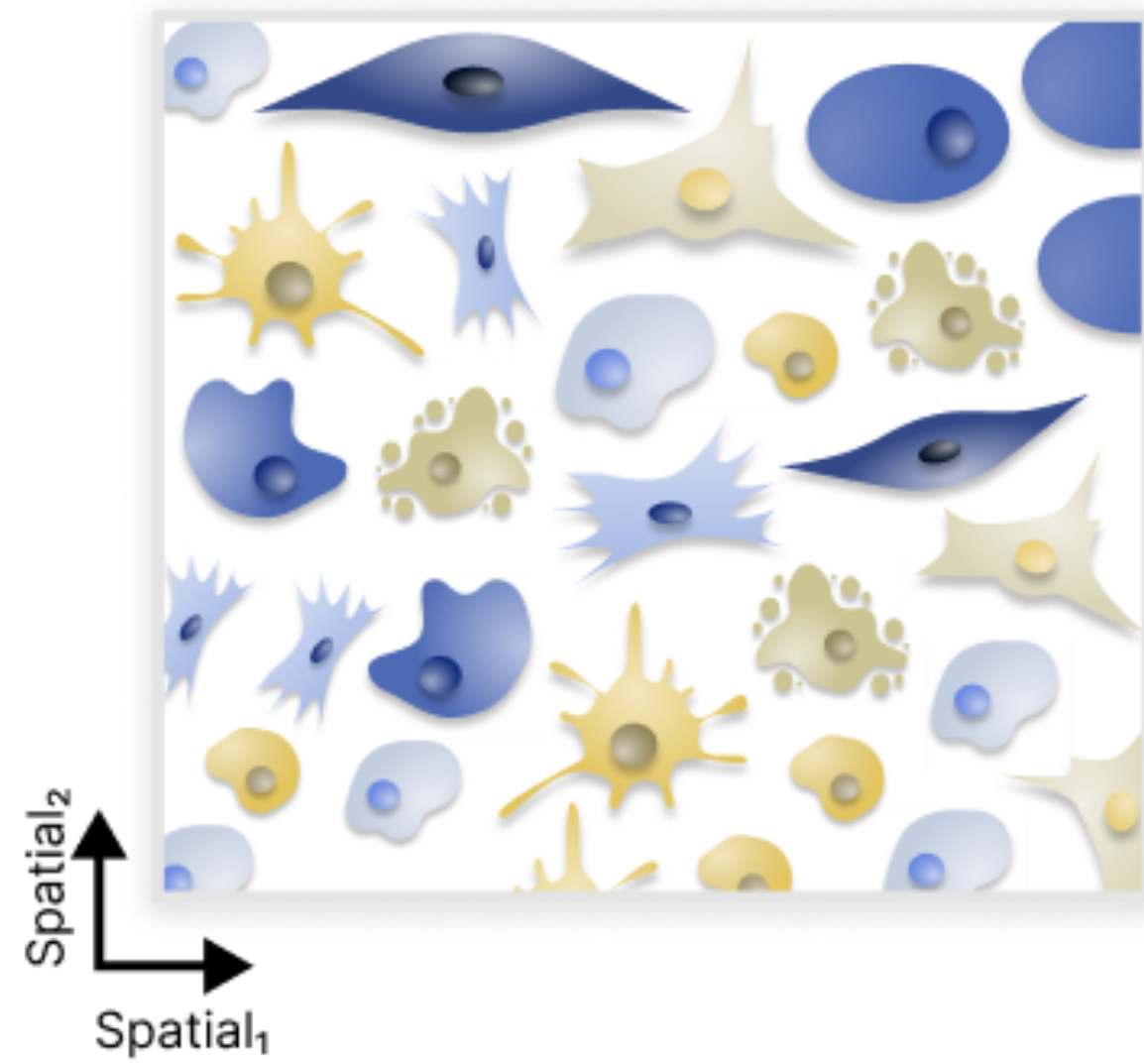
- Constraint cell-cell communication

# Defining spatial graphs of cells based on spatial proximity

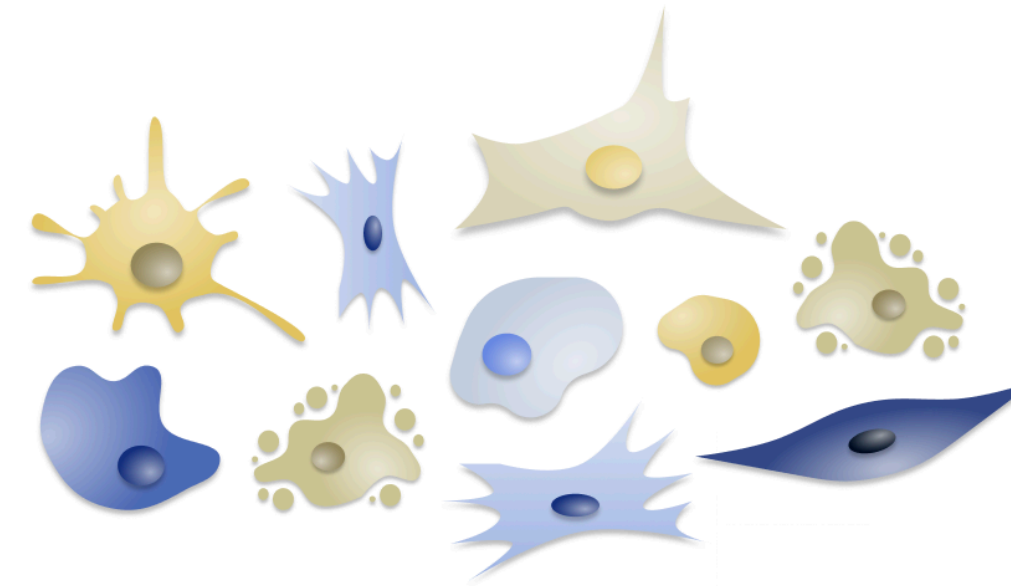
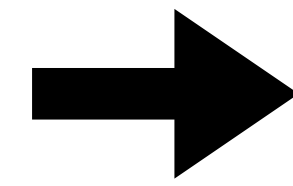


Segmented targeted spatial omics

# Defining spatial graphs of cells based on spatial proximity



Segmented targeted spatial omics

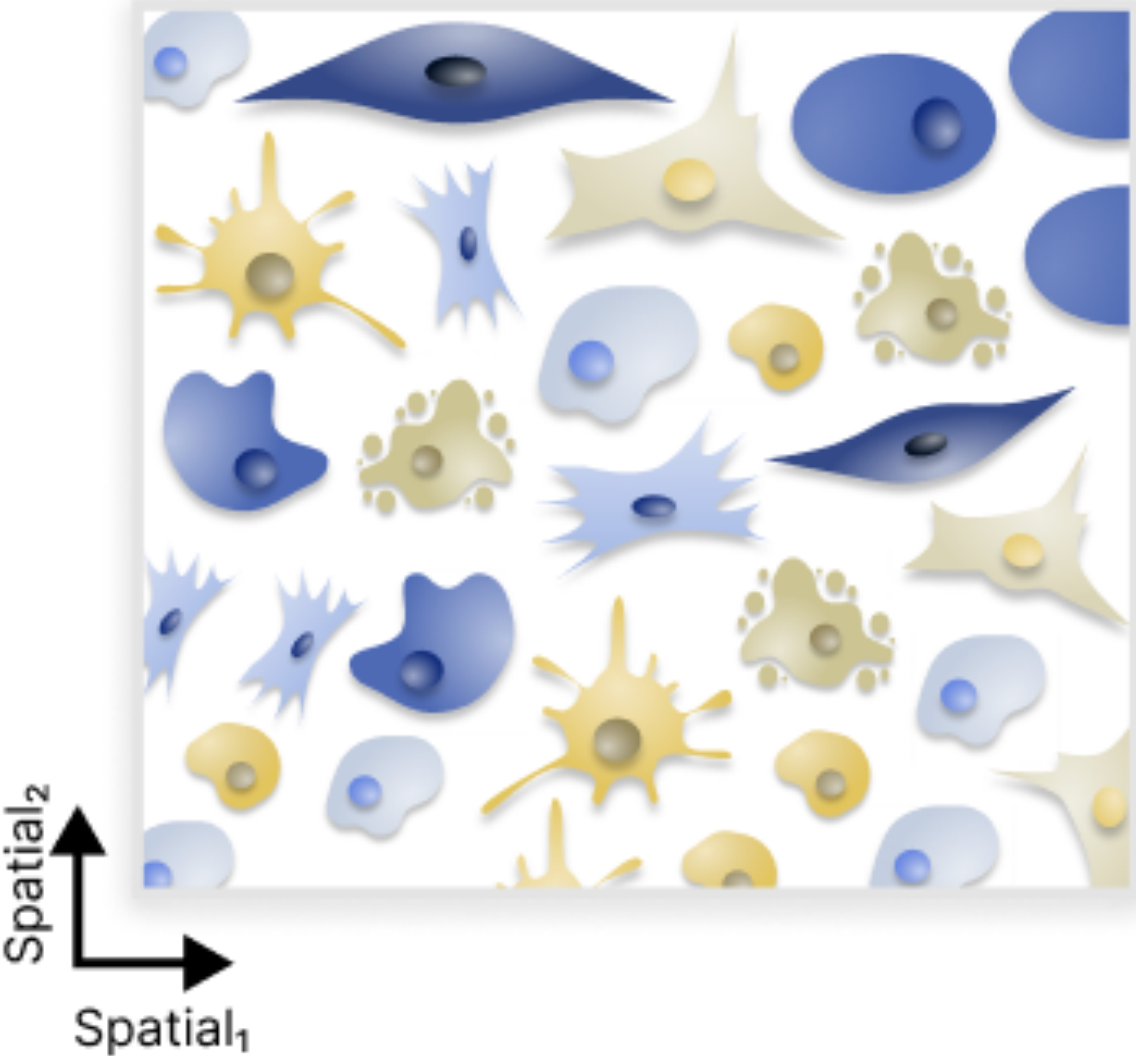


Cells resolved at their physical location

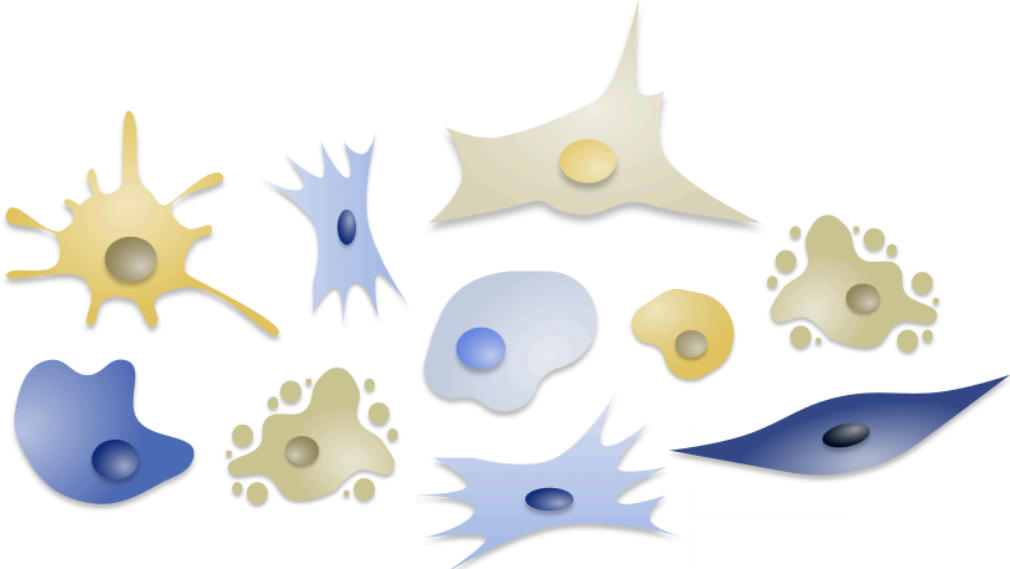
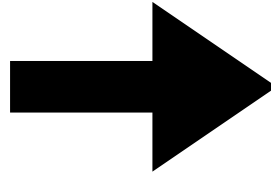
- Coordinates
- Gene expression vector
- Cell type annotations



# Defining spatial graphs of cells based on spatial proximity

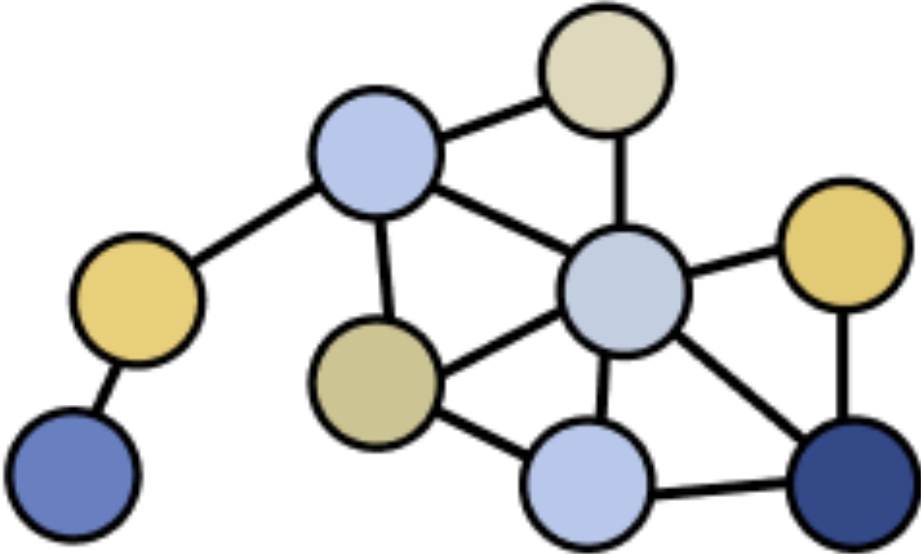
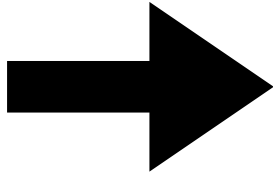


Segmented targeted spatial omics



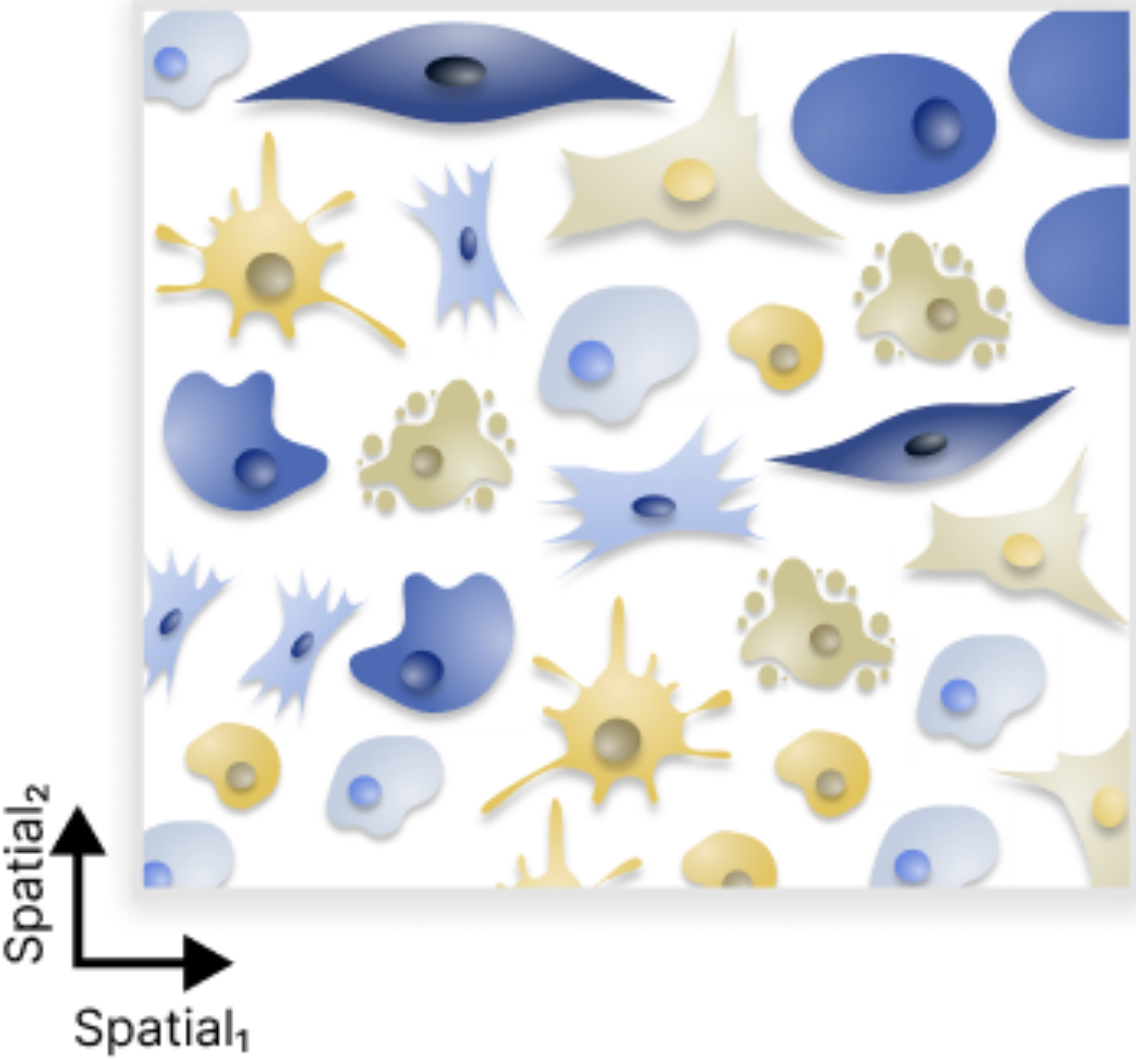
Cells resolved at their physical location

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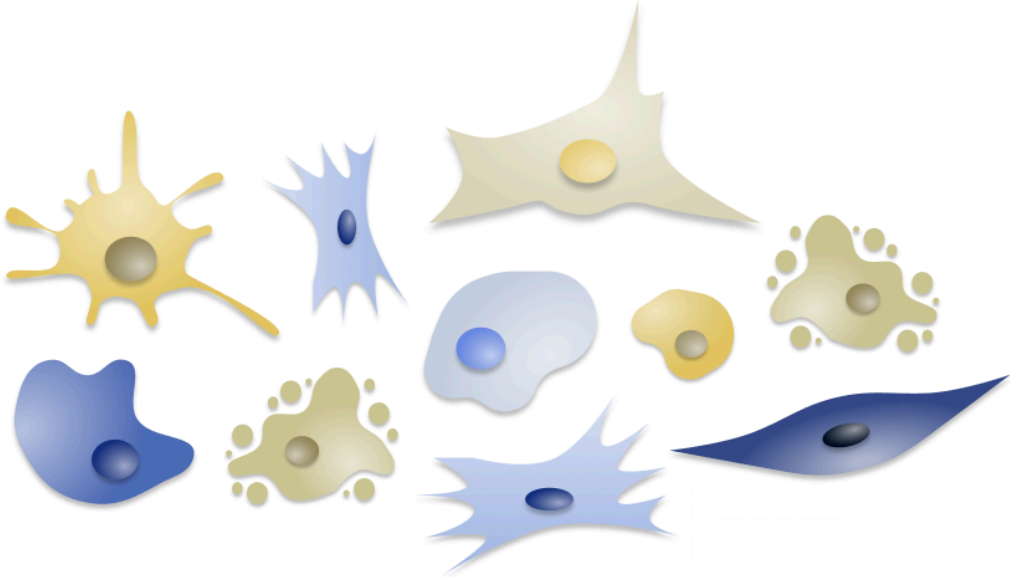
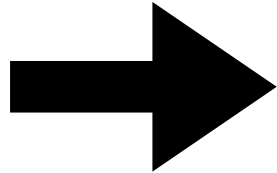


Spatial graph of cells

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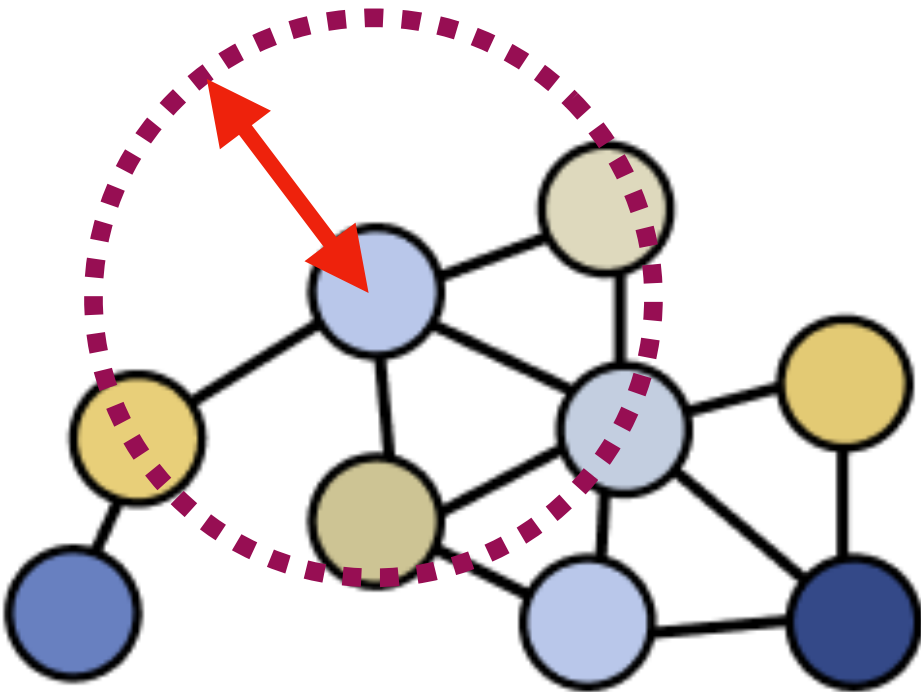
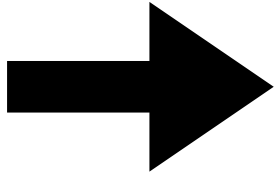


Segmented targeted spatial omics



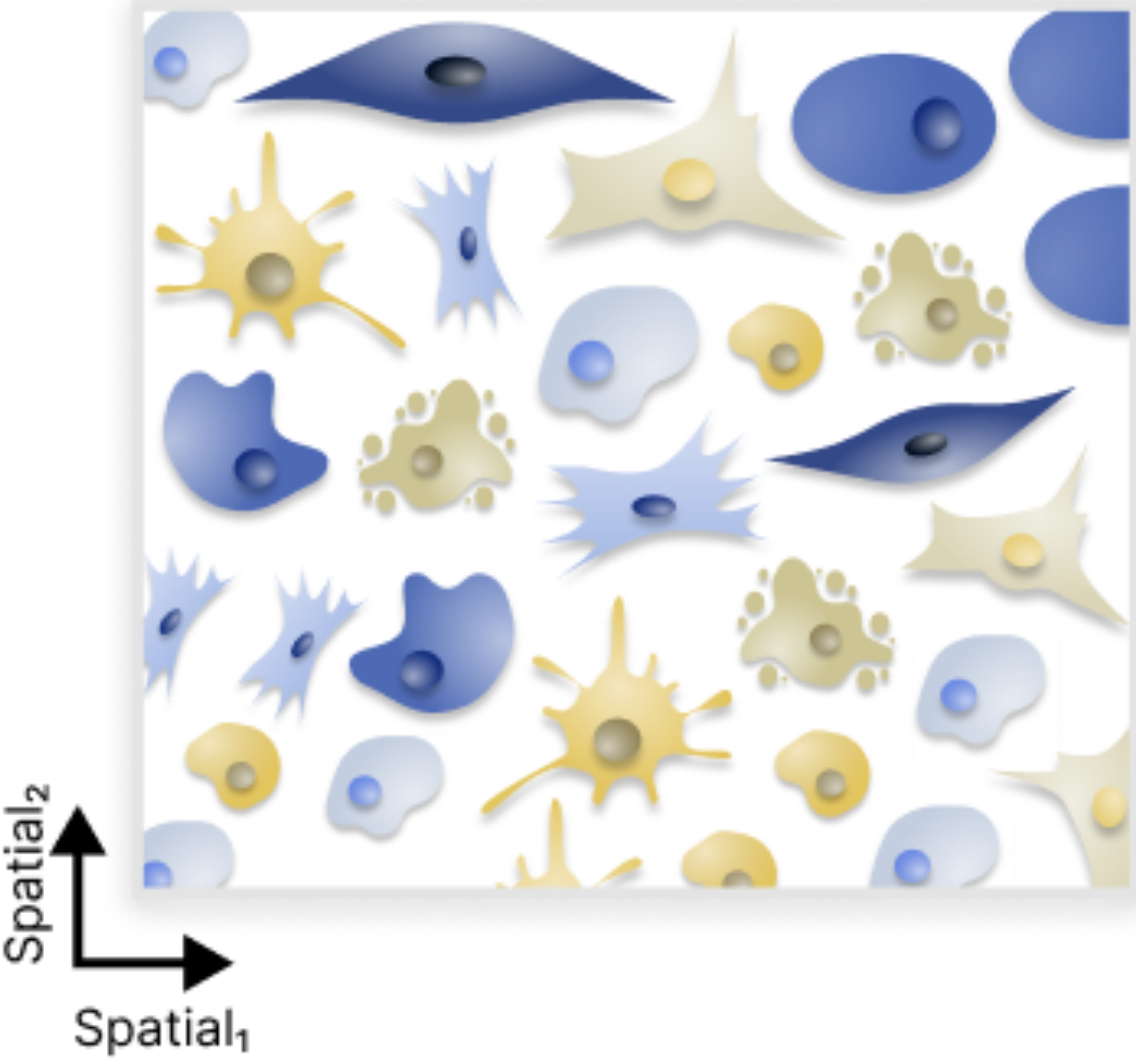
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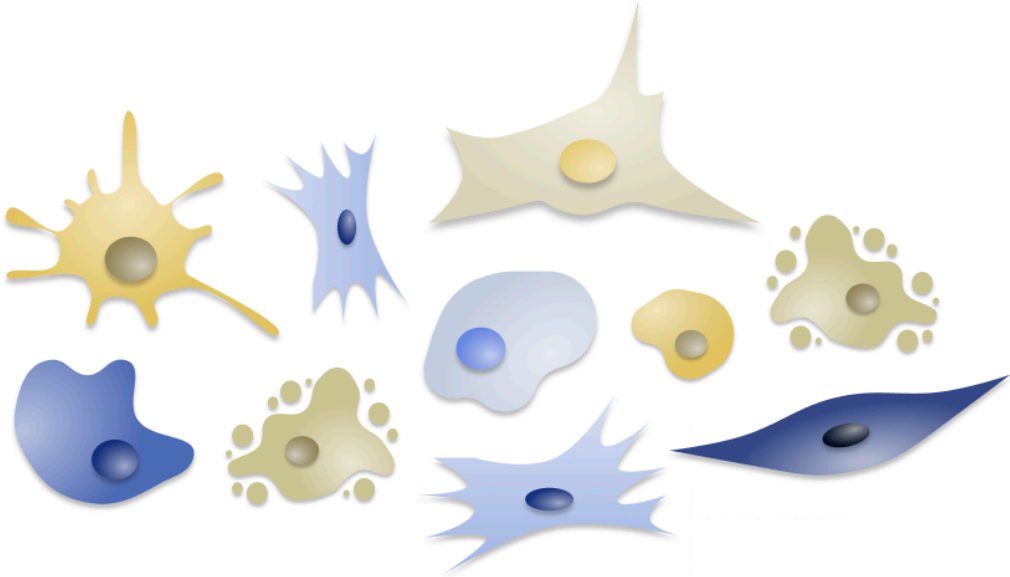
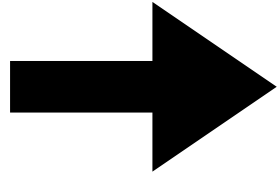


Spatial graph of cells

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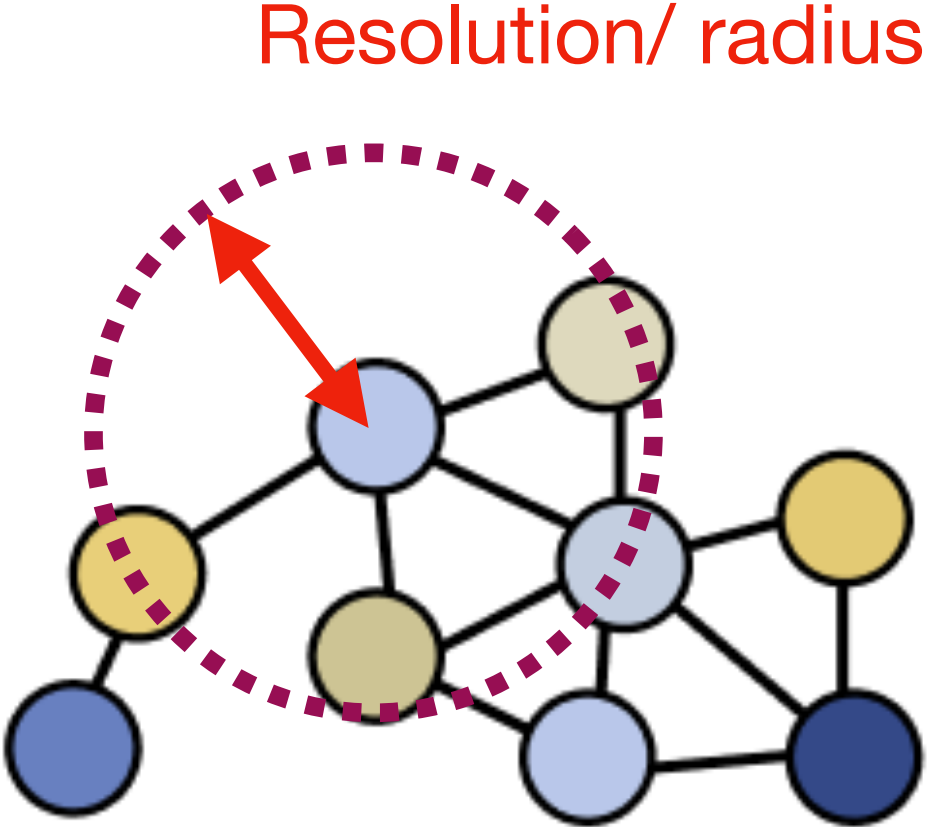
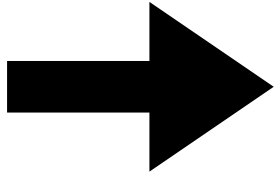


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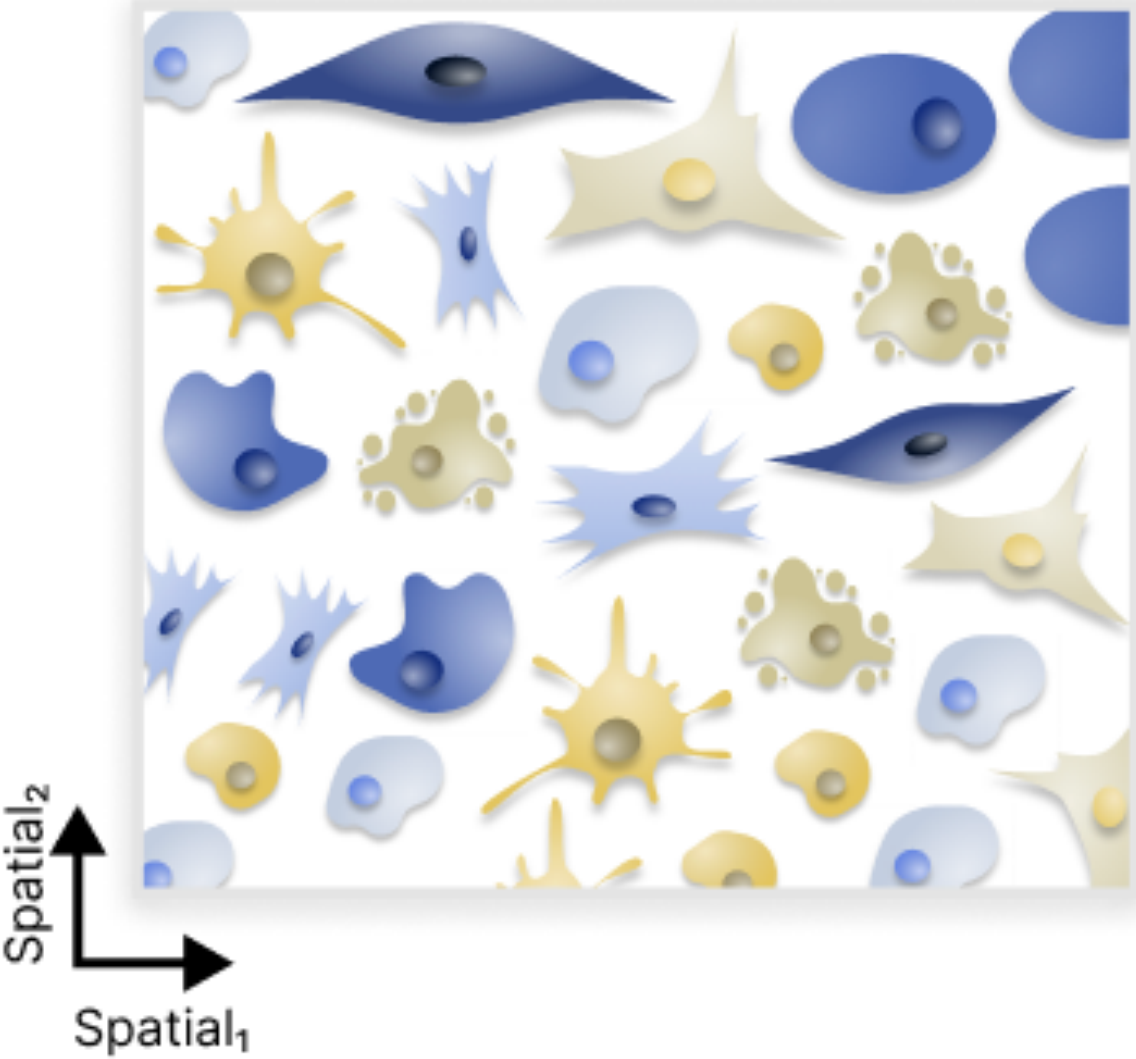
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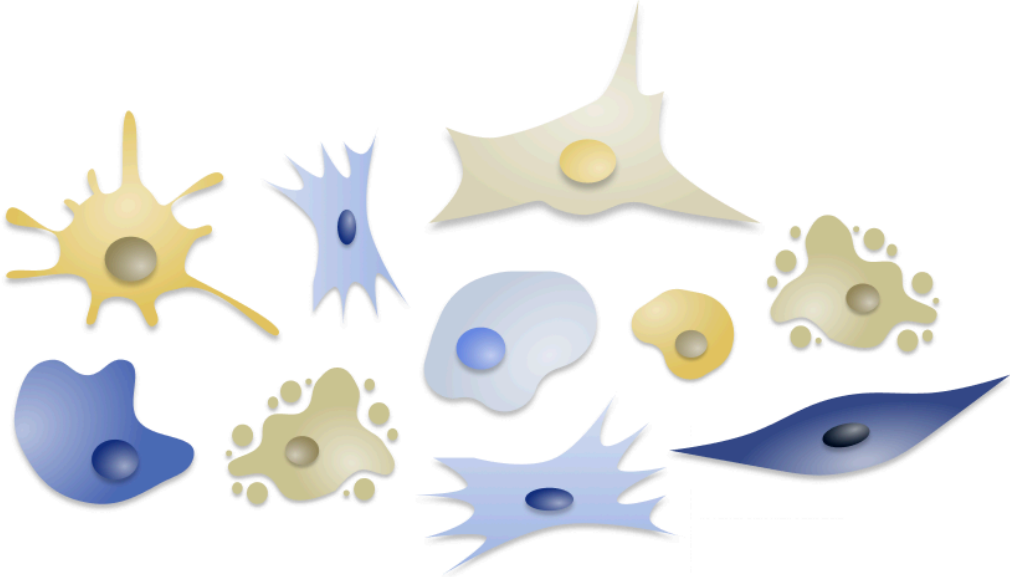
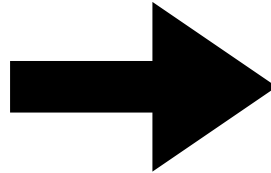


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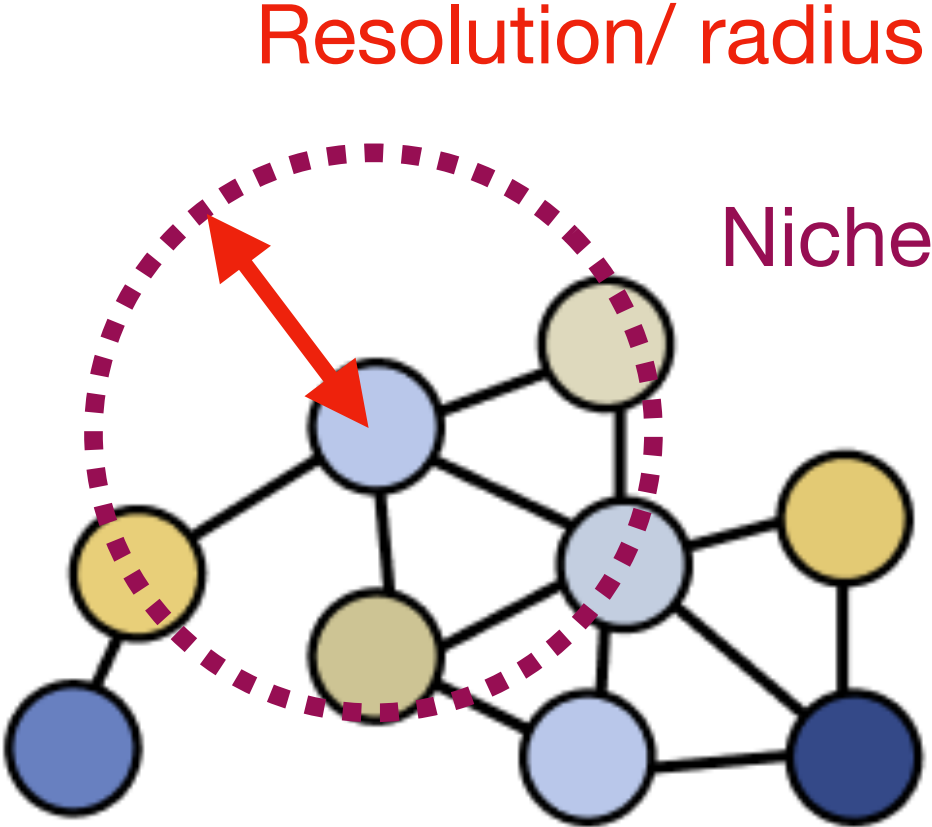
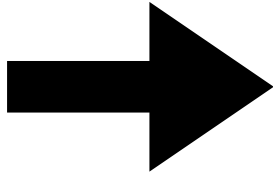


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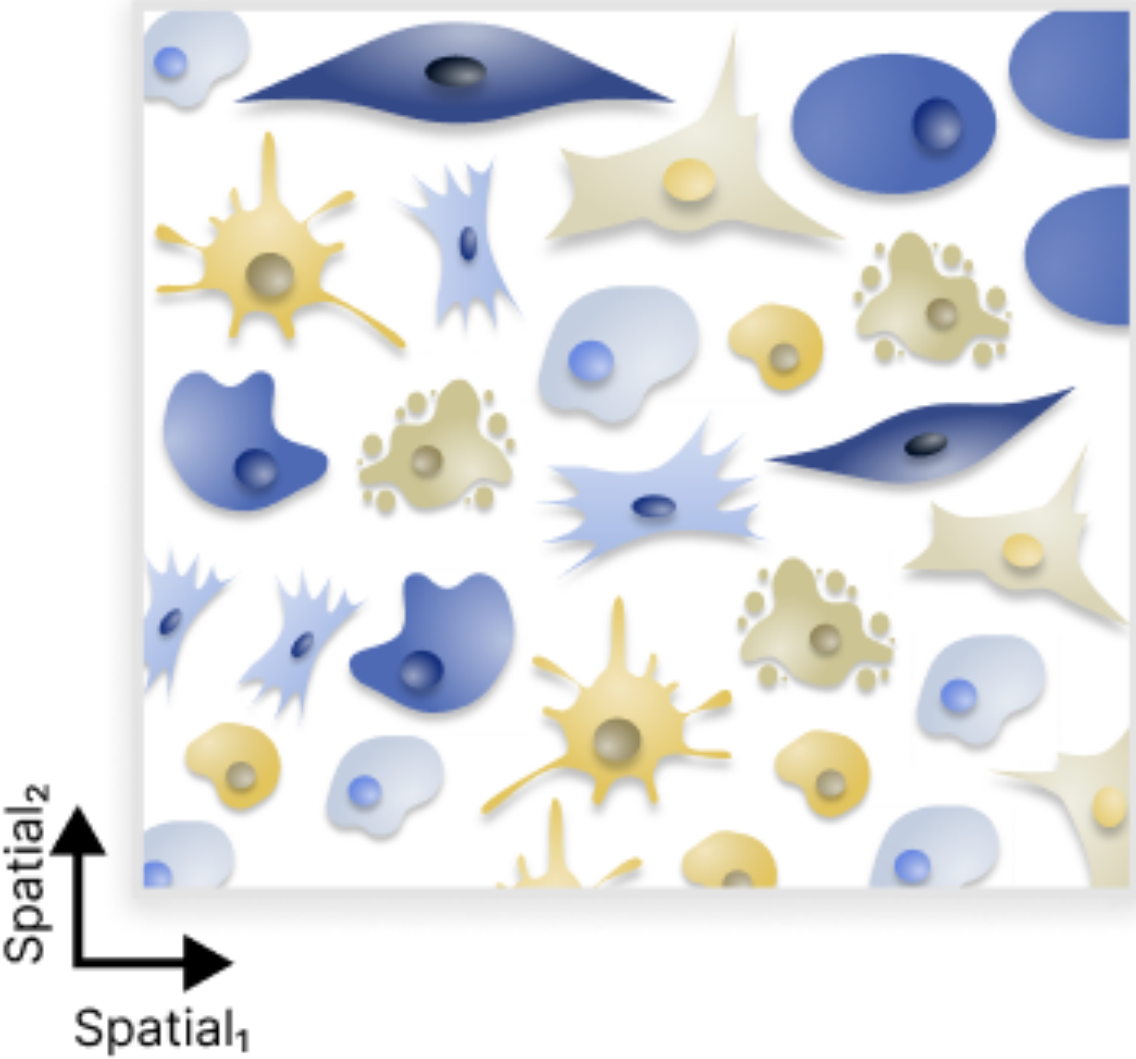
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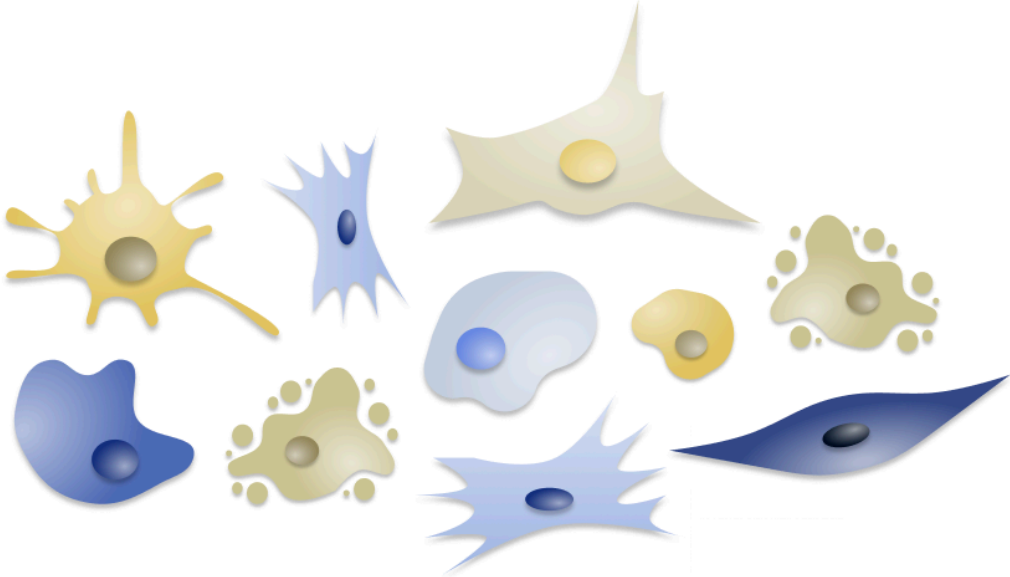
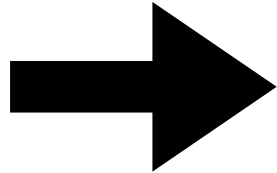


Spatial graph of cells

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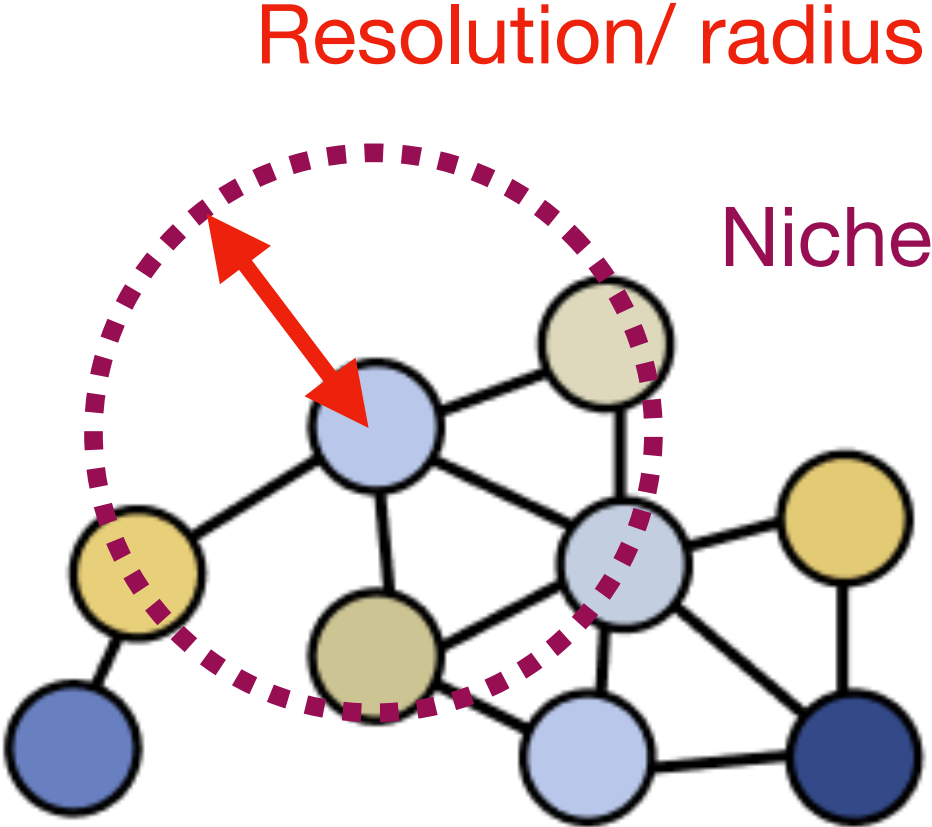
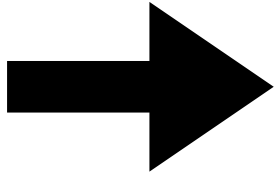


Segmented targeted spatial omics



Cells resolved at their physical location

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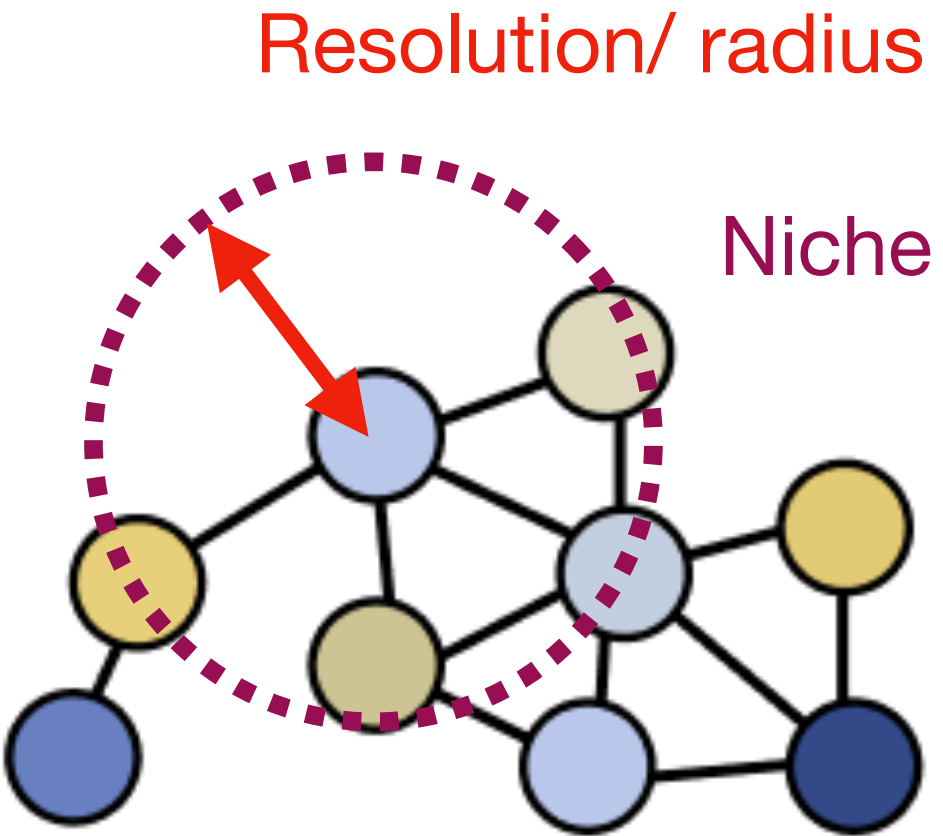
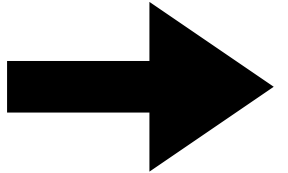
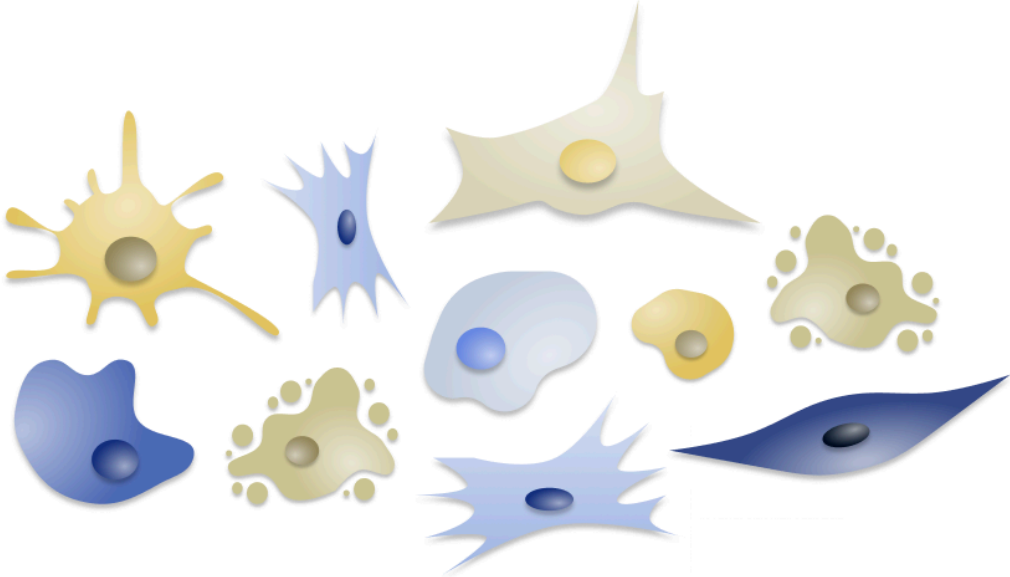
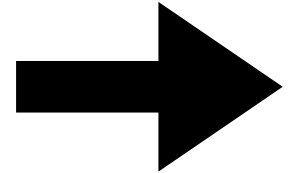
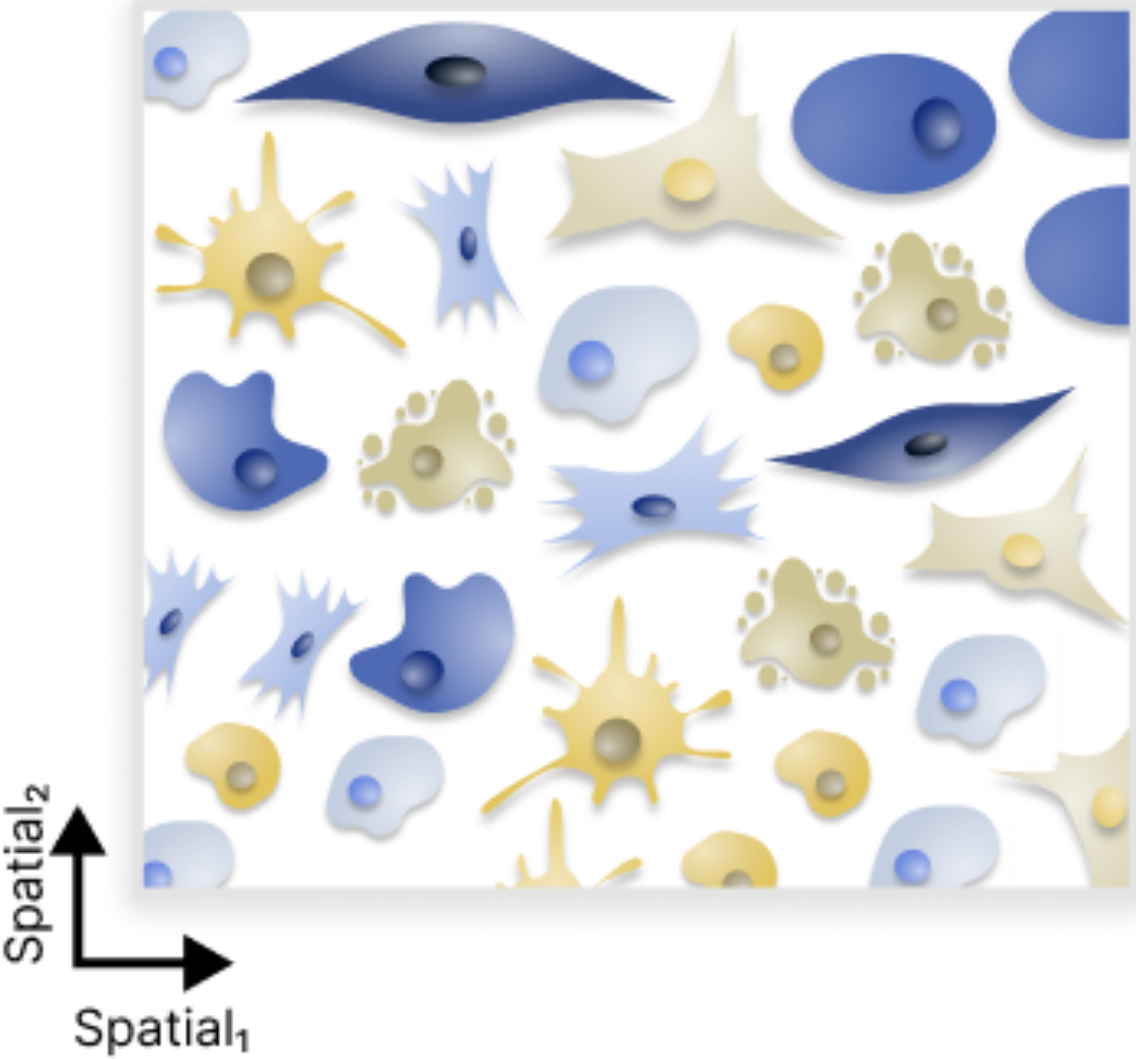


Spatial graph of cells

$A \in \{0;1\}^{\{c \times c\}}$  adjacency matrix

with  $a_{ij} = 1$  if  $d(x_i, x_j) \leq r$  with  $d$  being the euclidean distance between two cells in the slide

# Defining spatial graphs of cells based on spatial proximity

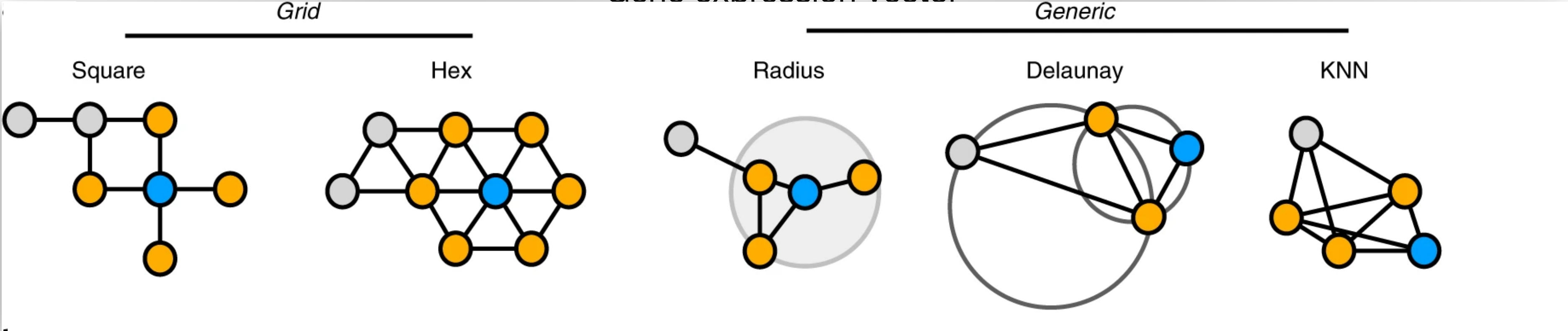


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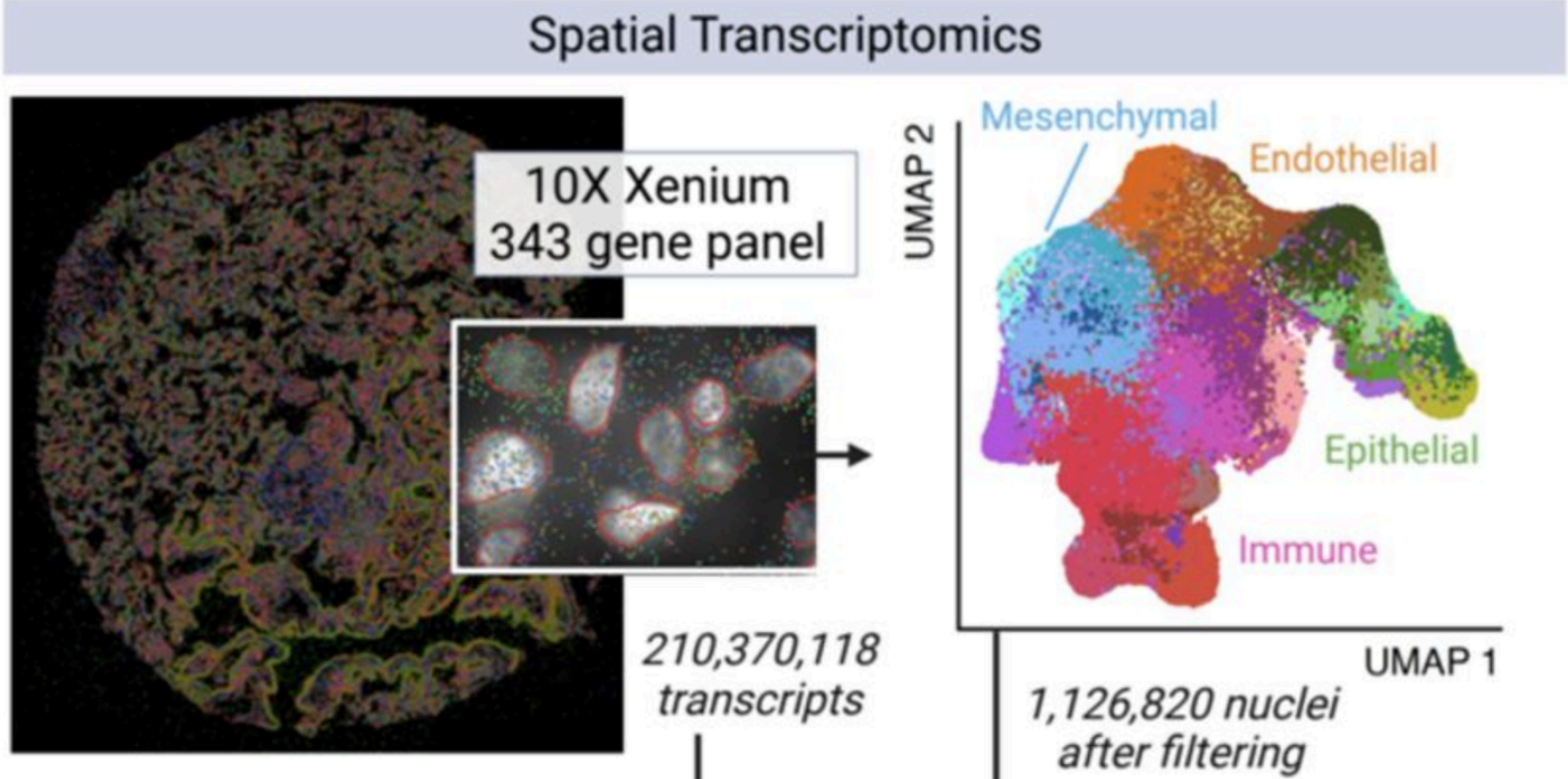
Segmented targeted spatial omics

Spatial graph of cells



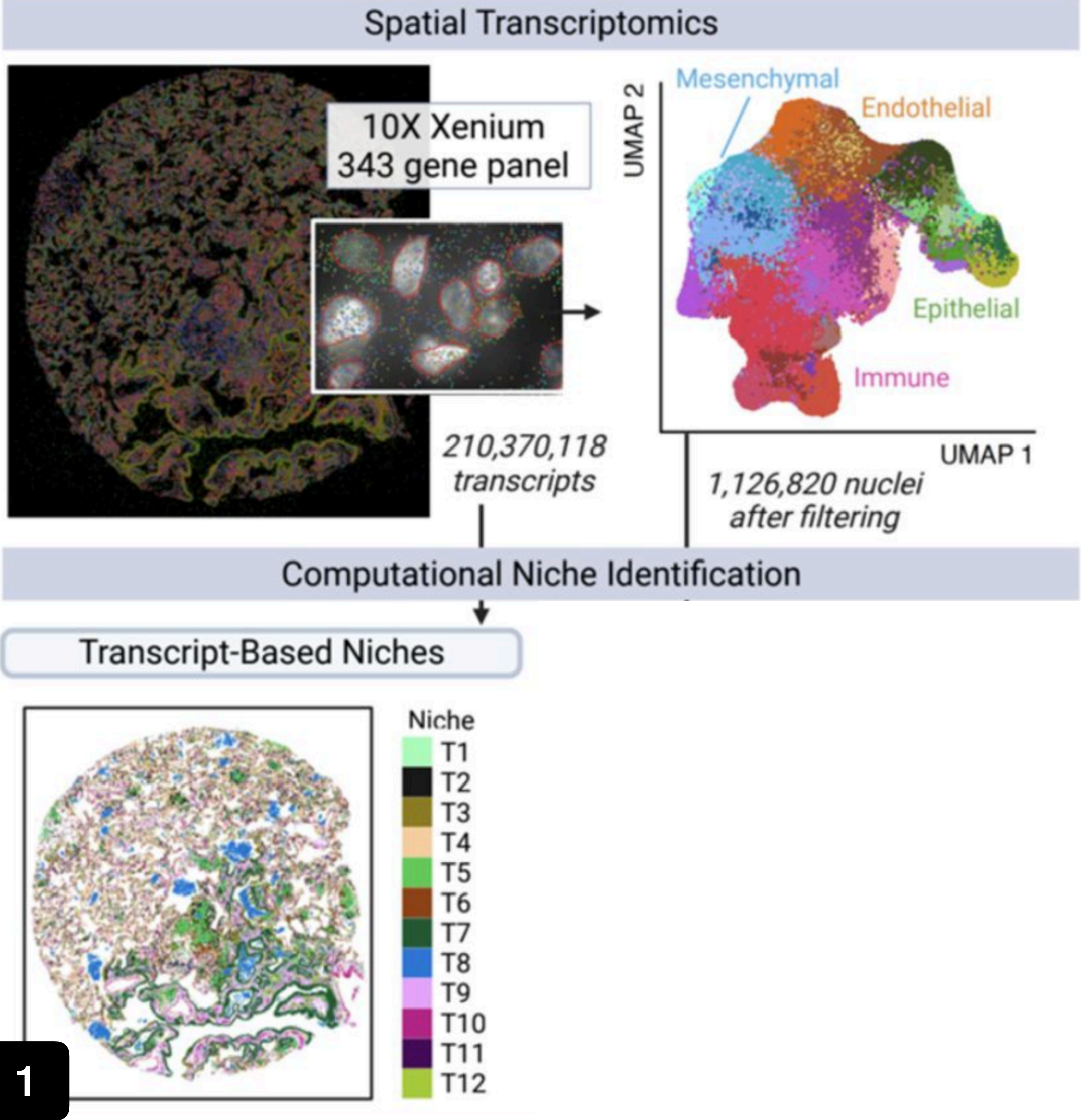
Adjacency matrix  
 $d(i, j) \leq r$  with  $d$  being  
 distance between two

# How to define niche labels in practice?



Vannan, A., *et al.* Image-based spatial transcriptomics identifies molecular niche dysregulation associated with distal lung remodeling in pulmonary fibrosis. *bioRxiv*, (2023).

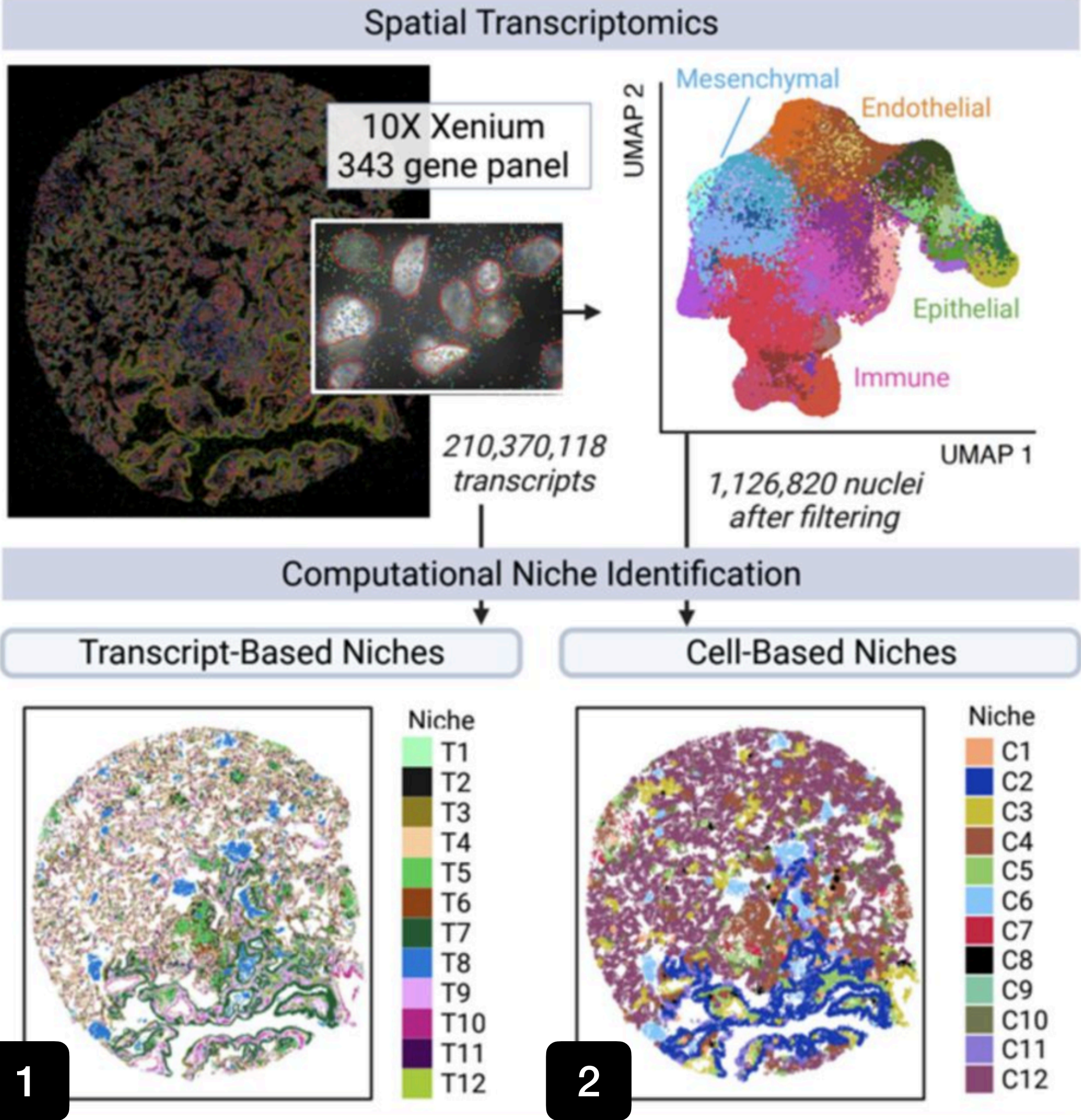
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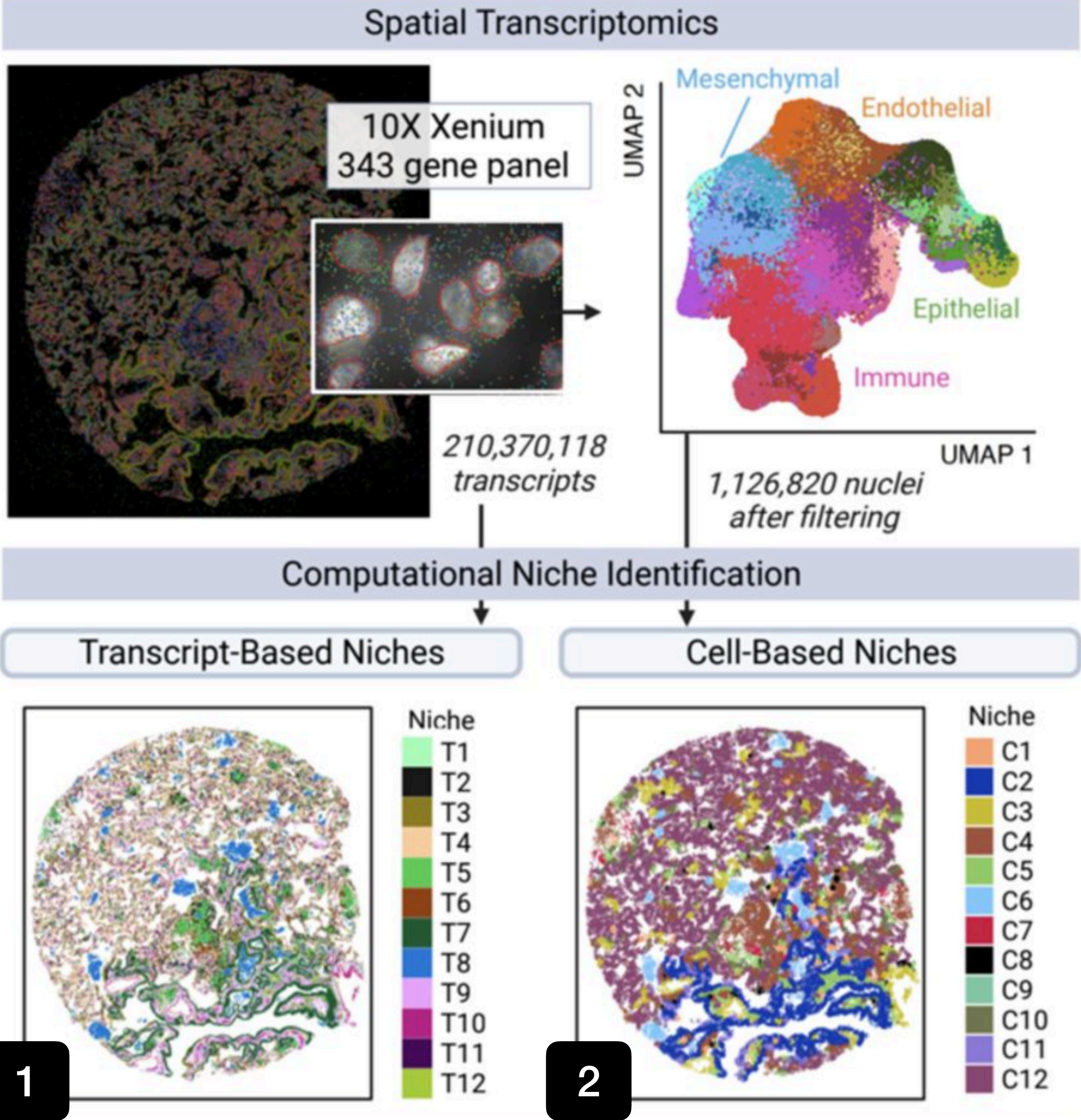


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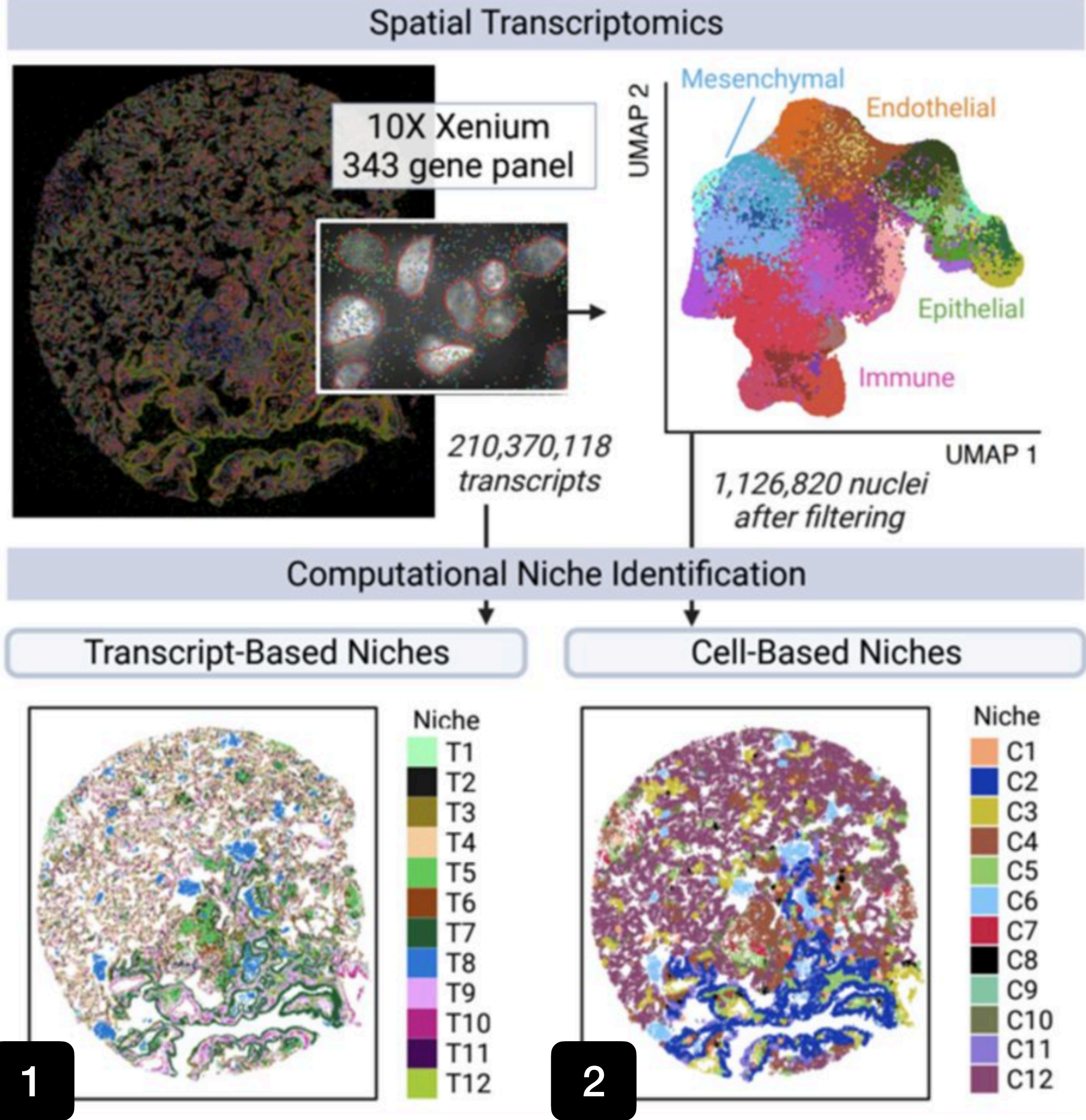
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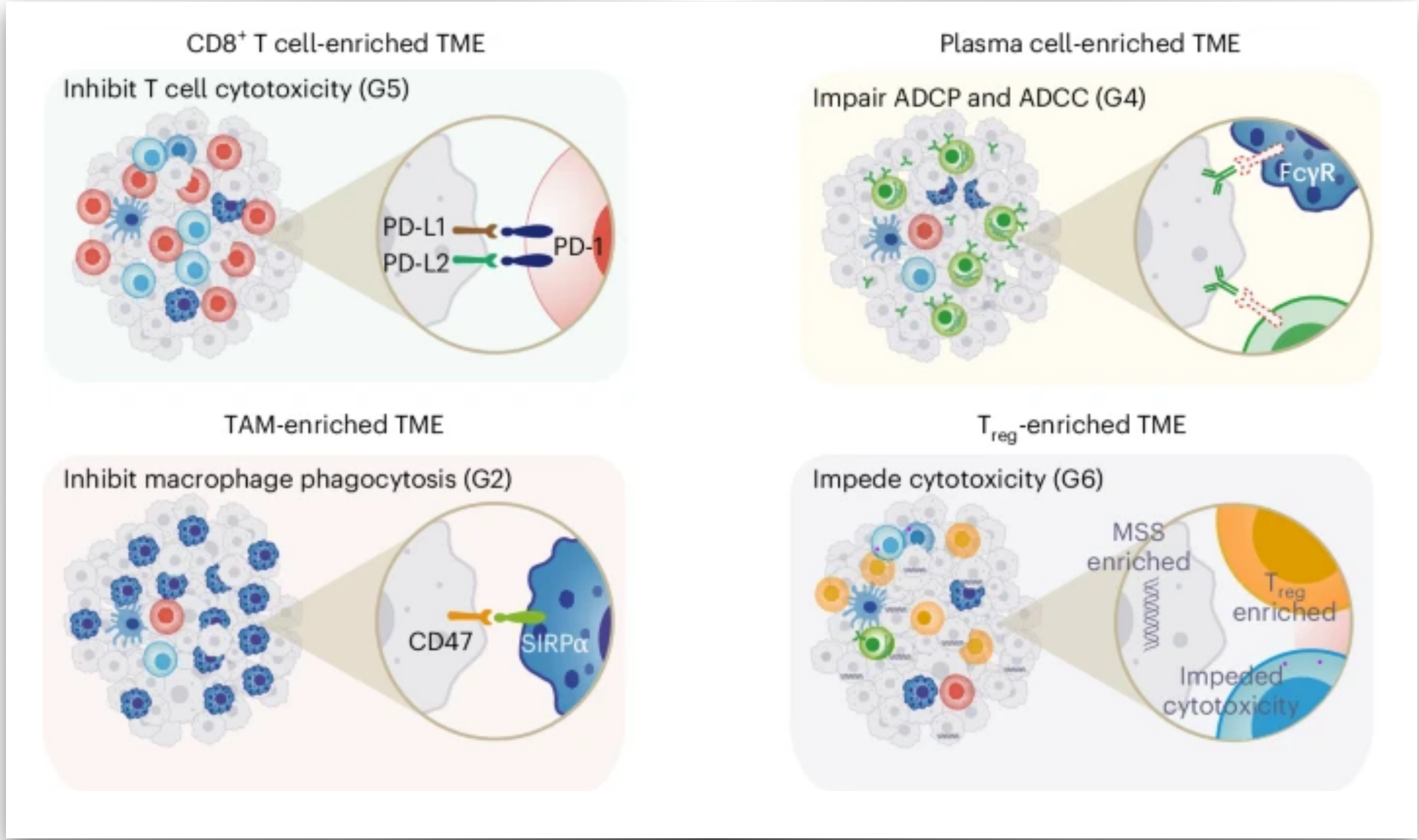
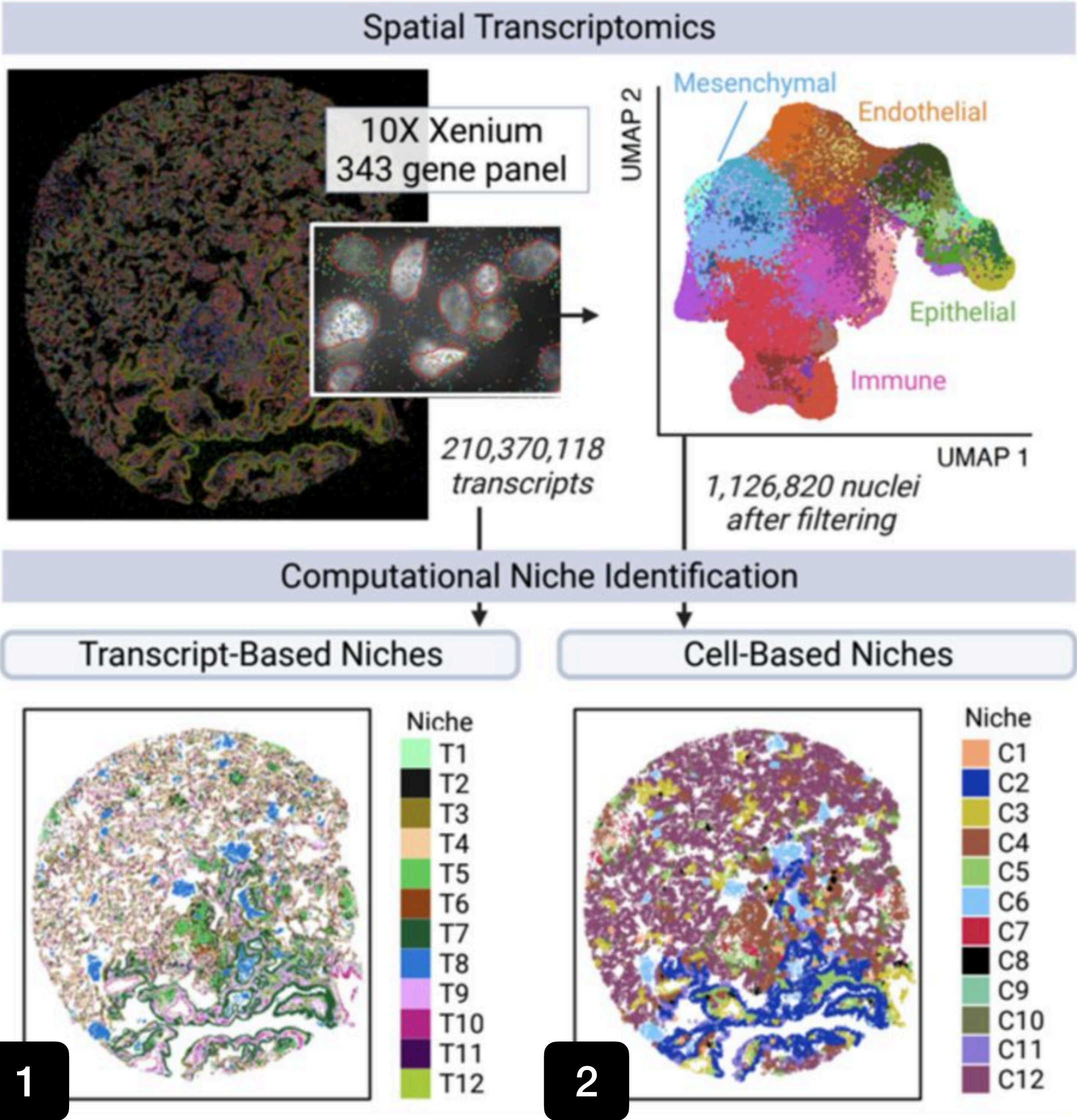


**Note:**

- Niche labels can be very tissue dependent
- Niche labels strongly depend on the specific use-case you are interested in
- Batch-effects might not be only technical variability, but biological differences

Vannan, A., et al. Image-based spatial transcriptomics identifies molecular niche dysregulation associated with distal lung remodeling in pulmonary fibrosis. *bioRxiv*, (2023).

# How to define niche labels in practice?



Chu, X., et al. Integrative single-cell analysis of human colorectal cancer reveals patient stratification with distinct immune evasion mechanisms. *Nat Cancer* 5, (2024).

3

**Communication-based Niches**

Vannan, A., et al. *bioRxiv*, (2023).

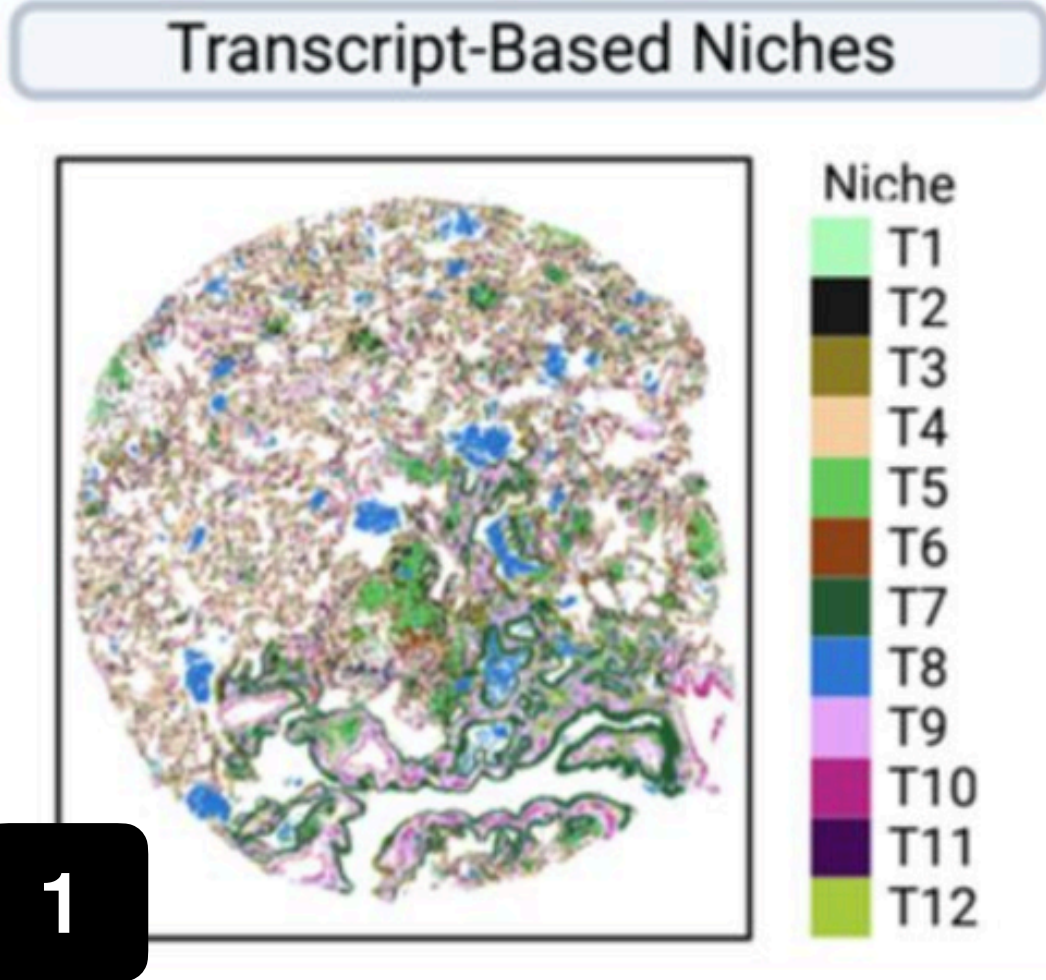
# Transcription-based niches

i.e. define a niche based on the expression profile of its surrounding neighbours

$A \in \{0;1\}^{c \times c}$  adjacency matrix

$Y \in \mathbb{R}^{+,c \times g}$  gene expression matrix

with  $c$  number of cells,  
 $g$  number of genes

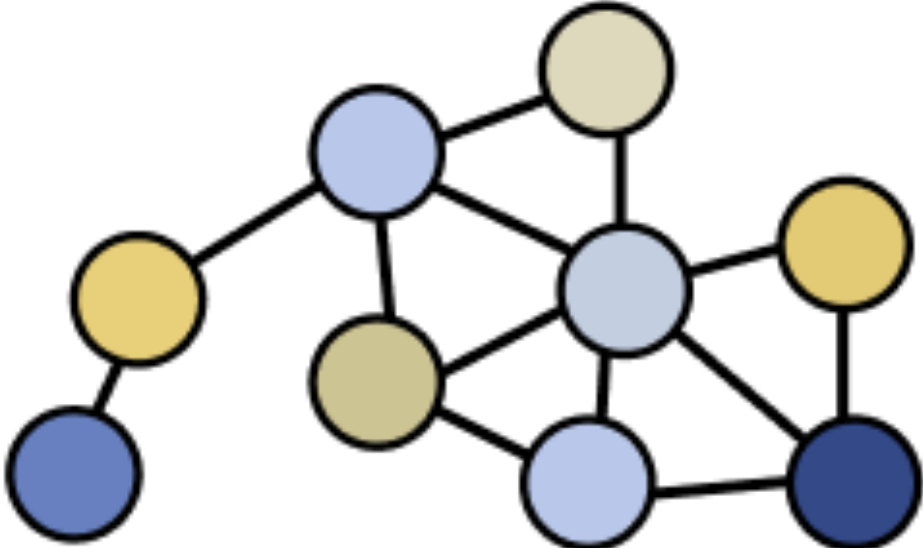


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Spatial graph of cells

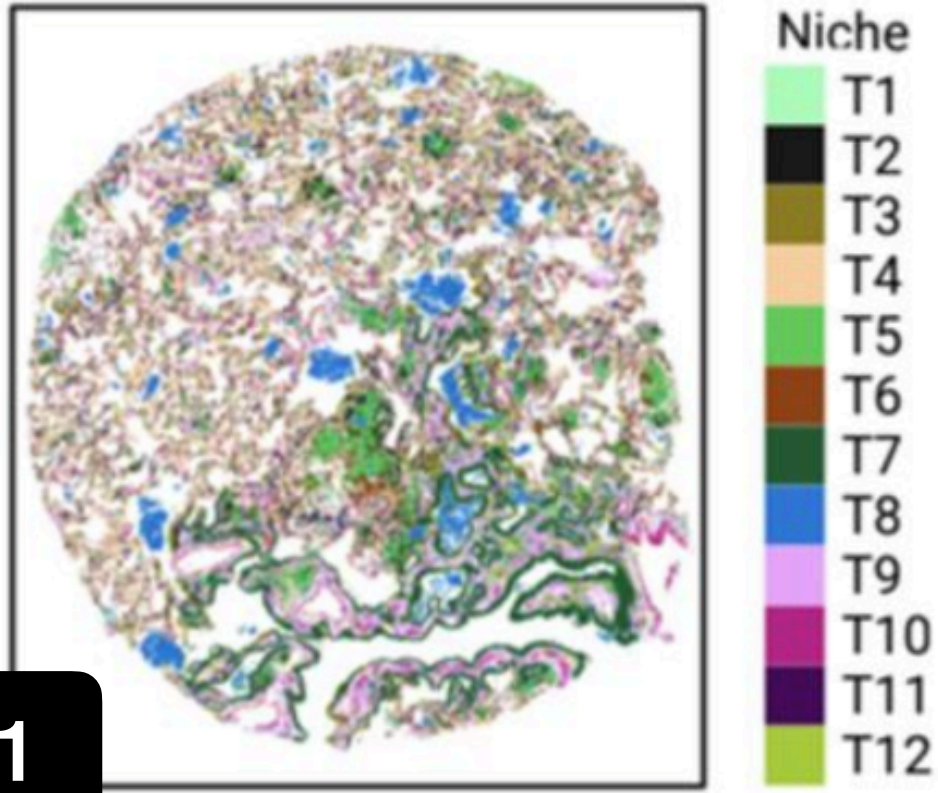


$$A \in \{0;1\}^{c \times c} \text{ adjacency matrix}$$

$$Y \in \mathbb{R}^{+, \{c \times g\}} \text{ gene expression matrix}$$

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## Transcript-Based Niches



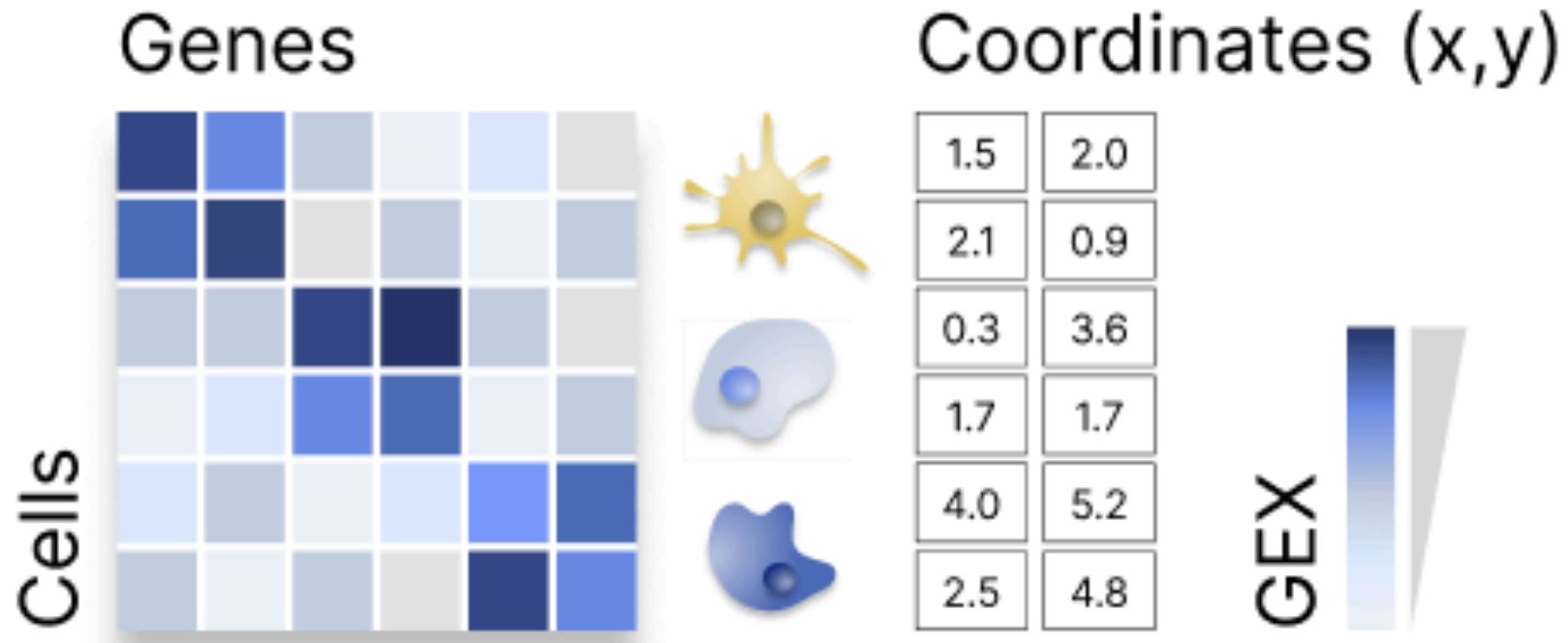
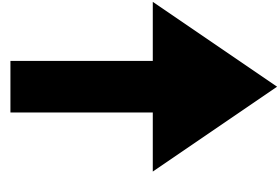
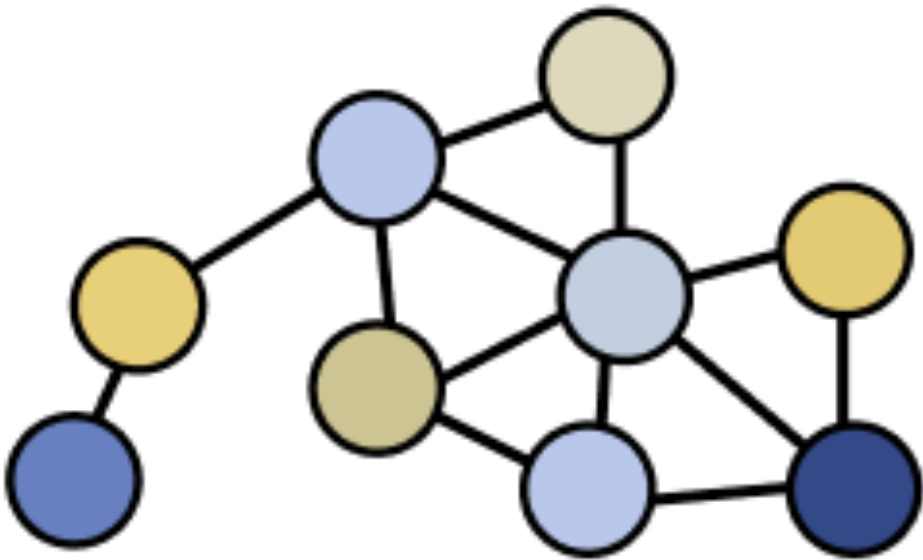
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Vannan, A., et al. *bioRxiv*, (2023).

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Spatial graph of cells

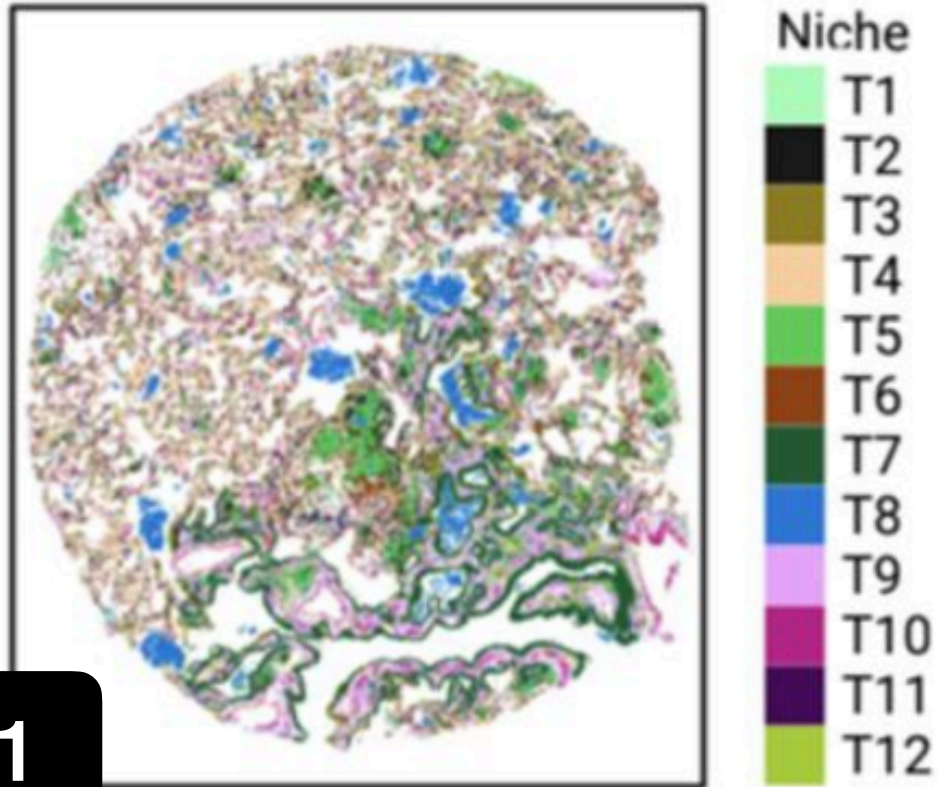


$A \in \{0;1\}^{\{c \times c\}}$  adjacency matrix

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Transcript-Based Niches

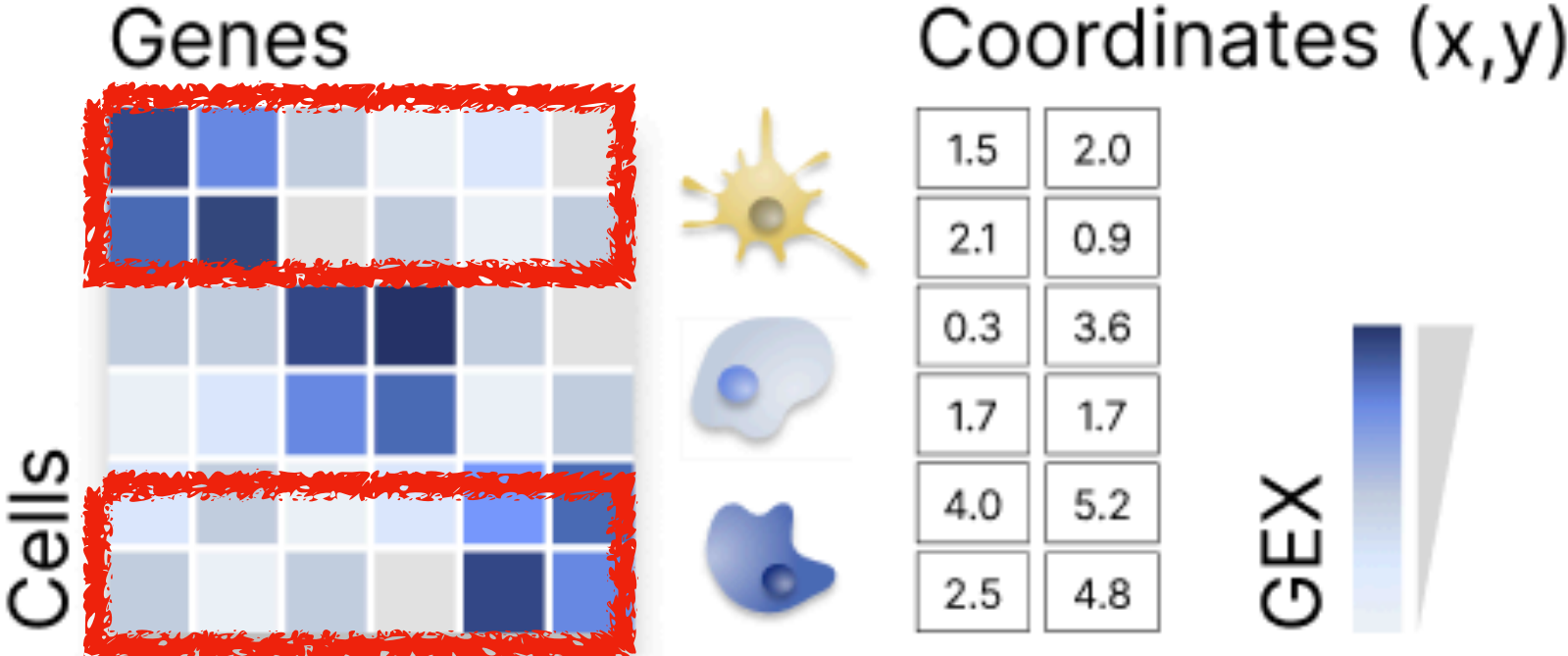
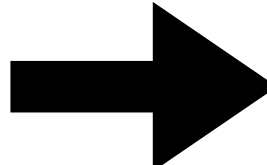
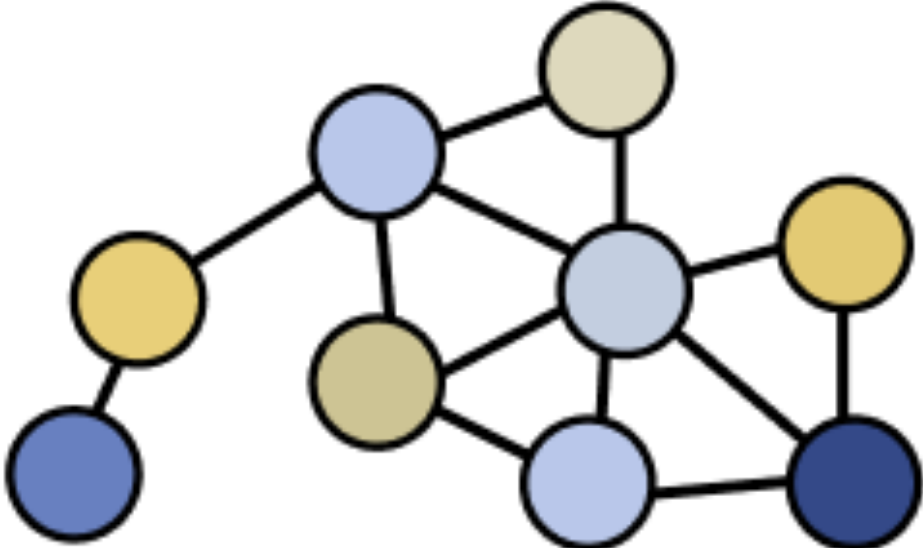


1

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Spatial graph of cells

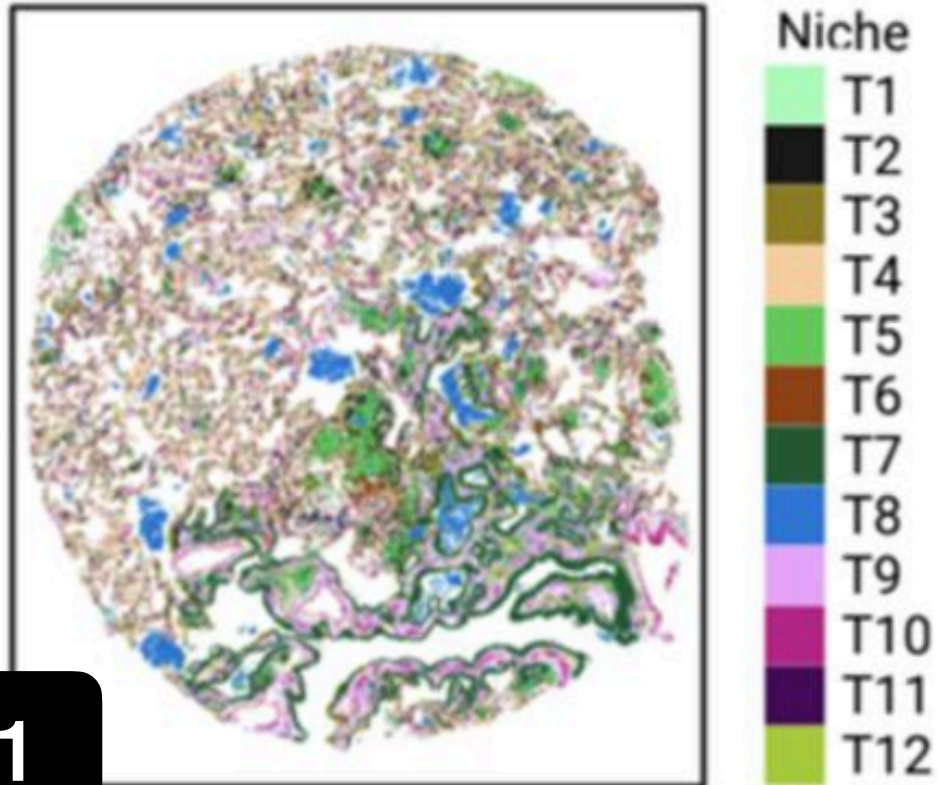


$A \in \{0;1\}^{\{c \times c\}}$  adjacency matrix

$Y \in \mathbb{R}^+_{\{c \times g\}}$  gene expression matrix

with c number of cells,  
g number of genes

Transcript-Based Niches



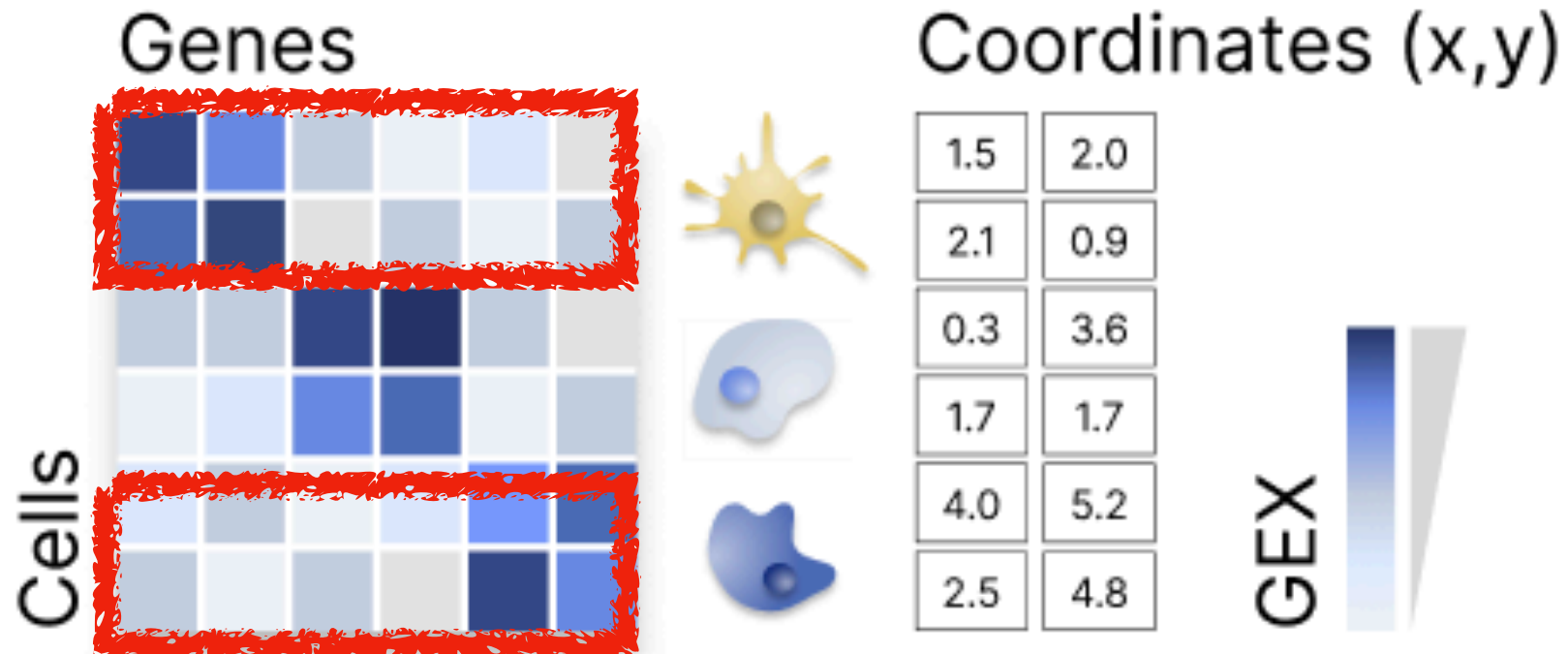
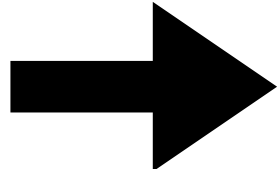
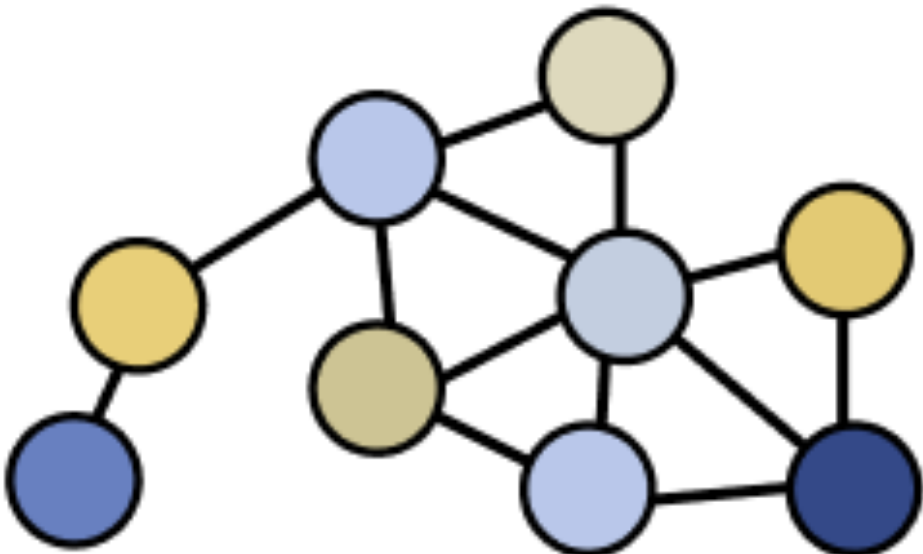
1



# Transcription-based niches

i.e. define a niche based on the expression profile of its surrounding neighbours

Spatial graph of cells



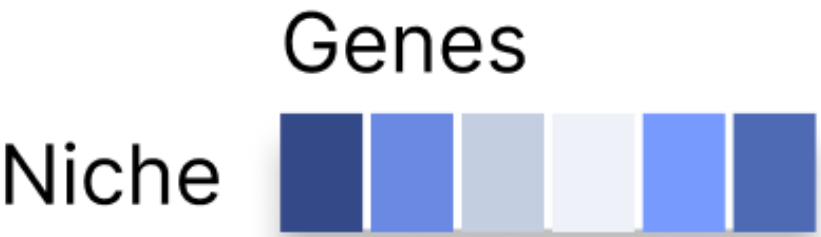
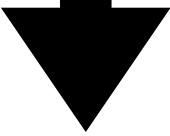
$A \in \{0;1\}^{\{c \times c\}}$  adjacency matrix

$Y \in \mathbb{R}^+_{\{c \times g\}}$  gene expression matrix

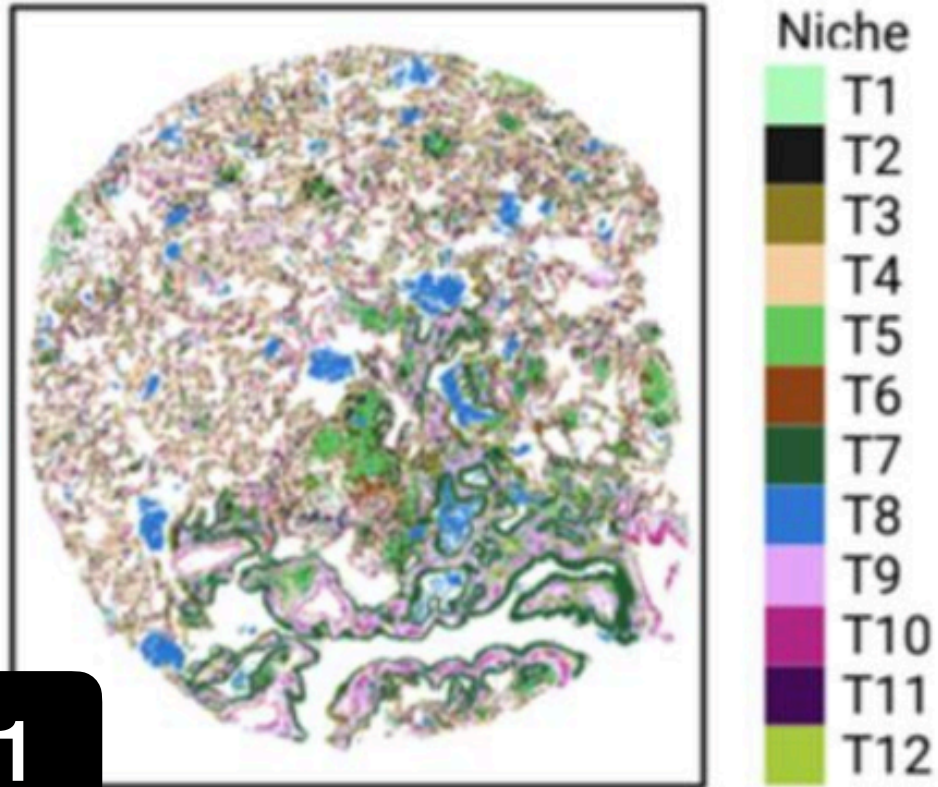
with  $c$  number of cells,  
 $g$  number of genes

Aggregation function

$$f(Y, A)$$



Transcript-Based Niches

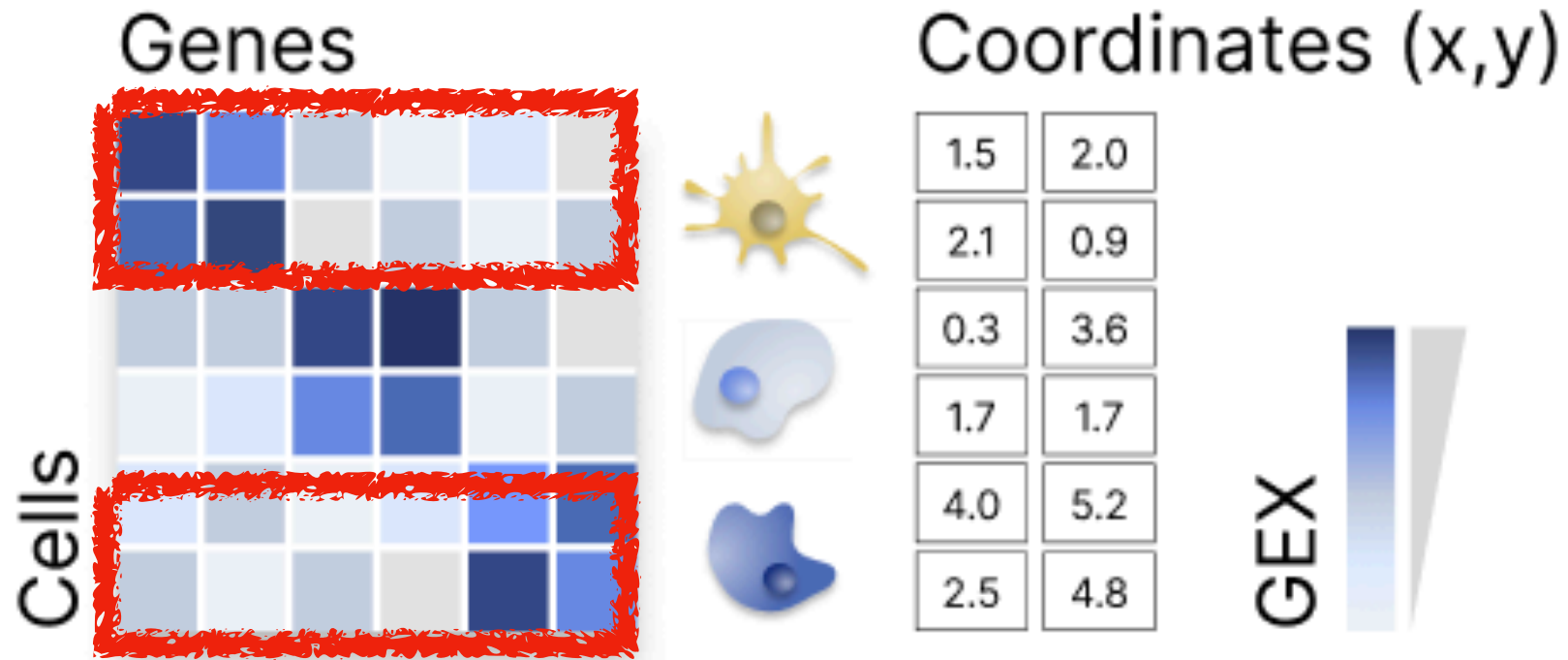
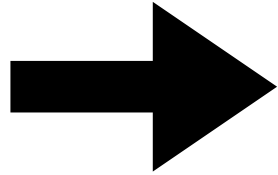
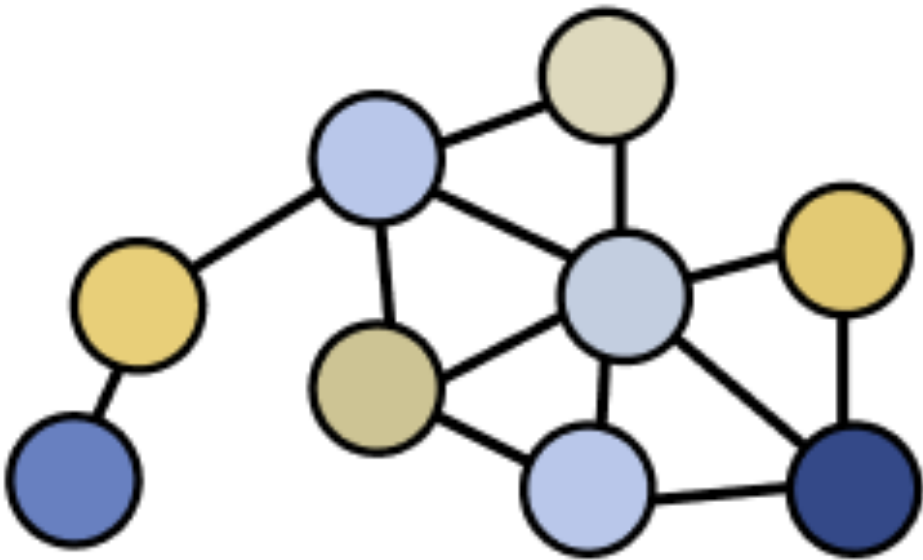


1

# Transcription-based niches

i.e. define a niche based on the expression profile of its surrounding neighbours

Spatial graph of cells



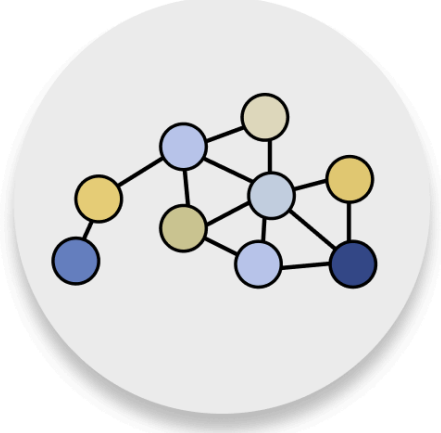
$A \in \{0;1\}^{\{c \times c\}}$  adjacency matrix

$Y \in \mathbb{R}^+_{\{c \times g\}}$  gene expression matrix

with  $c$  number of cells,  
 $g$  number of genes

Aggregation function

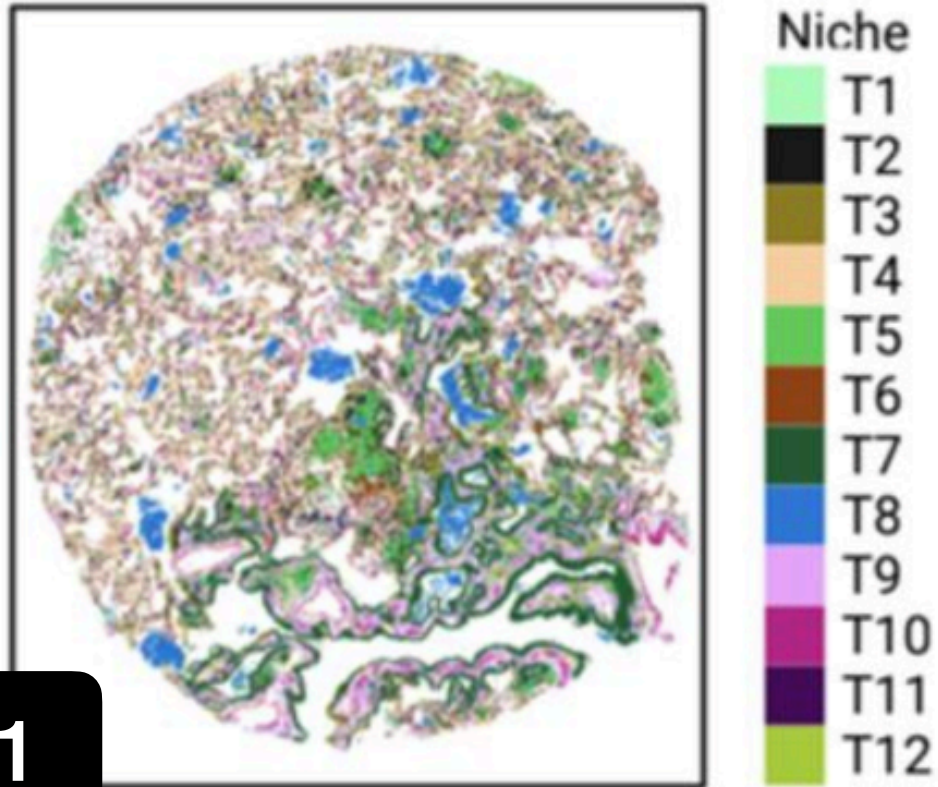
$$f(Y, A)$$



Trivial example:  
pseudo Visium spots

$$\sum Y \cdot A$$

Transcript-Based Niches

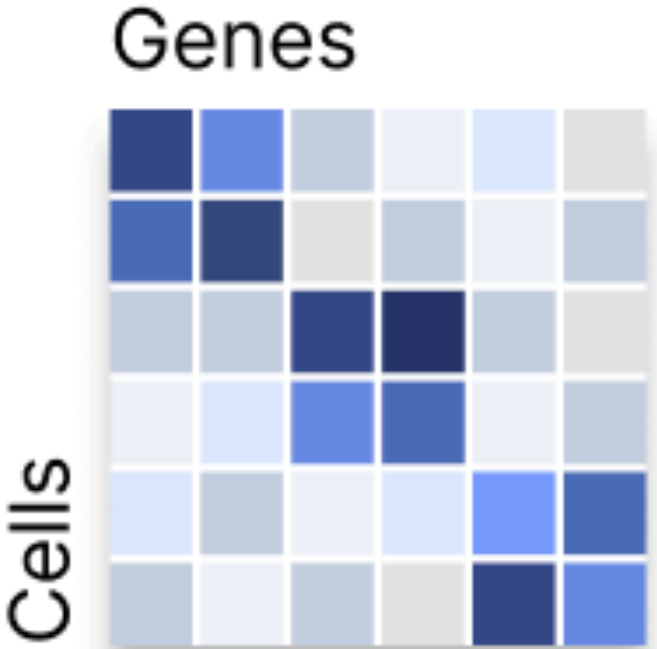
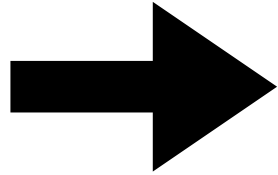
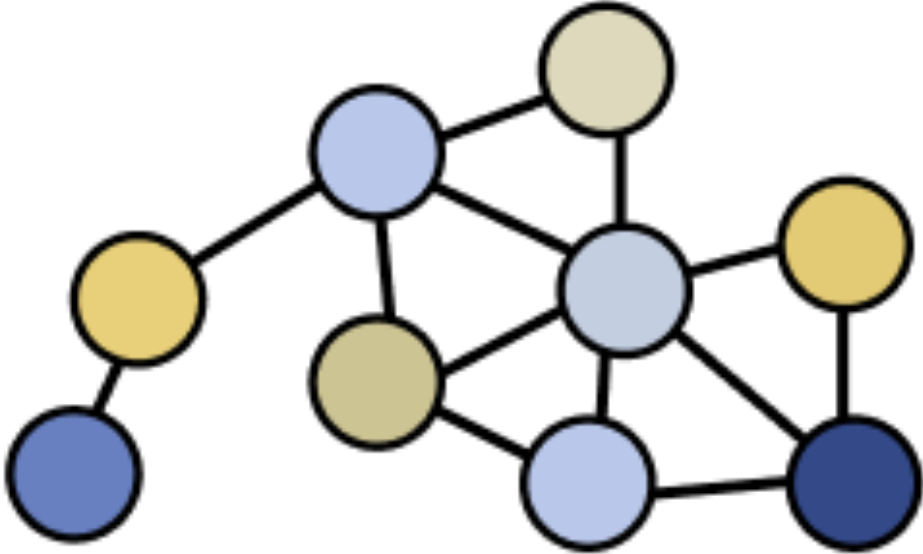


1

# Transcription-based niches

i.e. define a niche based on the expression profile of its surrounding neighbours

Spatial graph of cells



Coordinates (x,y)

$A \in \{0;1\}^{c \times c}$  adjacency matrix

Article | [Open access](#) | Published: 27 February 2024

**BANKSY unifies cell typing and tissue domain segmentation for scalable spatial omics data analysis**

Vipul Singhal, Nigel Chou, Joseph Lee, Yifei Yue, Jinyue Liu, Wan Kee Chock, Li Lin, Yun-Ching Chang, Erica Mei Ling Teo, Jonathan Aow, Hwee Kuan Lee, Kok Hao Chen & Shyam Prabhakar

*Nature Genetics* 56, 431–441 (2024) | [Cite this article](#)

Aggreg

For each gene  $q$ , we computed the mean expression in the neighborhood of cell  $u \in \mathcal{U}$  as:

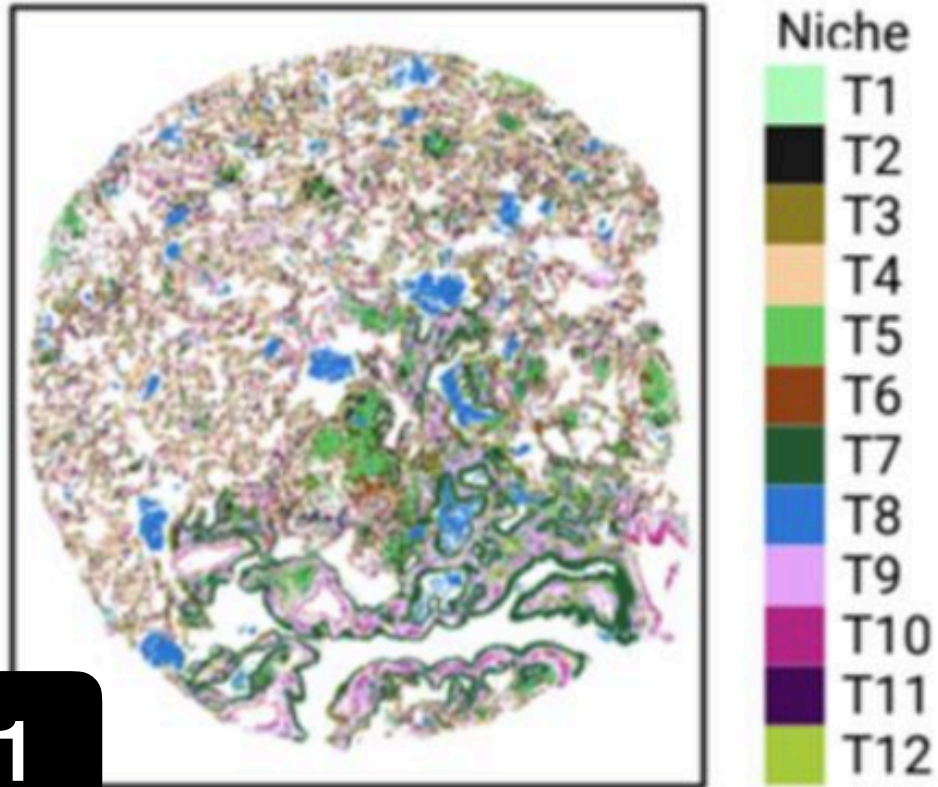
$$M_u^{(q)} = \sum_{v \in \eta_{k_{\text{geom}}}^u} g_v^{(q)} \Gamma_{uv}^{k_{\text{geom}}}$$

where  $g_v^{(q)}$  is the expression of the  $q$ th gene in neighboring cell  $v$  and the term  $\Gamma_{uv}^{k_{\text{geom}}}$  is a Gaussian weighting envelope defined as:

$$\Gamma_{uv}^{k_{\text{geom}}} = \frac{\exp \frac{-r_{uv}^2}{r_{uv}^2}}{\sum_{w \in \eta_{k_{\text{geom}}}^u} \left( \exp \frac{-r_{uw}^2}{r_{uw}^2} \right)}$$



Transcript-Based Niches



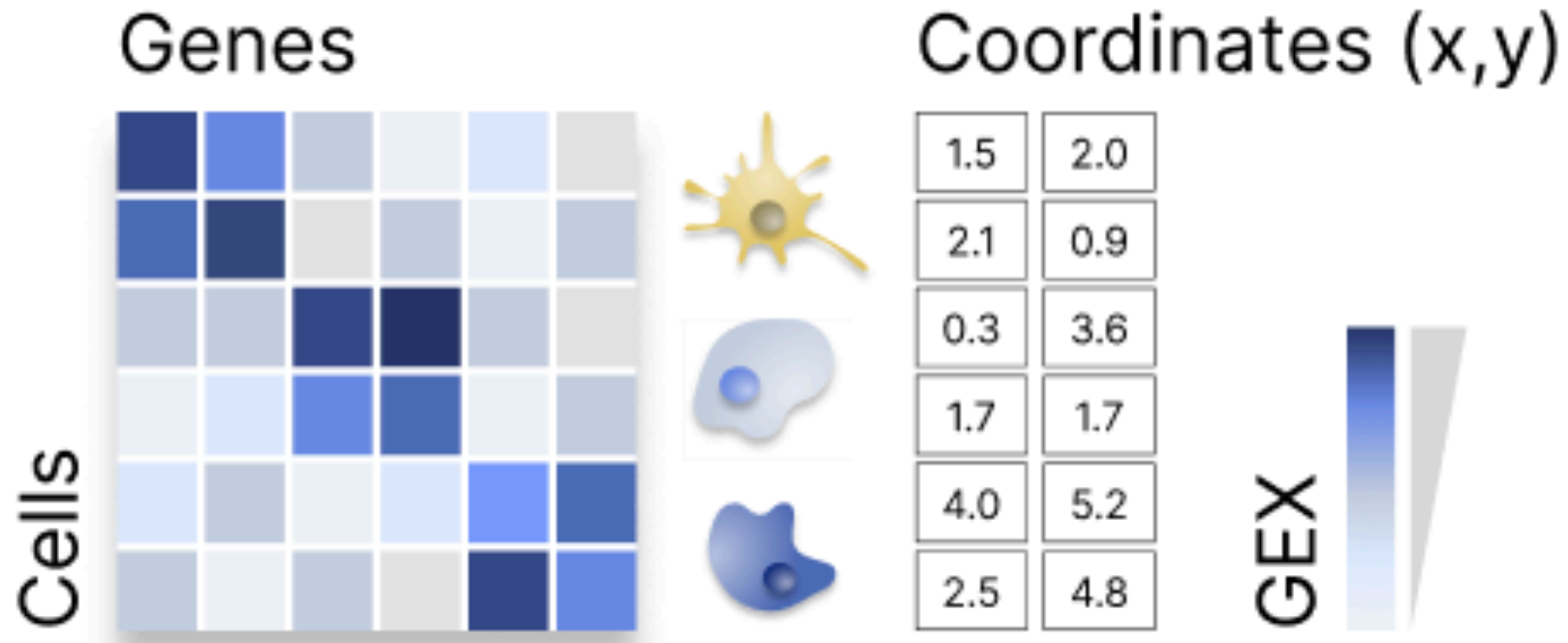
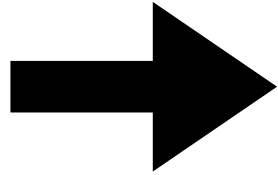
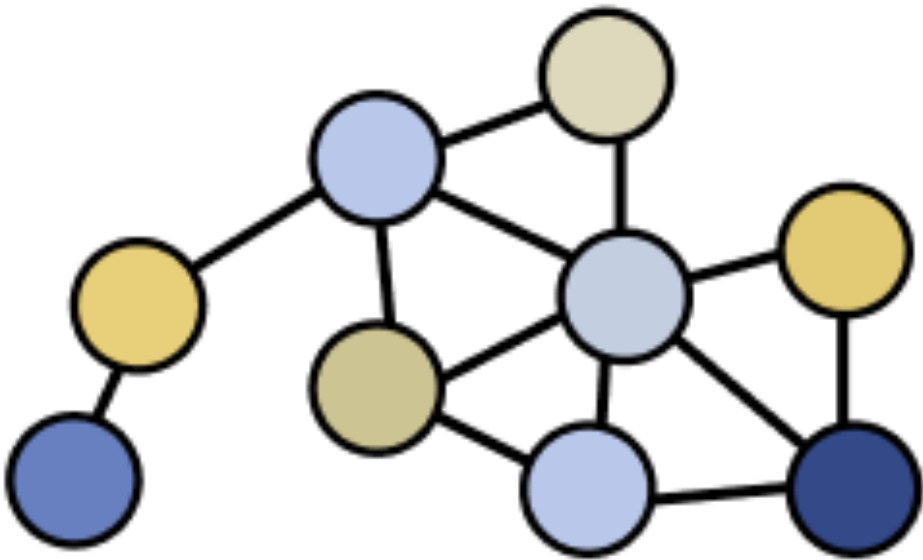
1

Vannan, A., et al. *bioRxiv*, (2023).

# Transcription-based niches

i.e. define a niche based on the expression profile of its surrounding neighbours

Spatial graph of cells



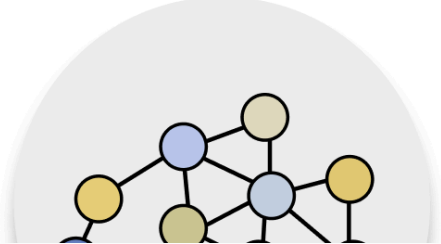
$A \in \{0;1\}^{\{c \times c\}}$  adjacency matrix

$Y \in \mathbb{R}^+_{\{c \times g\}}$  gene expression matrix

with  $c$  number of cells,  
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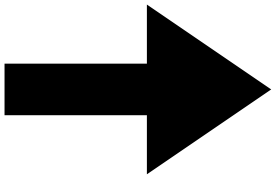
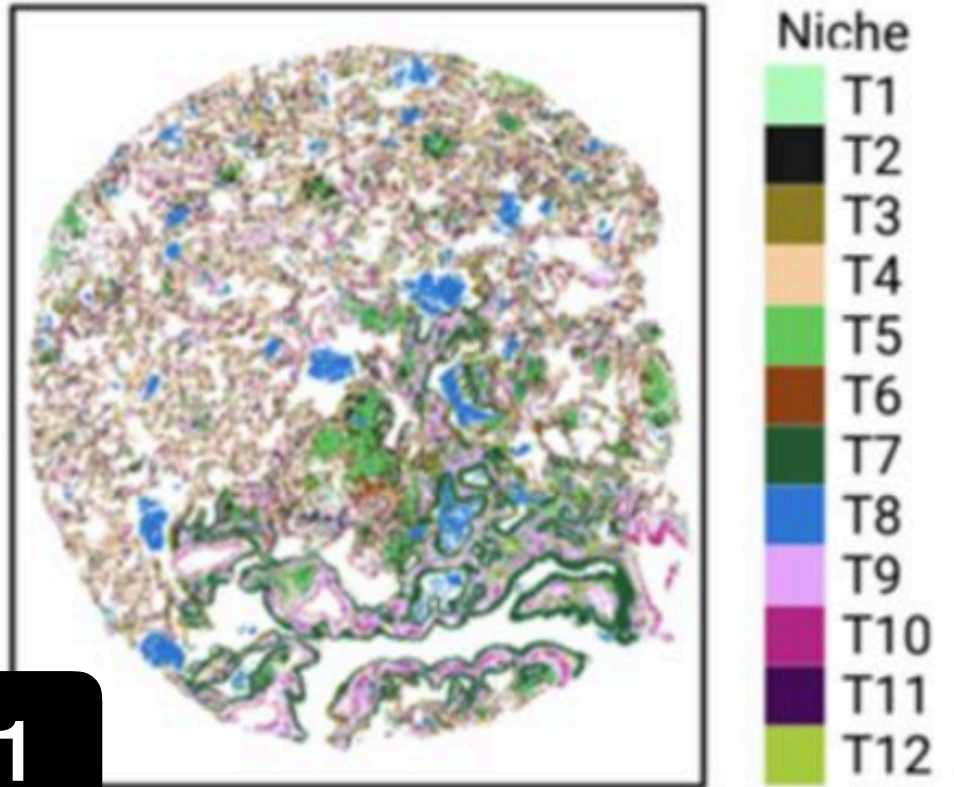
Aggregation function

$$f(Y, A)$$



Trivial example:  
pseudo Visium  $\sum_i Y \cdot A$

Transcript-Based Niches



```
import scanpy as sc

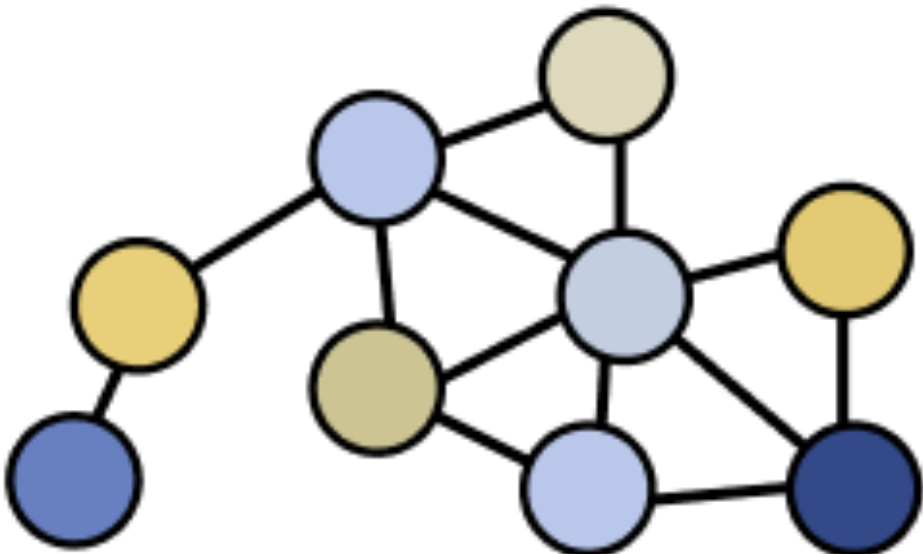
sc.pp.neighbors(adata, use_rep="X_niche",
                key_added="niche_connectivities")
sc.tl.leiden(adata,
             adjacency="niche_connectivities")
```

1

# Cell-based niches

i.e. define a niche based on the composition of neighbouring cell types

Spatial graph of cells

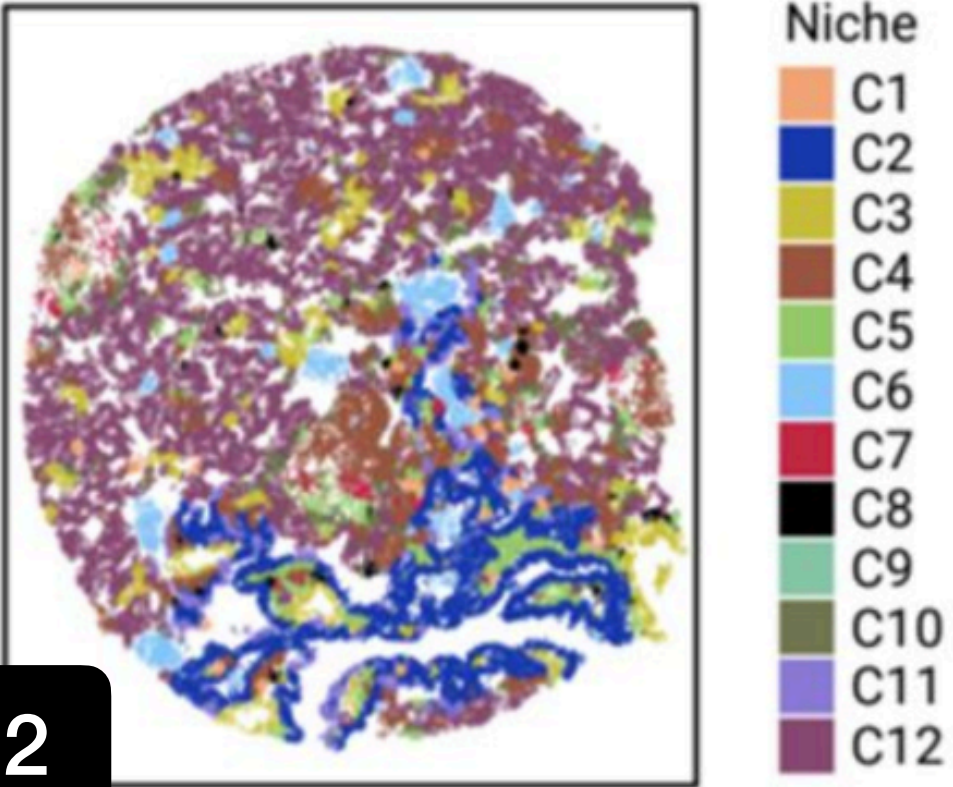


$$A \in \{0,1\}^{\{c \times c\}} \text{ adjacency matrix}$$

$$X \in \{0,1\}^{\{c \times d\}} \text{ one-hot encoded cell-type matrix}$$

with  $c$  number of cells,  
 $d$  number of cell-types

Cell-Based Niches

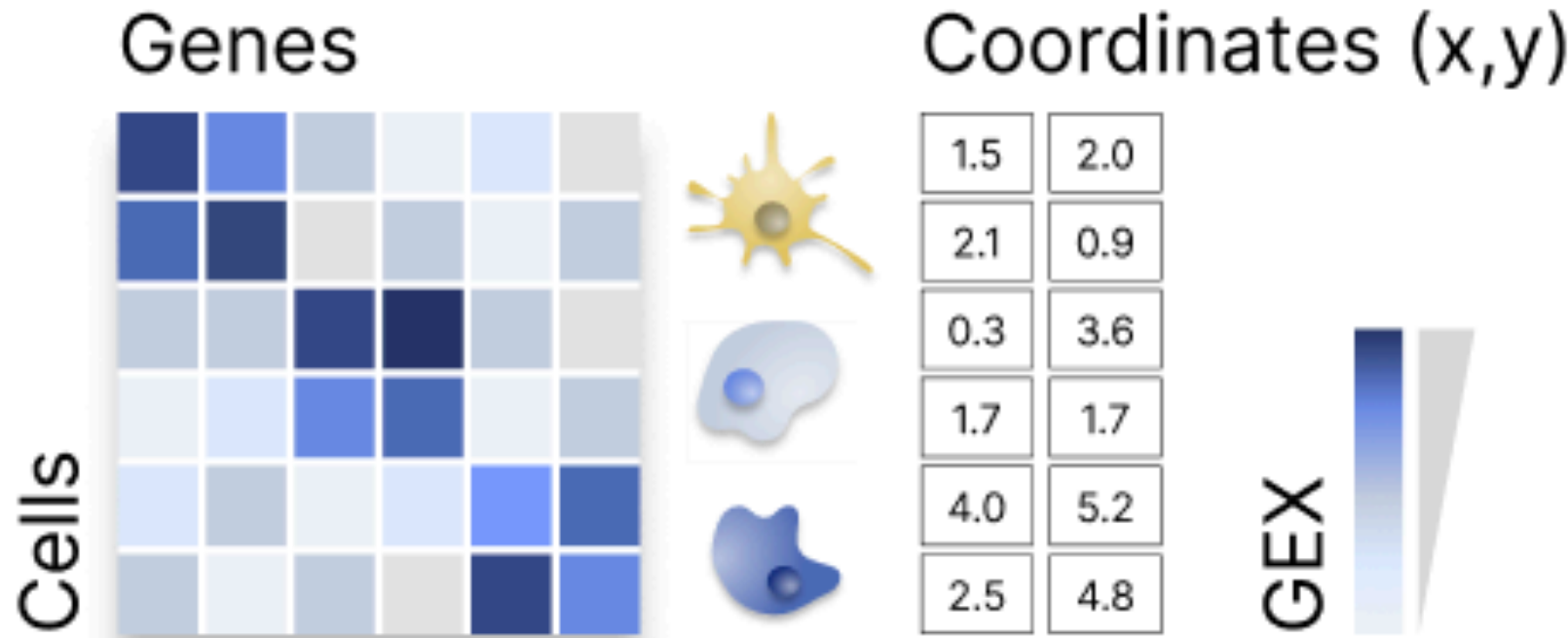
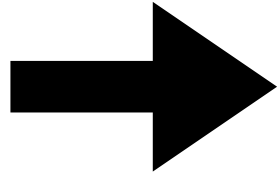
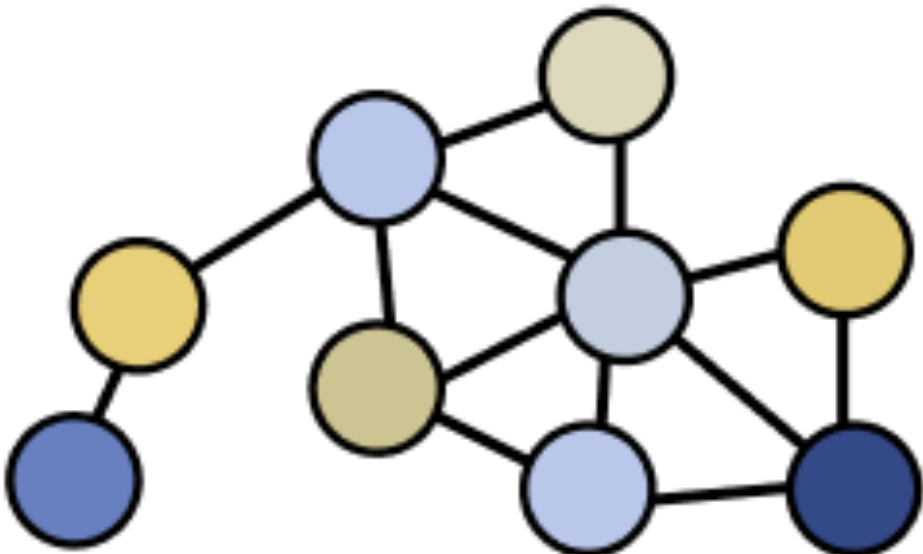


2

# Cell-based niches

i.e. define a niche based on the composition of neighbouring cell types

Spatial graph of cells

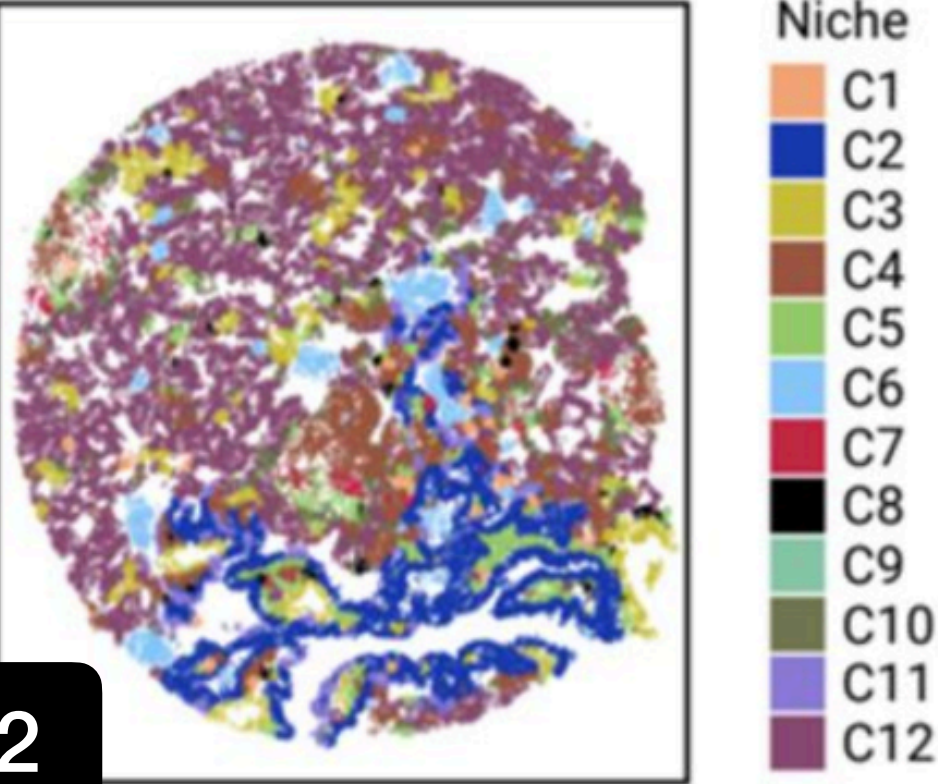


$A \in \{0,1\}^{c \times c}$  adjacency matrix

$X \in \{0,1\}^{c \times d}$  one-hot encoded cell-type matrix

with c number of cells,  
d number of cell-types

Cell-Based Niches

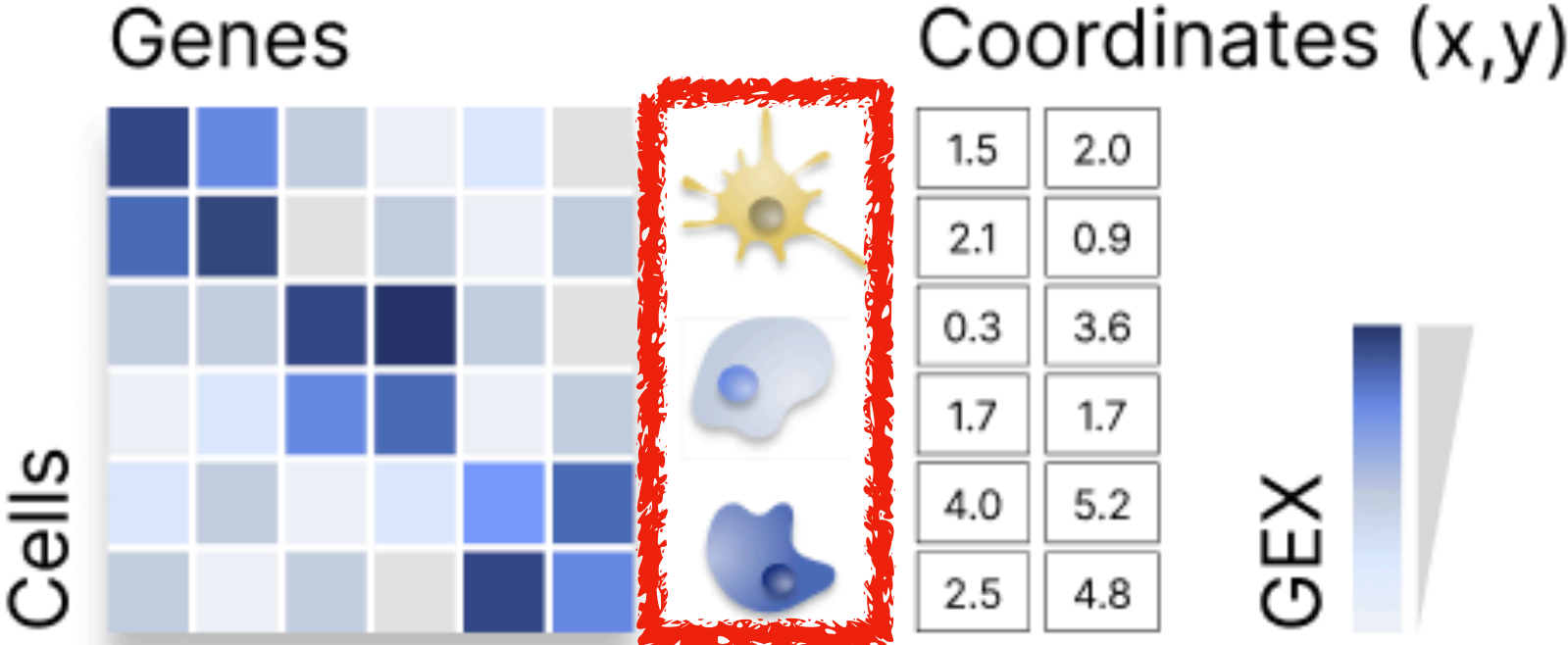
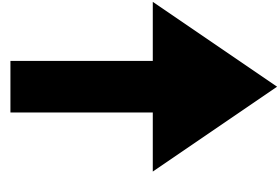
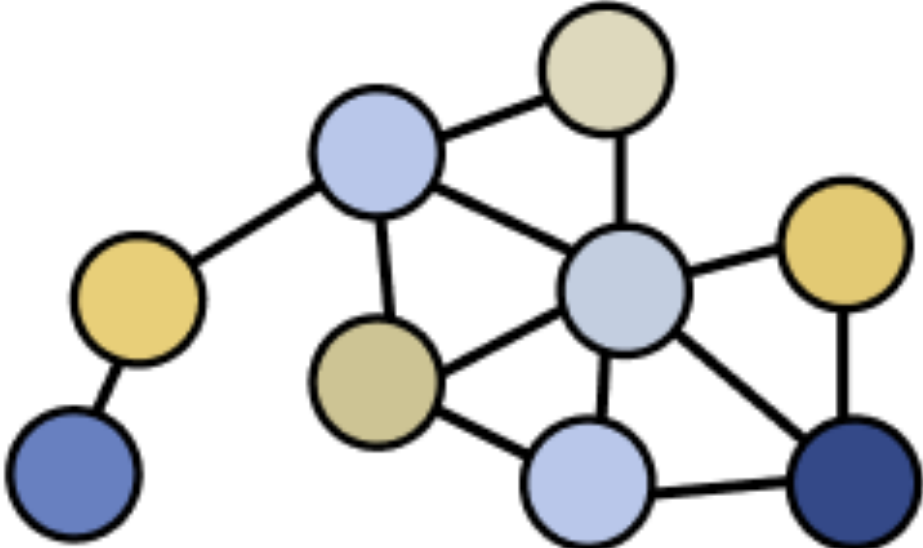


2

# Cell-based niches

i.e. define a niche based on the composition of neighbouring cell types

Spatial graph of cells

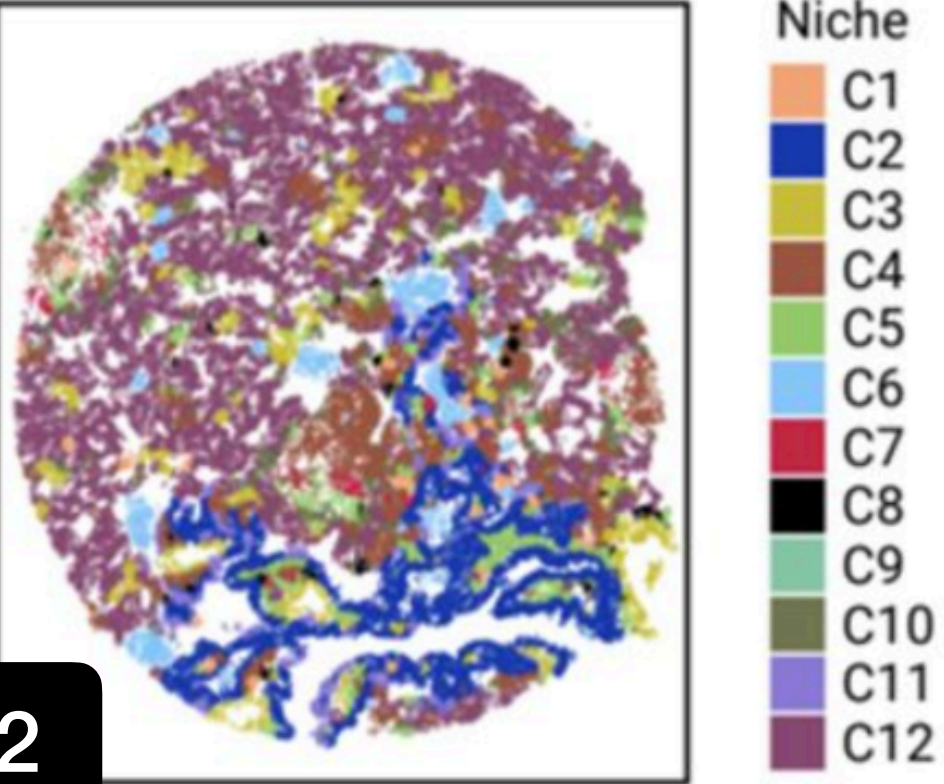


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Cell-Based Niches

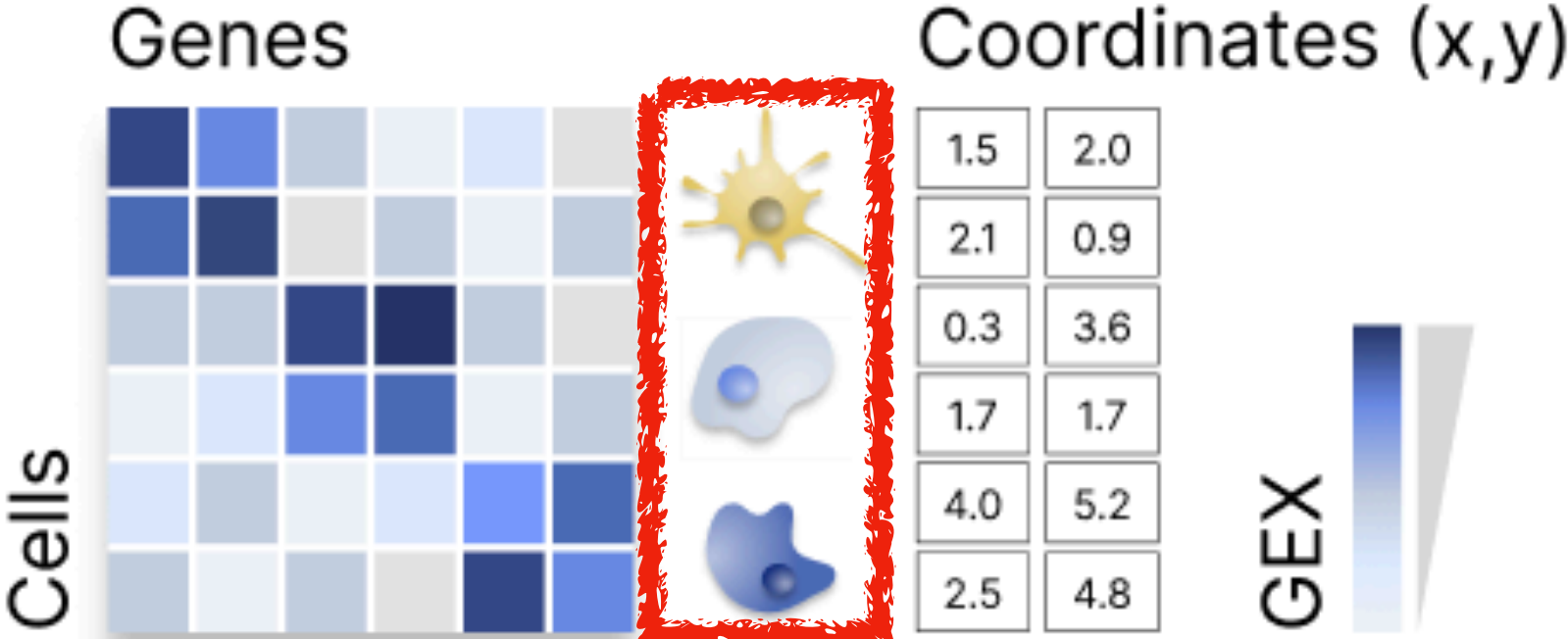
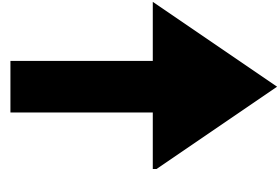
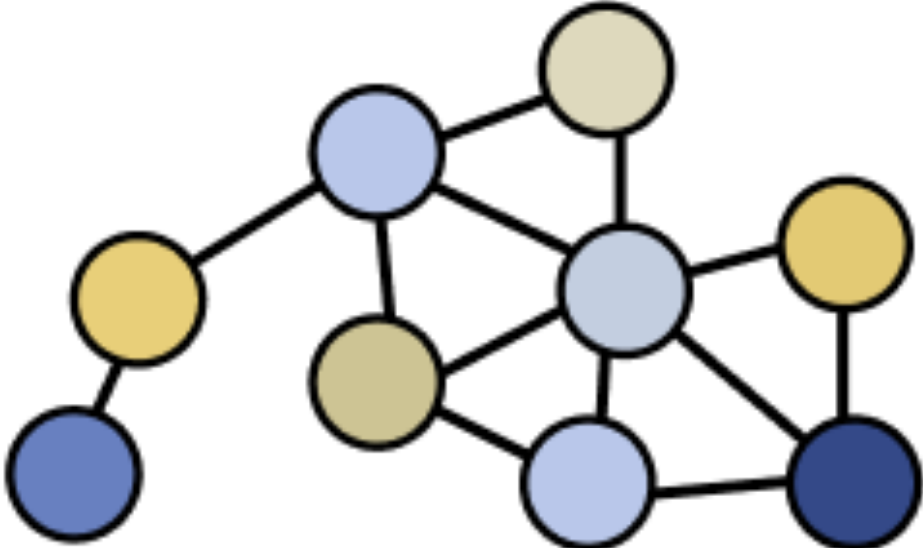


2

# Cell-based niches

i.e. define a niche based on the composition of neighbouring cell types

Spatial graph of cells



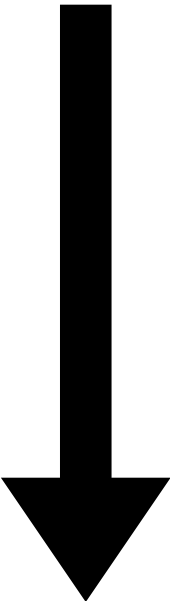
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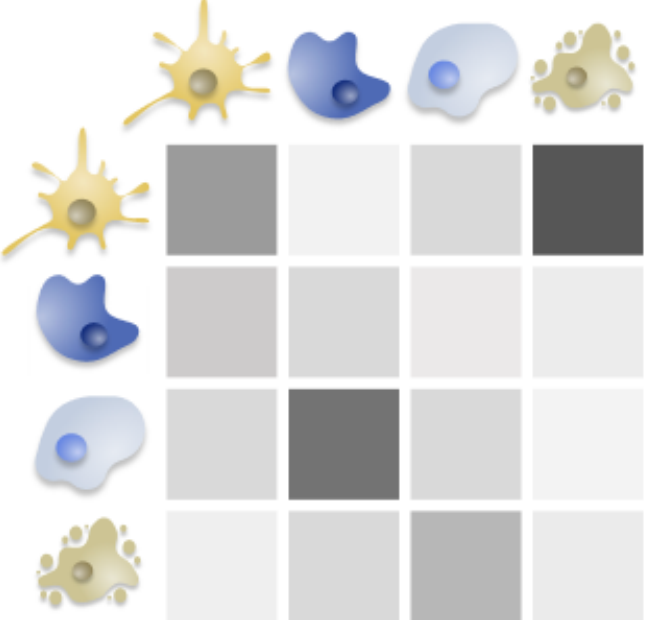
with  $c$  number of cells,  
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Aggregation function

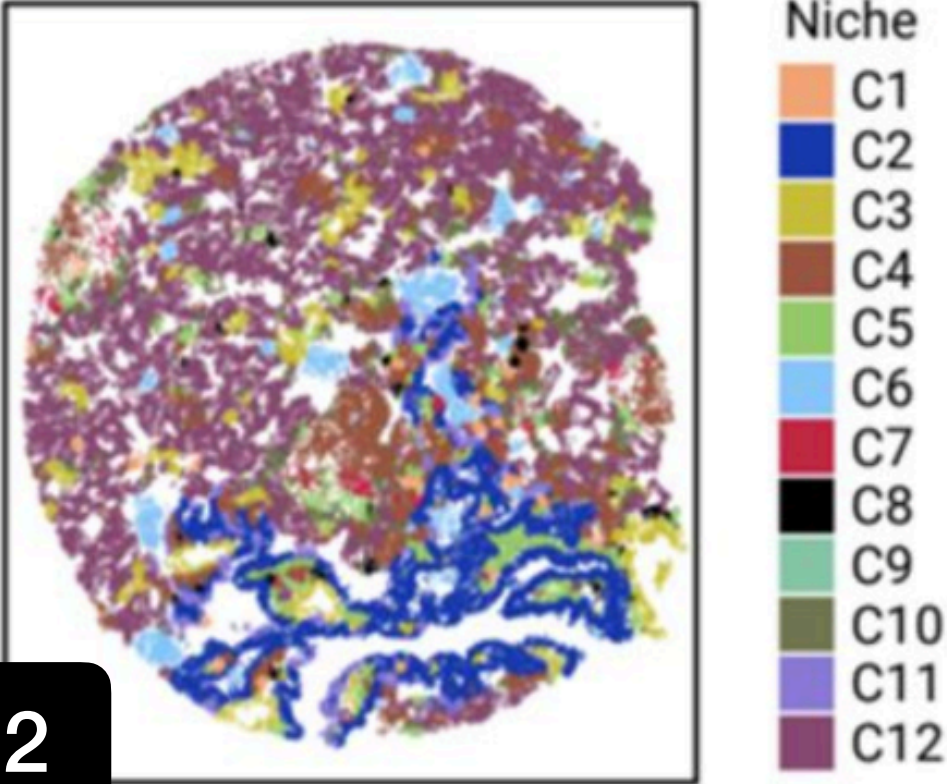
$$f(X, A)$$



Cell-type composition of the niche



Cell-Based Niches



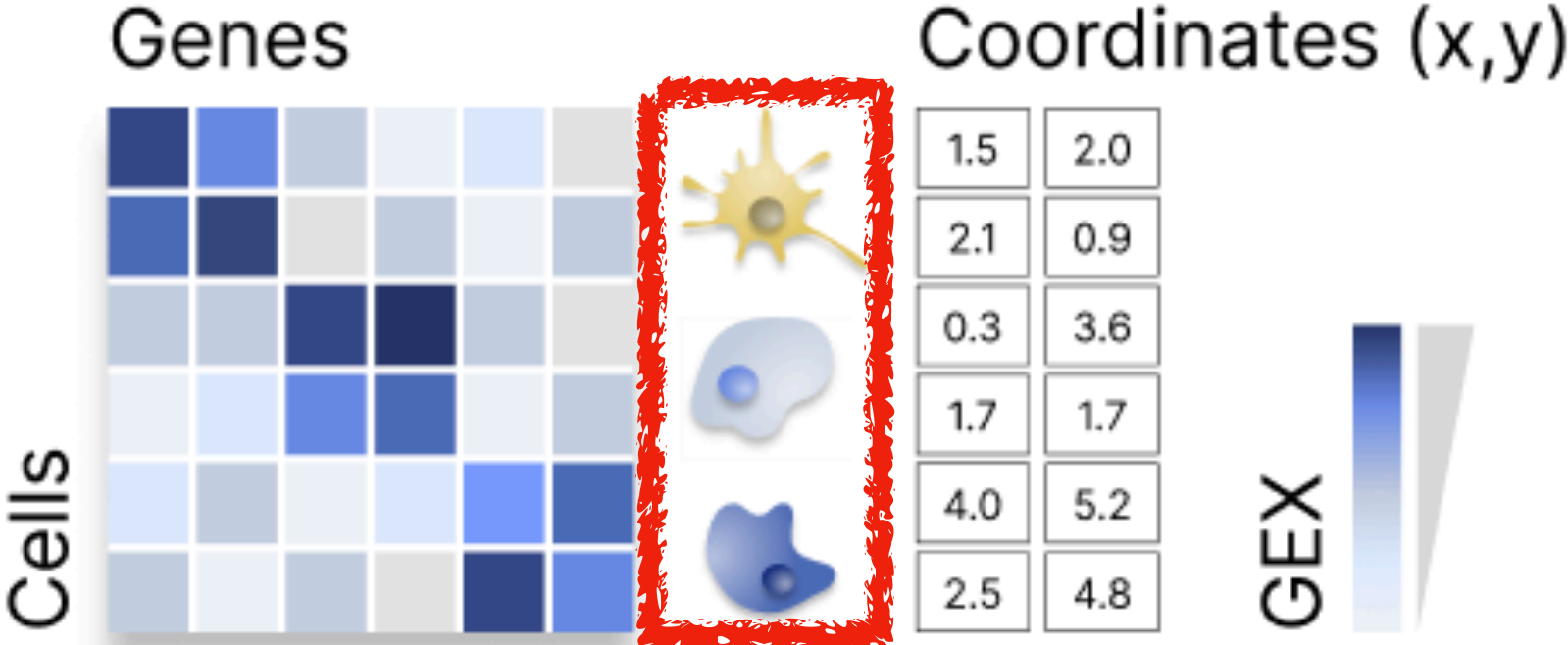
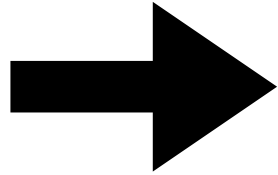
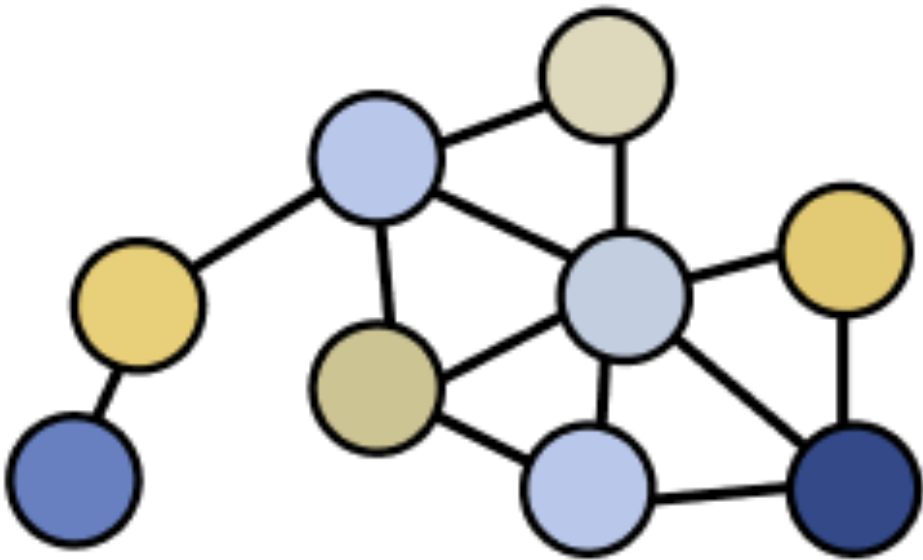
2



# Cell-based niches

i.e. define a niche based on the composition of neighbouring cell types

Spatial graph of cells



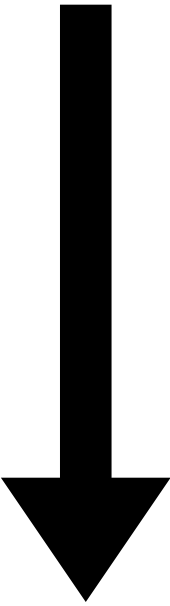
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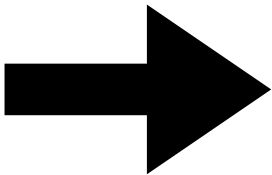
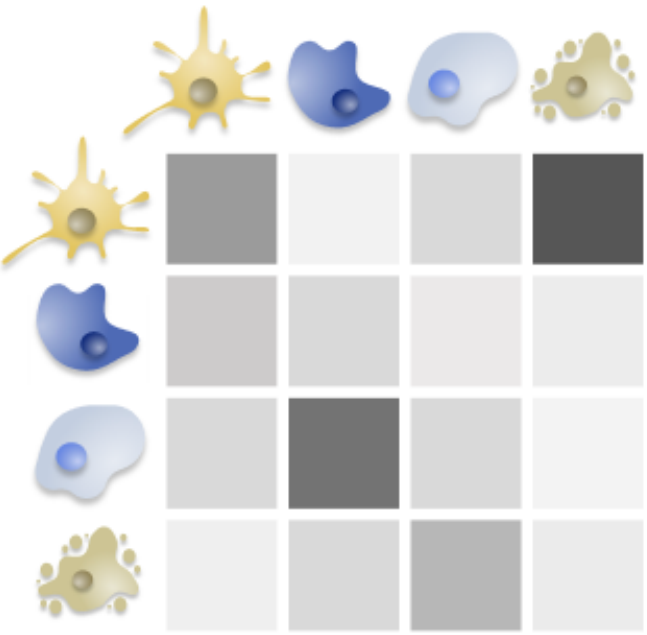
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$$f(X, A)$$



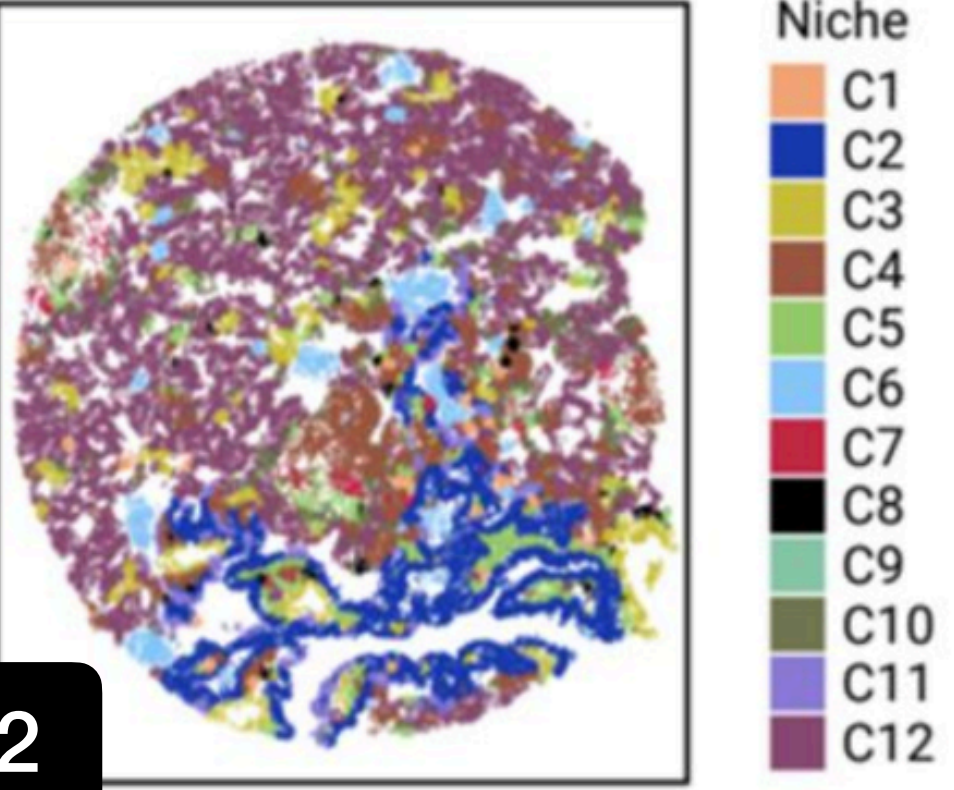
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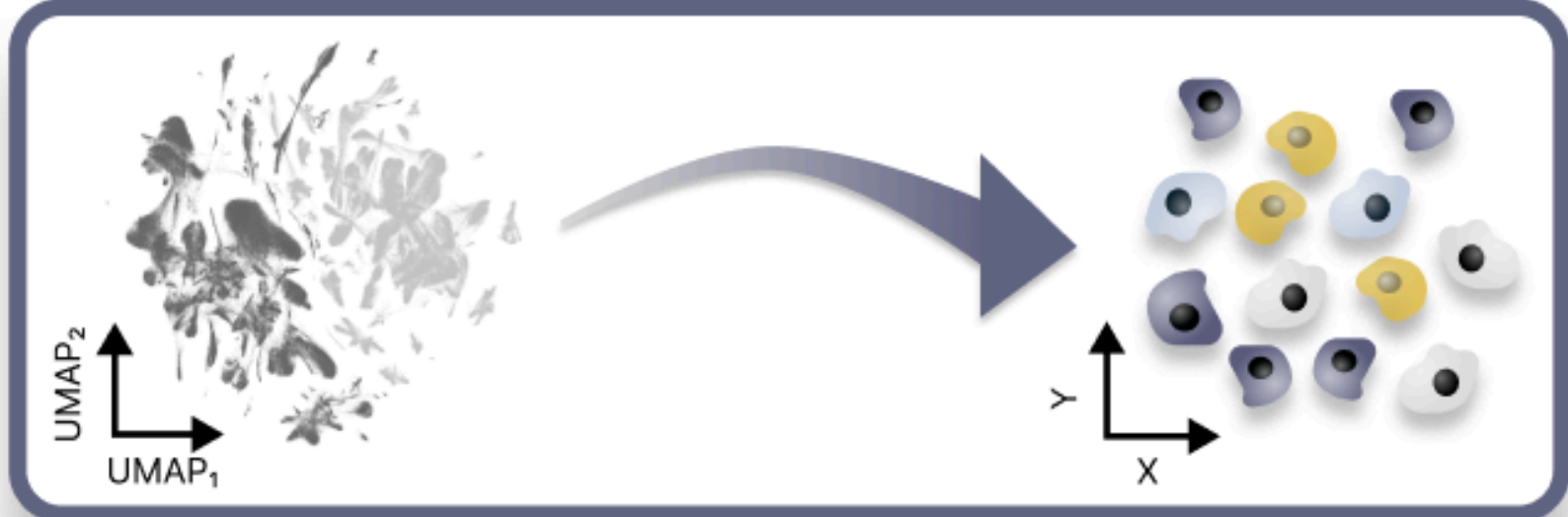
Cell-Based Niches



2

# Can we transfer niche labels to dissociated single-cell data?

**Spatial cell type label transfer**



# Can we transfer niche labels to dissociated single-cell data?

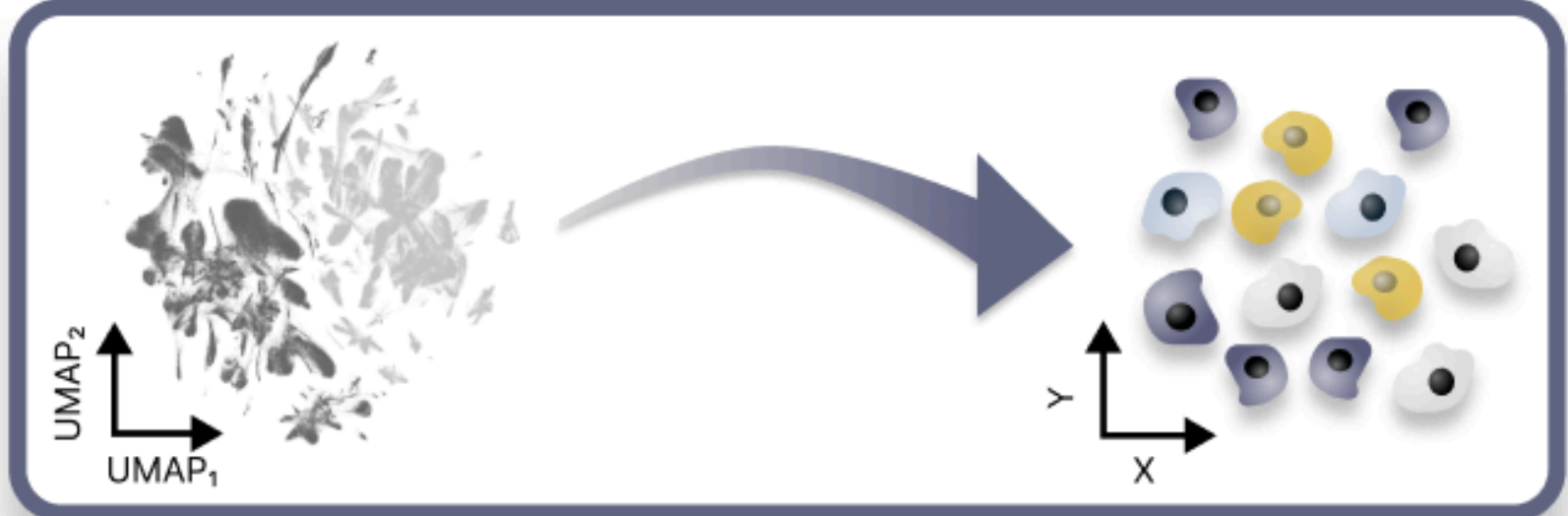


Alejandro Tejada-Lapuerta



Fabian J. Theis

## Spatial cell type label transfer



### Nicheformer: a foundation model for single-cell and spatial omics

Anna C. Schaar, Alejandro Tejada-Lapuerta, Giovanni Palla, Robert Gutgesell, Lennard Halle, Mariia Minaeva, Larsen Vornholz, Leander Dony, Francesca Drummer, Mojtaba Bahrami, Fabian J. Theis

doi: <https://doi.org/10.1101/2024.04.15.589472>

# Can we transfer niche labels to dissociated single-cell data?

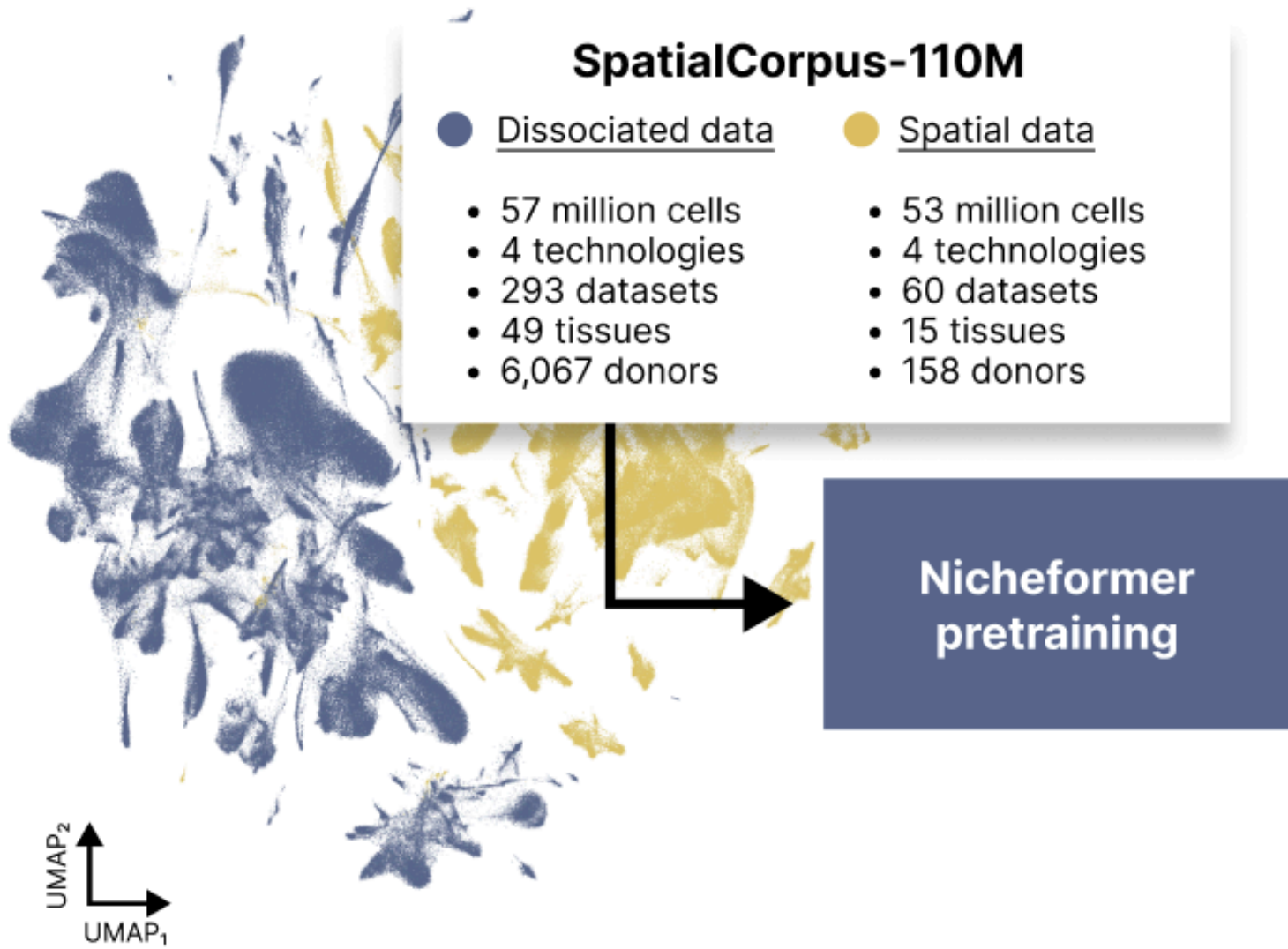


Alejandro Tejada-Lapuerta

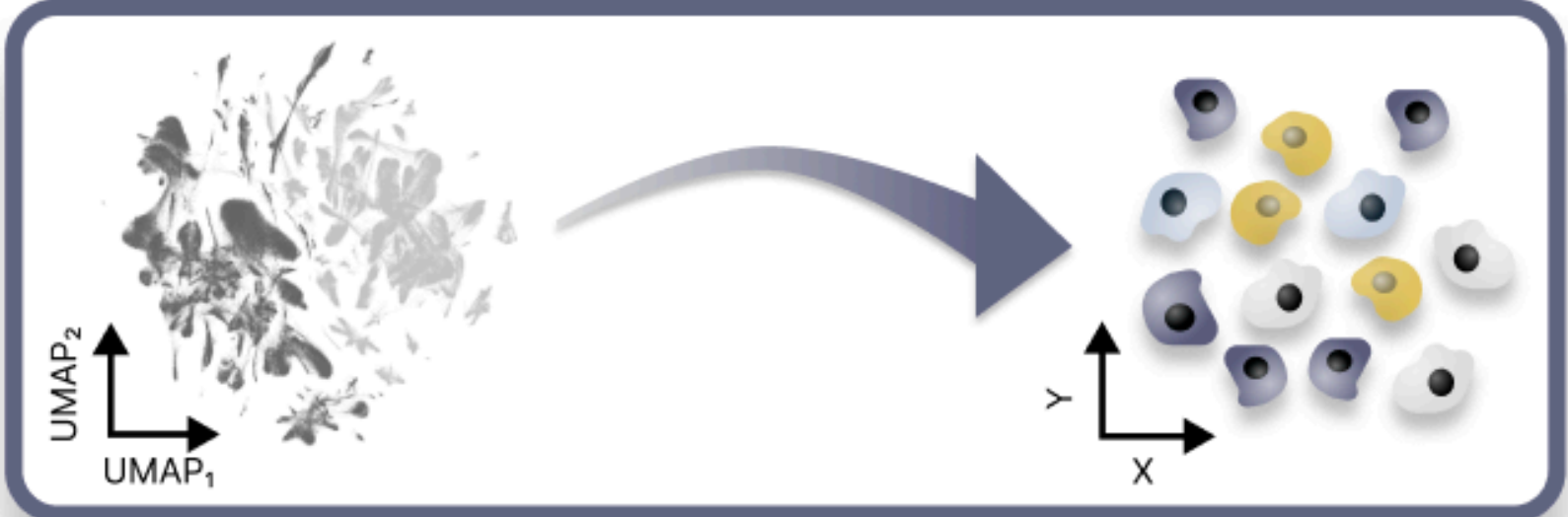


Fabian J. Theis

## Pretraining: cellular representation



## Spatial cell type label transfer



## Nicheformer: a foundation model for single-cell and spatial omics

[id](#) Anna C. Schaar, [id](#) Alejandro Tejada-Lapuerta, [id](#) Giovanni Palla, [id](#) Robert Gutgesell, [id](#) Lennard Halle, [id](#) Mariia Minaeva, [id](#) Larsen Vornholz, [id](#) Leander Dony, Francesca Drummer, [id](#) Mojtaba Bahrami, [id](#) Fabian J. Theis

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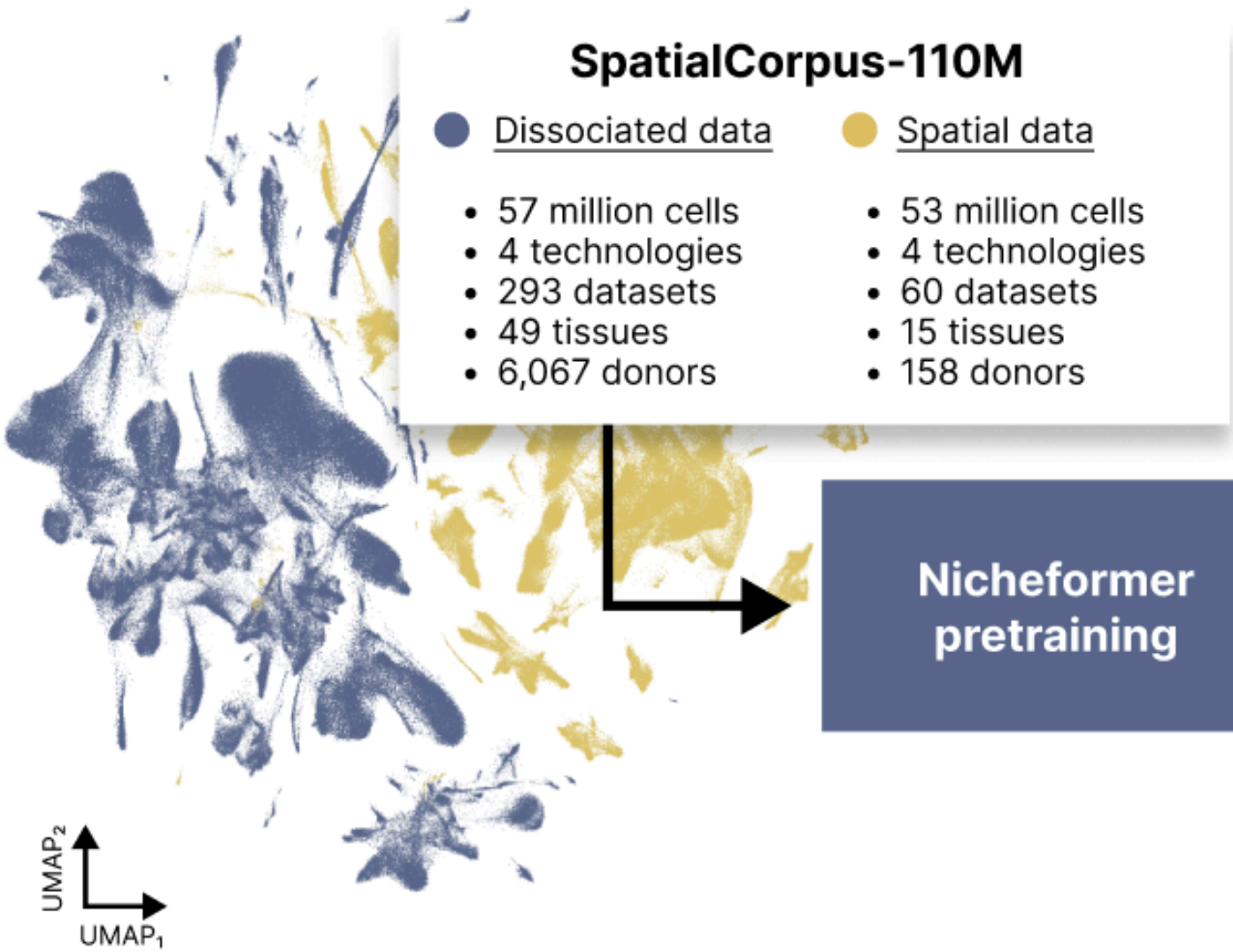


Alejandro Tejada-Lapuerta

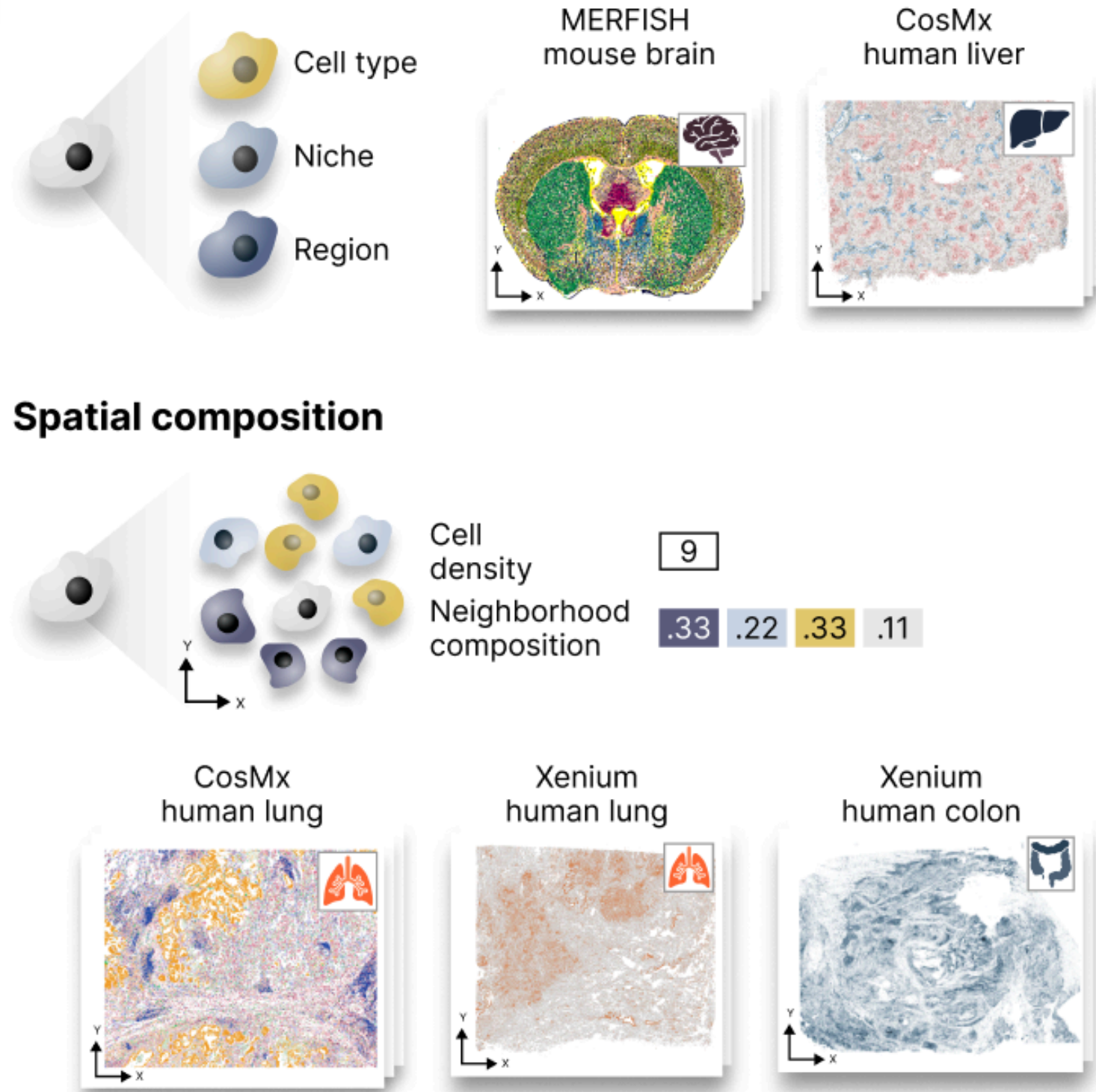


Fabian J. Theis

## Pretraining: cellular representation



## Fine-tuning: spatial tasks



## Spatial cell type label transfer

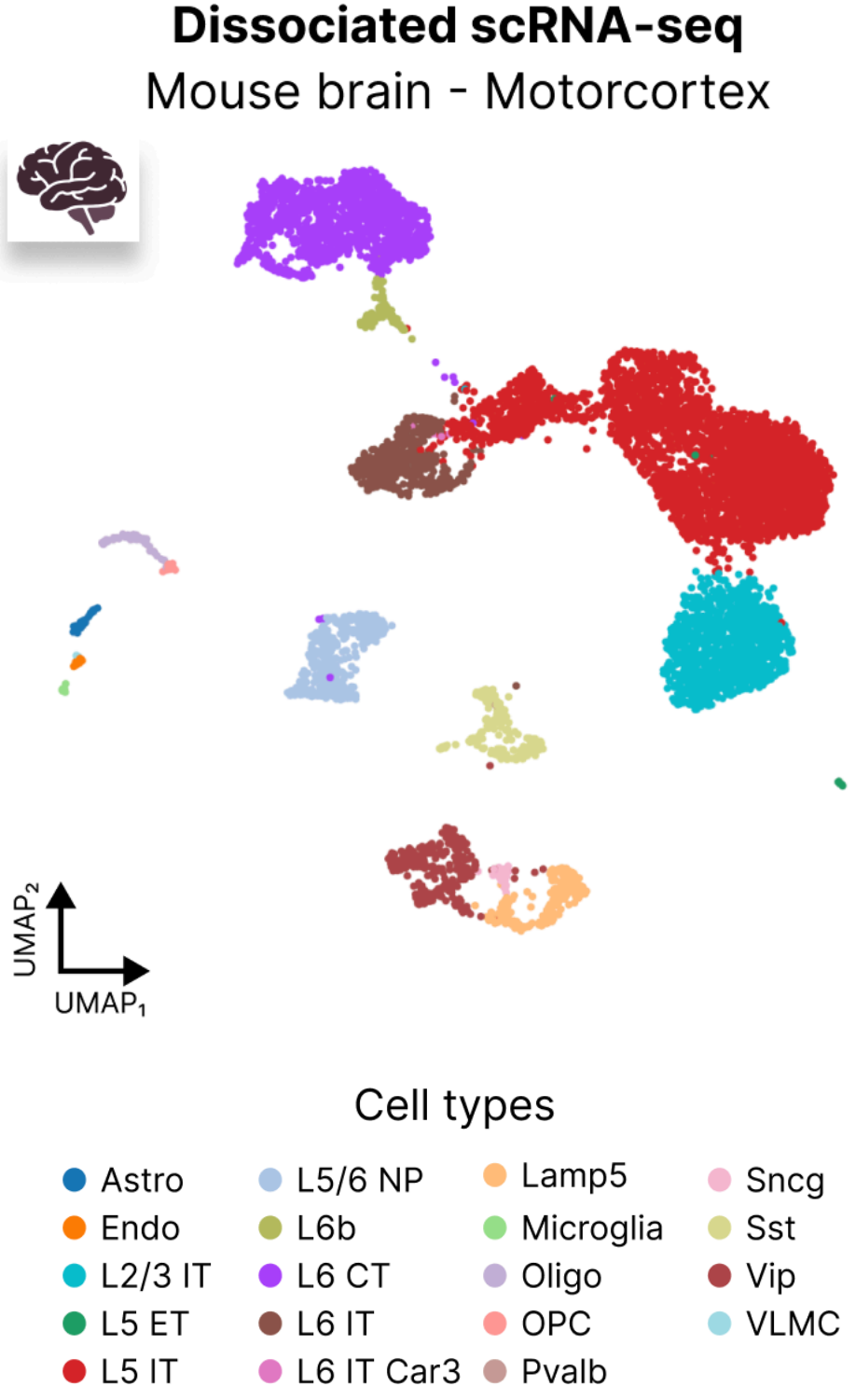


## Nicheformer: a foundation model for single-cell and spatial omics

[iD](#) Anna C. Schaar, [iD](#) Alejandro Tejada-Lapuerta, [iD](#) Giovanni Palla, [iD](#) Robert Gutgesell, [iD](#) Lennard Halle, [iD](#) Mariia Minaeva, [iD](#) Larsen Vornholz, [iD](#) Leander Dony, [iD](#) Francesca Drummer, [iD](#) Mojtaba Bahrami, [iD](#) Fabian J. Theis

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# Nicheformer spatial label transfer

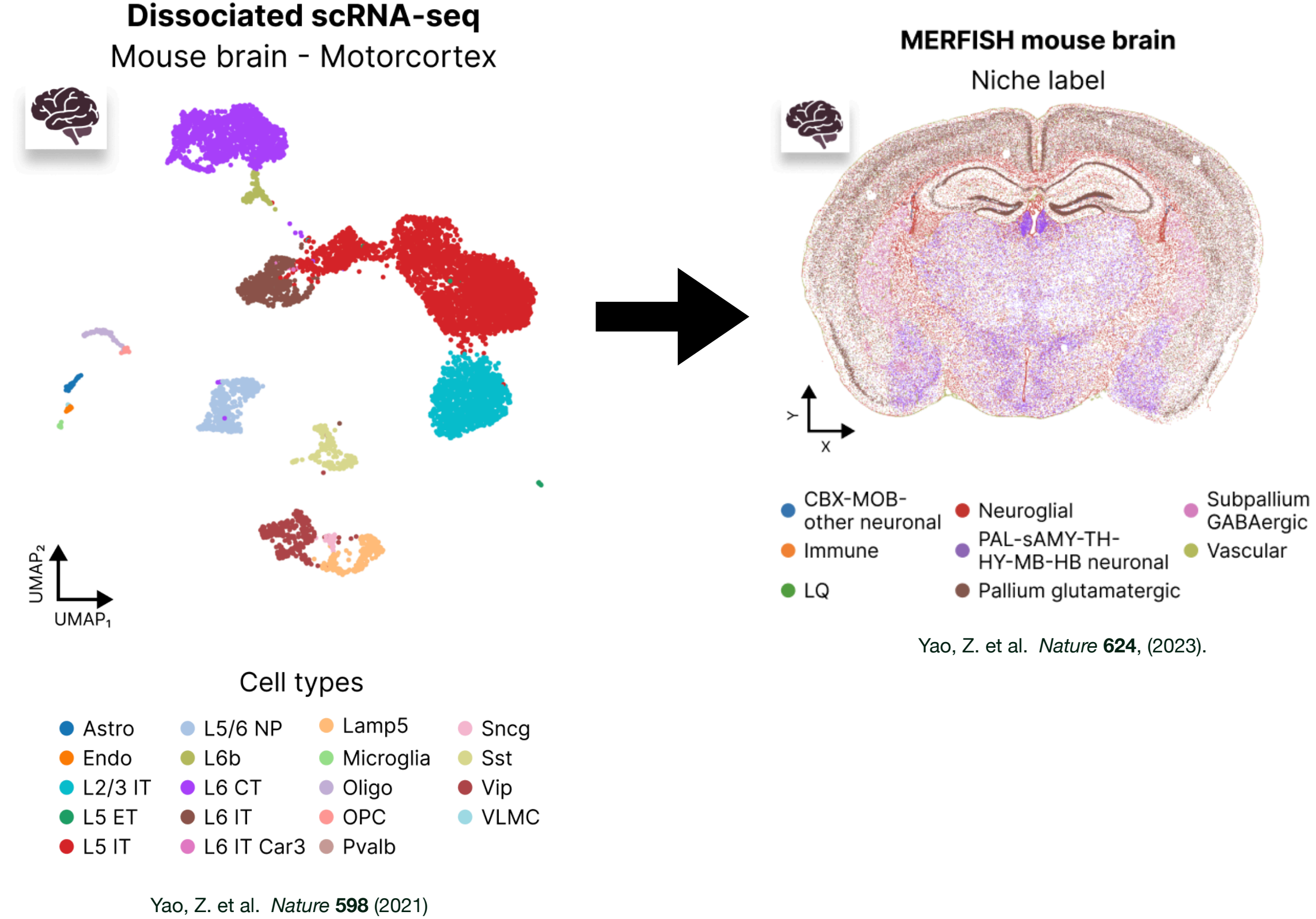


Yao, Z. et al. *Nature* **598** (2021)

Yao, Z. et al. A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. *Nature* **598**, 103–110 (2021).

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# Nicheformer spatial label transfer

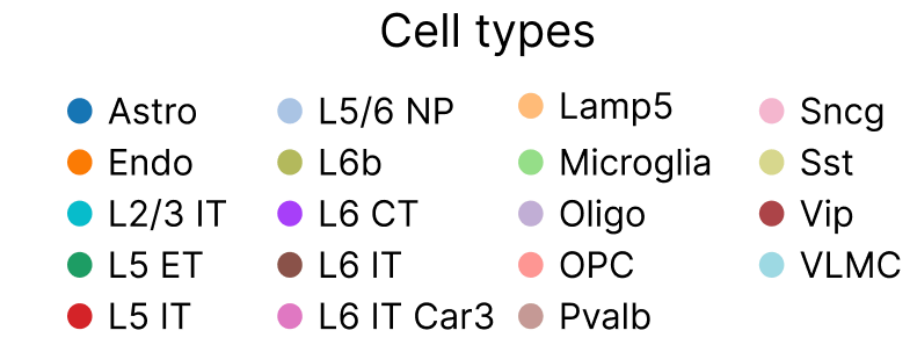
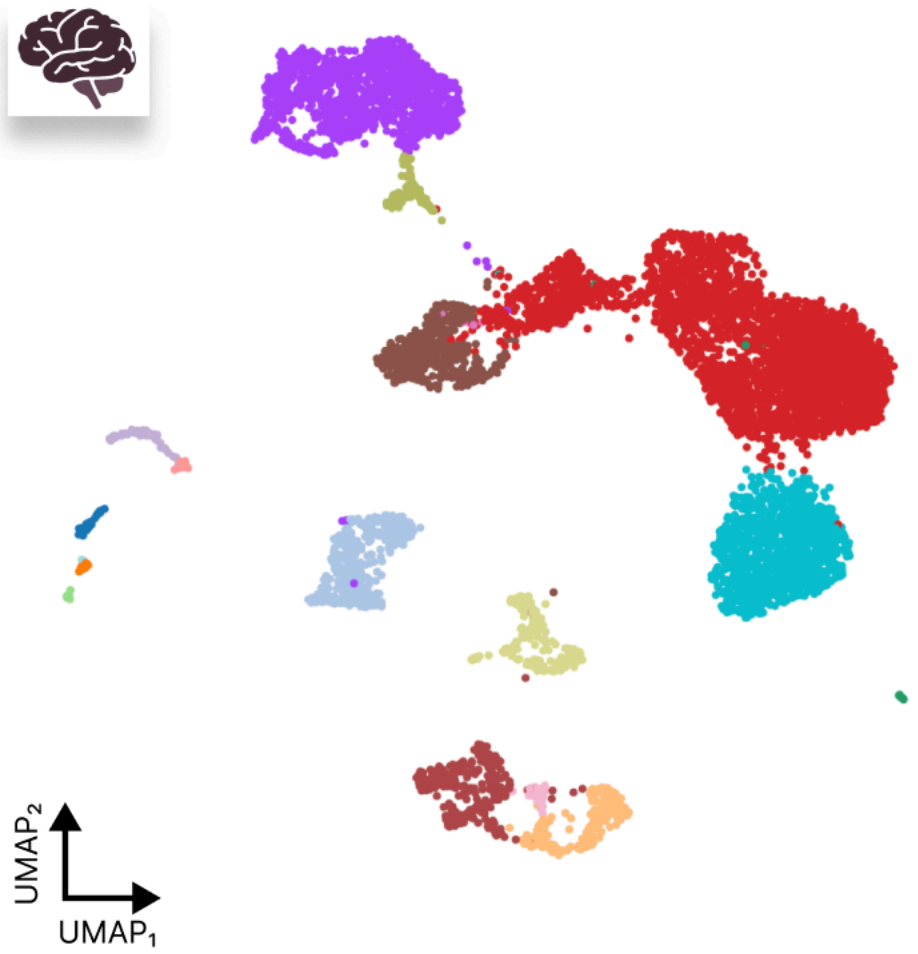


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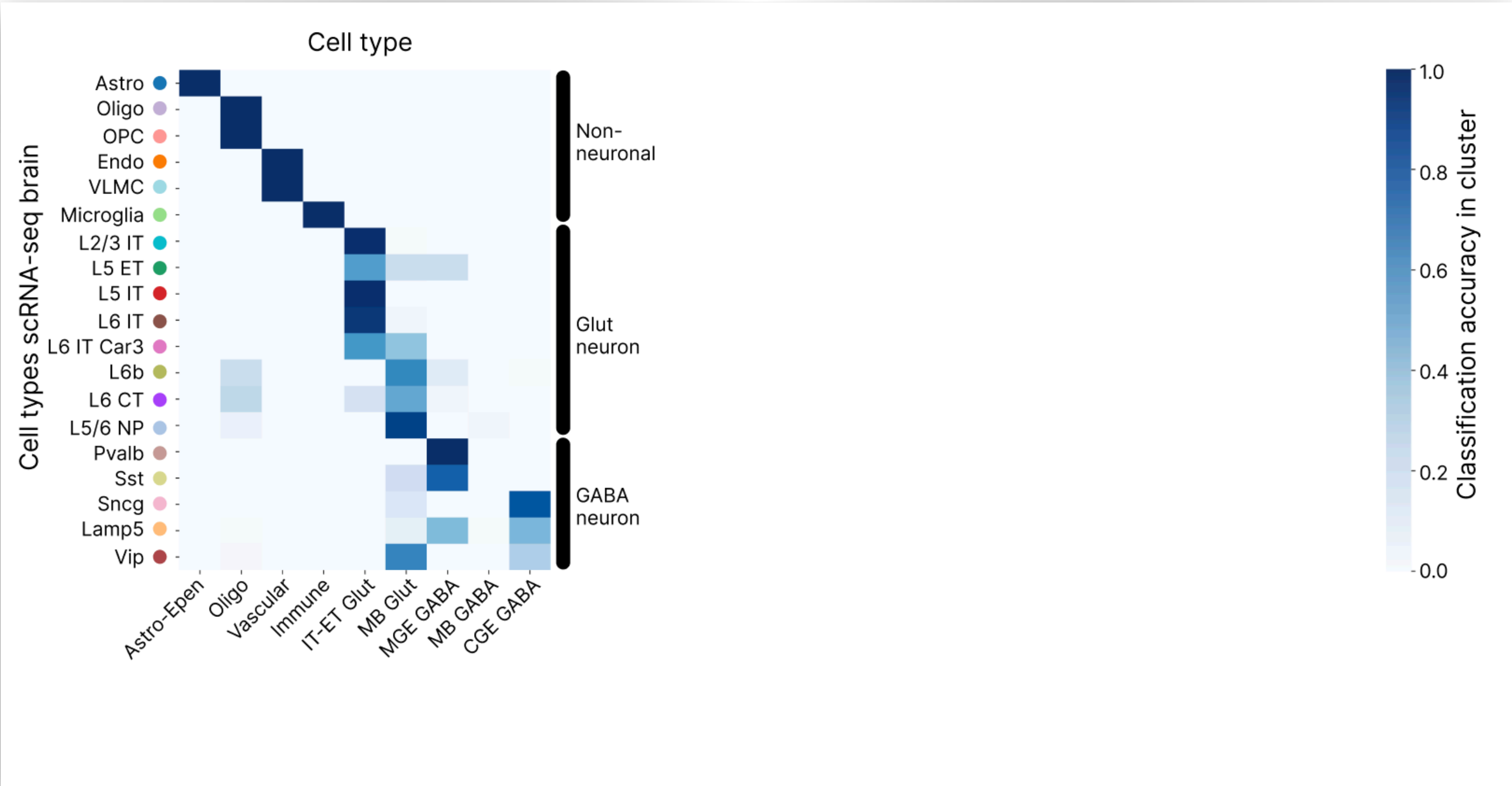
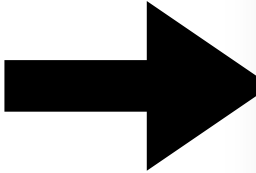
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# Nicheformer spatial label transfer

**Dissociated scRNA-seq**  
 Mouse brain - Motorcortex



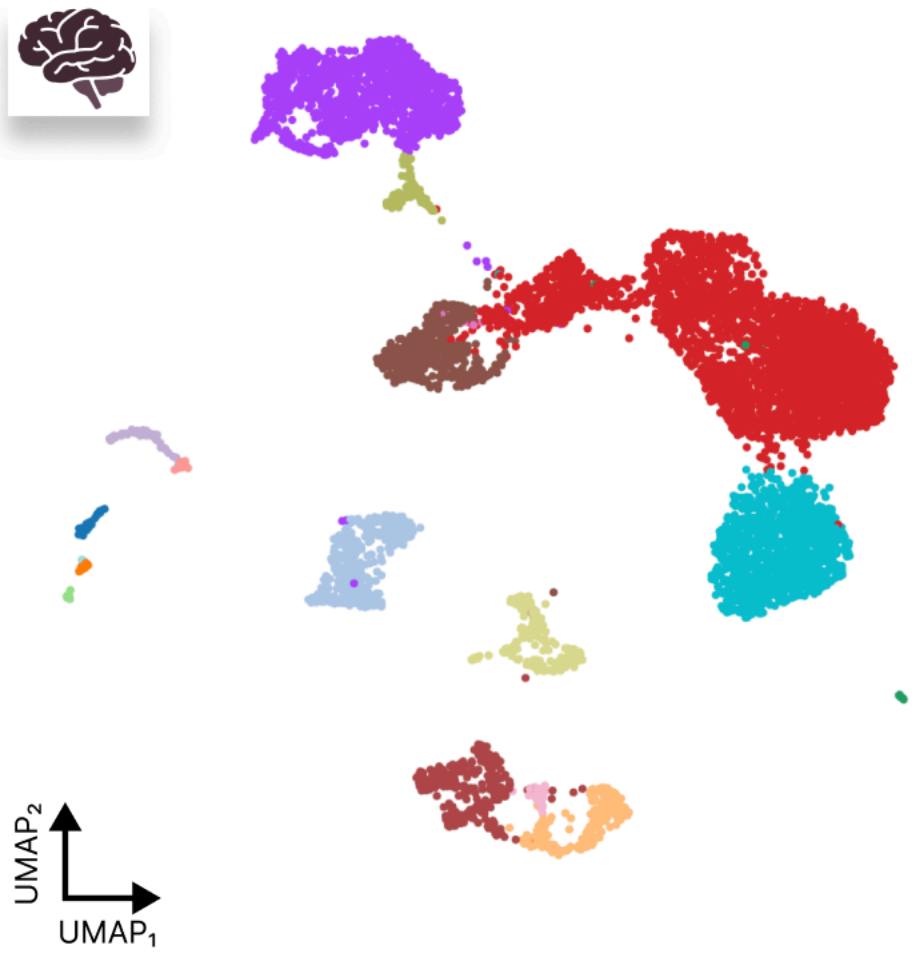
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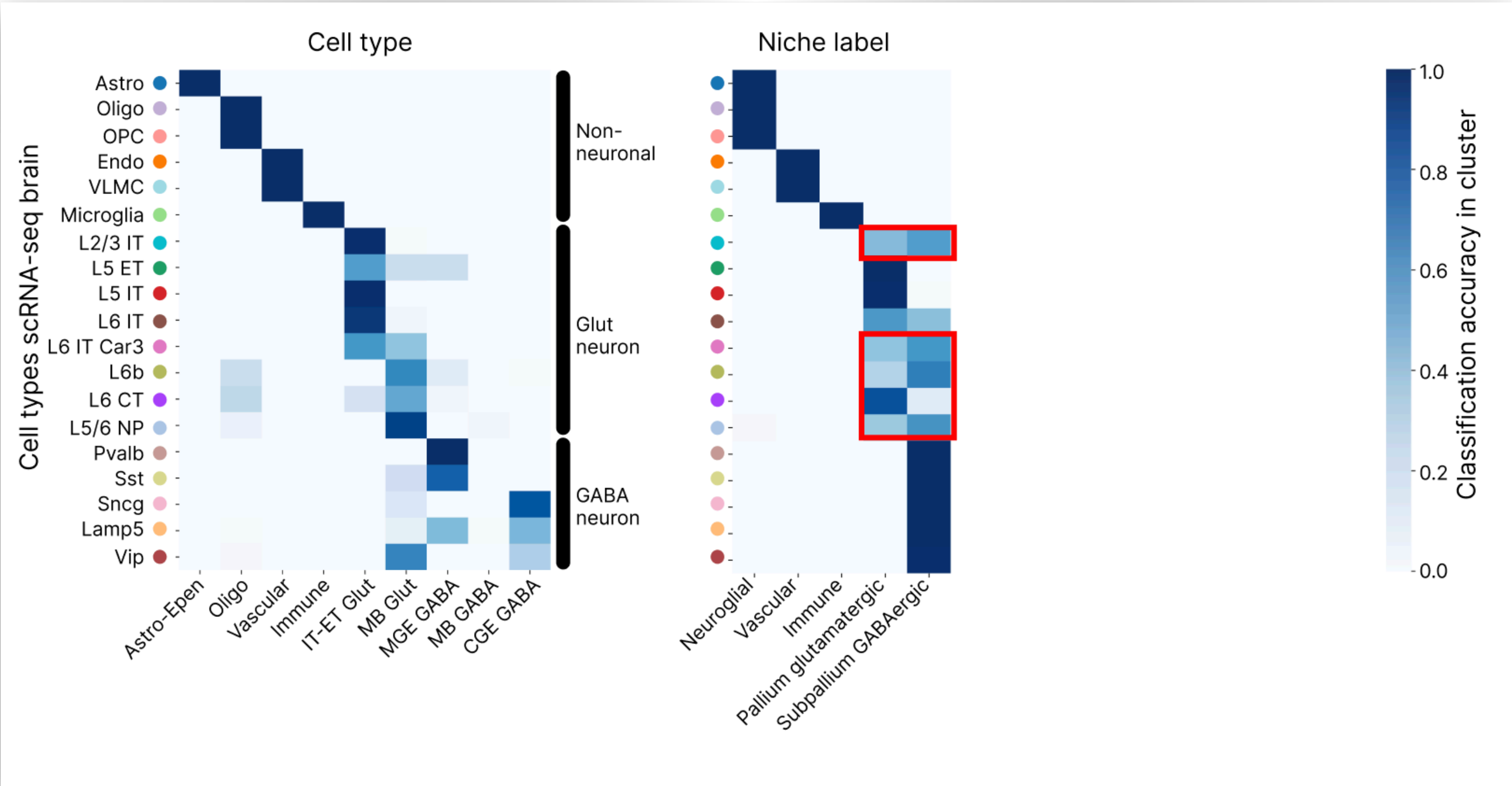
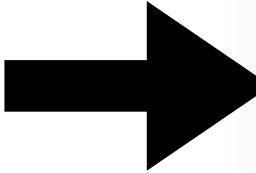
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**Dissociated scRNA-seq**  
 Mouse brain - Motorcortex



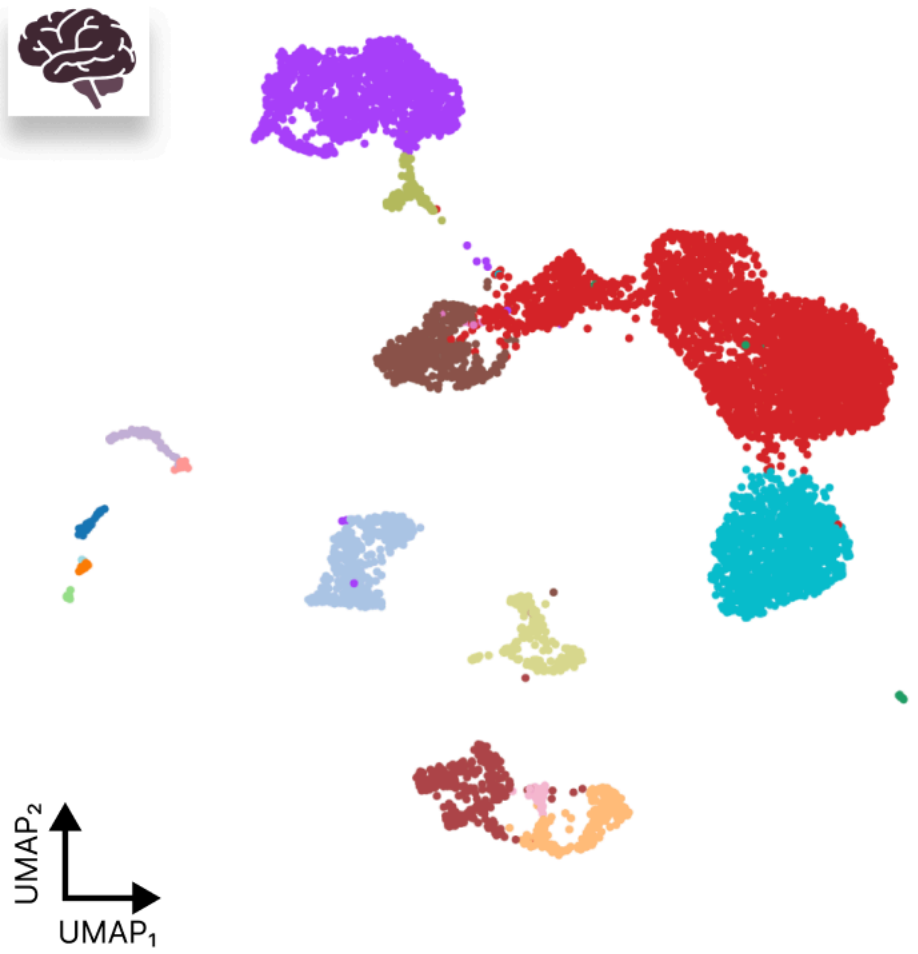
- Cell types**
- Astro
  - Endo
  - L2/3 IT
  - L5 ET
  - L5 IT
  - L5/6 NP
  - L6b
  - L6 CT
  - L6 IT
  - L6 IT Car3
  - Lamp5
  - Lamp5
  - Vip
  - Sncg
  - Sst
  - Microglia
  - Oligo
  - OPC
  - VLMC

Yao, Z. et al. *Nature* **598** (2021)



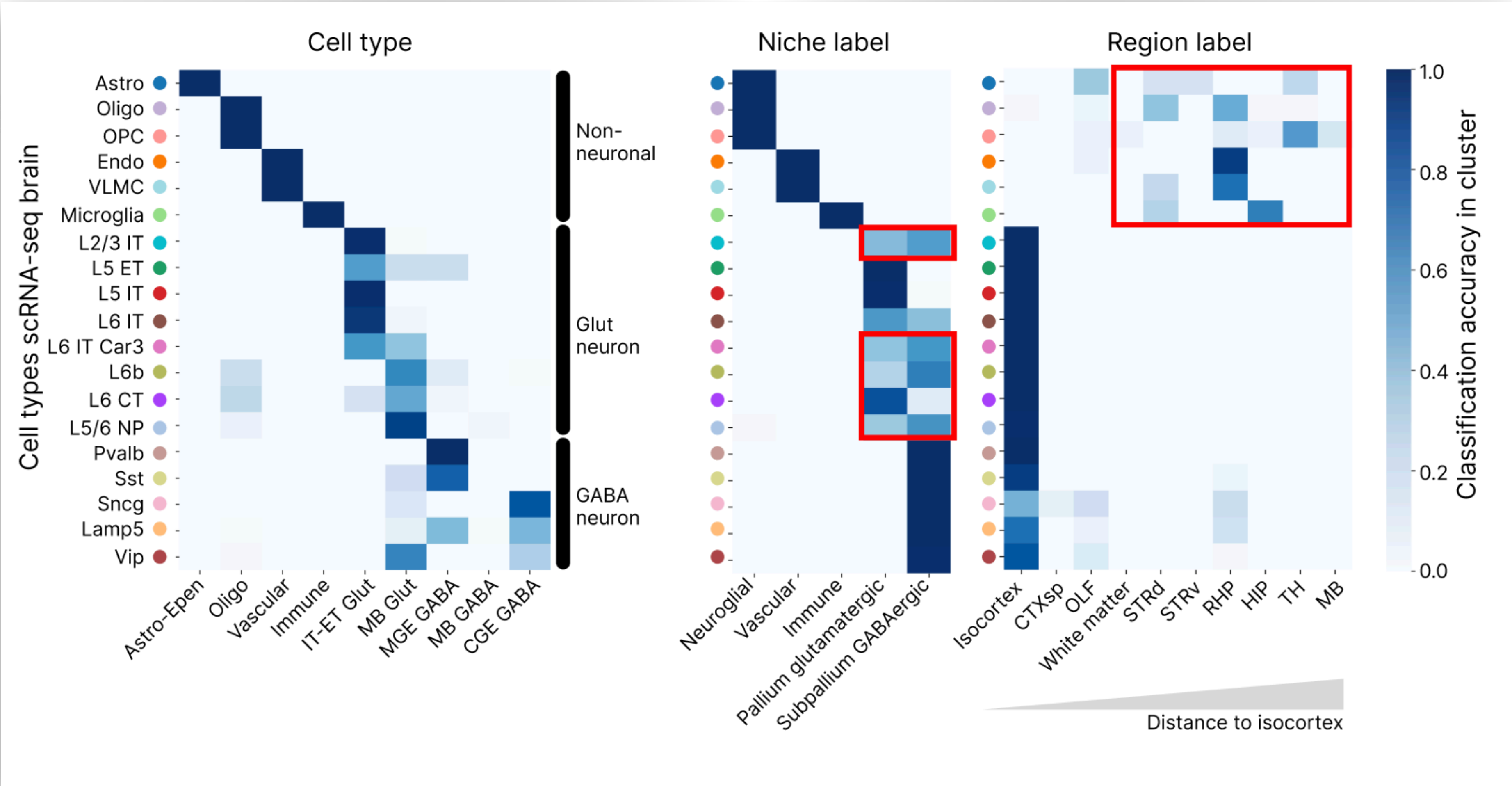
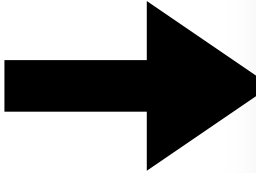
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 Mouse brain - Motorcortex

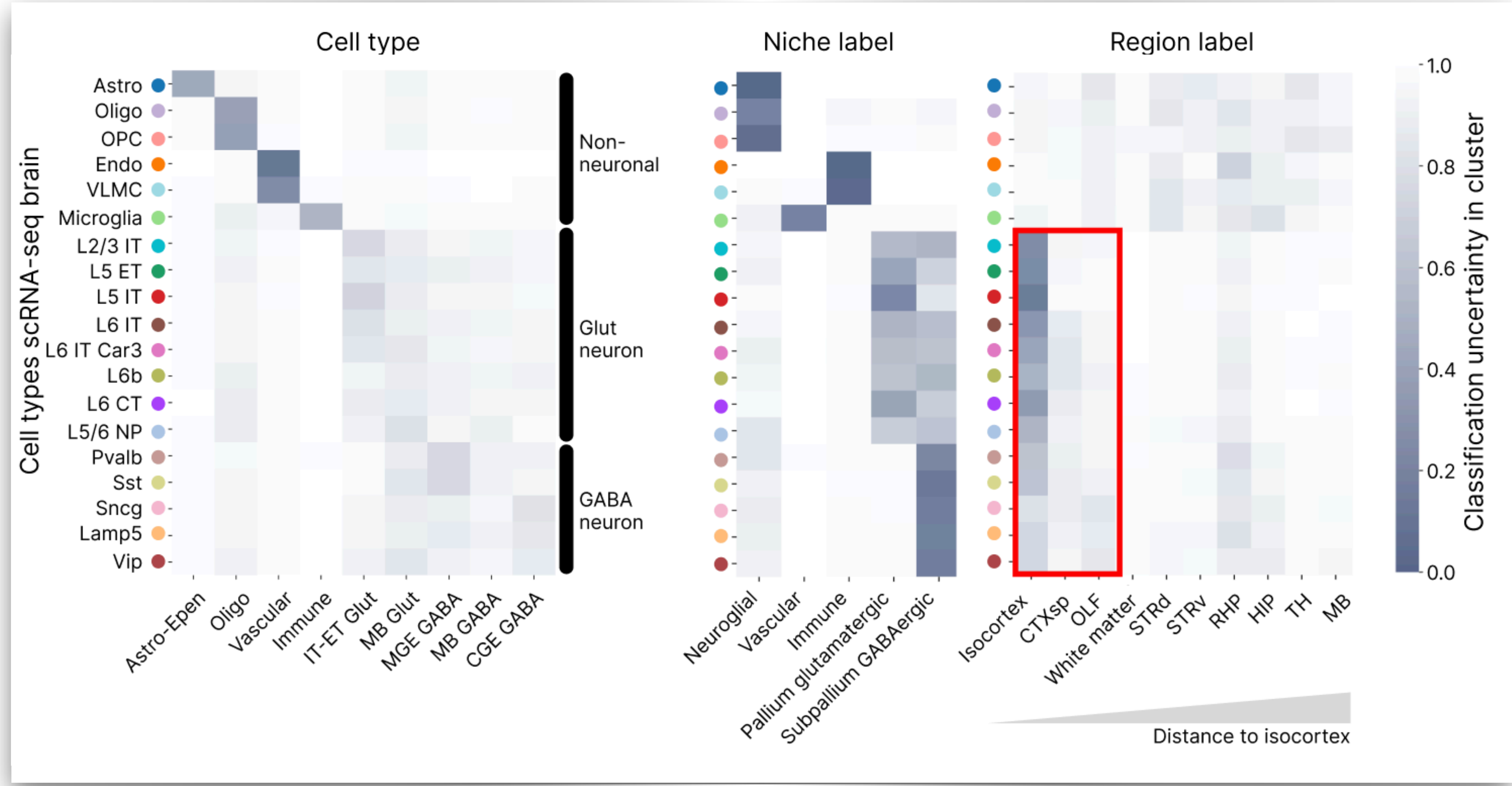
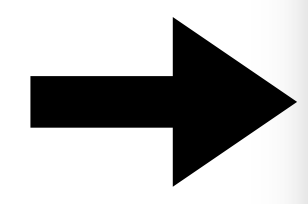
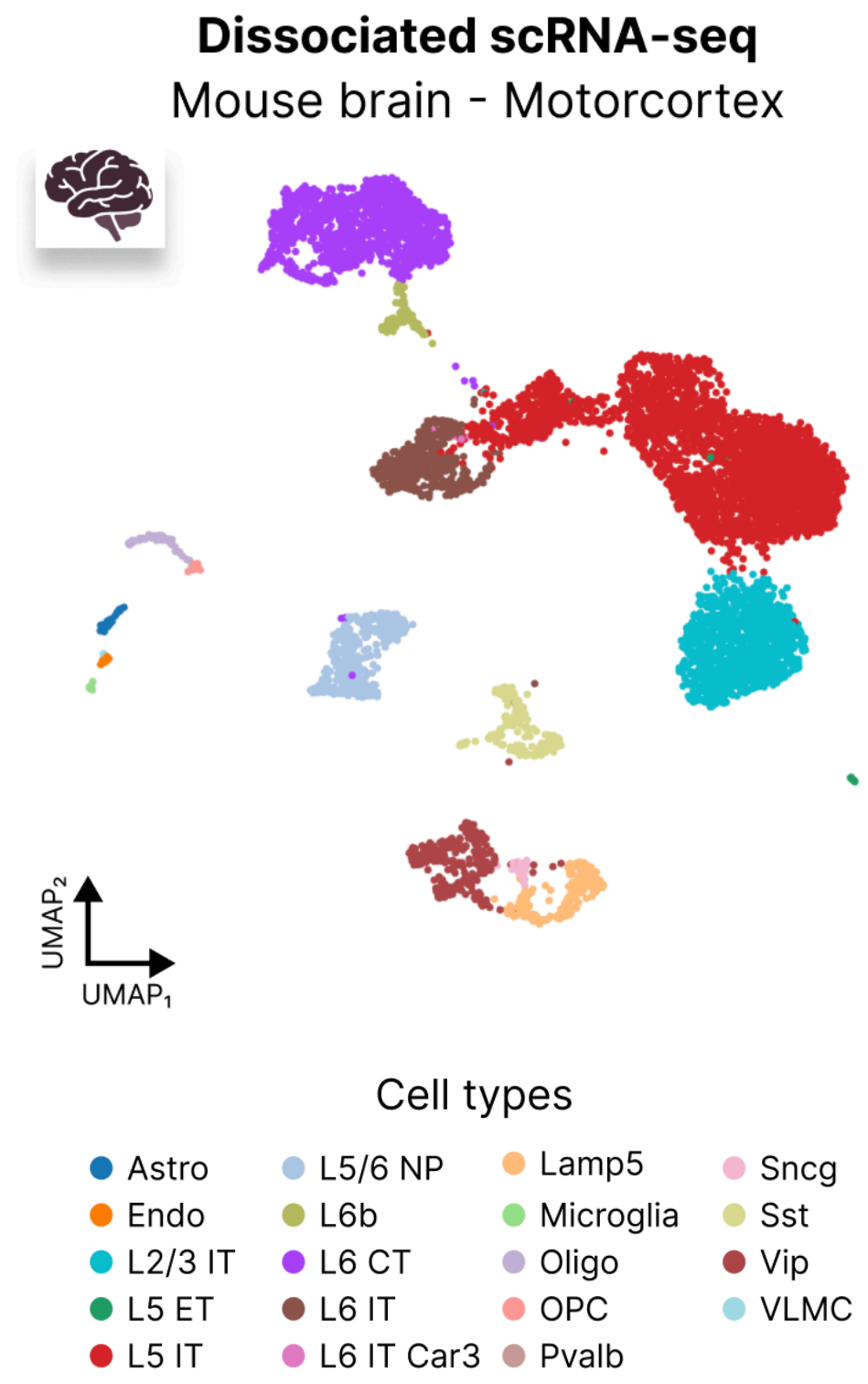


- Cell types**
- Astro
  - Endo
  - L2/3 IT
  - L5 ET
  - L5 IT
  - L5/6 NP
  - L6b
  - L6 CT
  - L6 IT
  - L6 IT Car3
  - Lamp5
  - Lamp5
  - Vip
  - Sncg
  - Sst
  - Microglia
  - Oligo
  - OPC
  - VLMC

Yao, Z. et al. *Nature* **598** (2021)

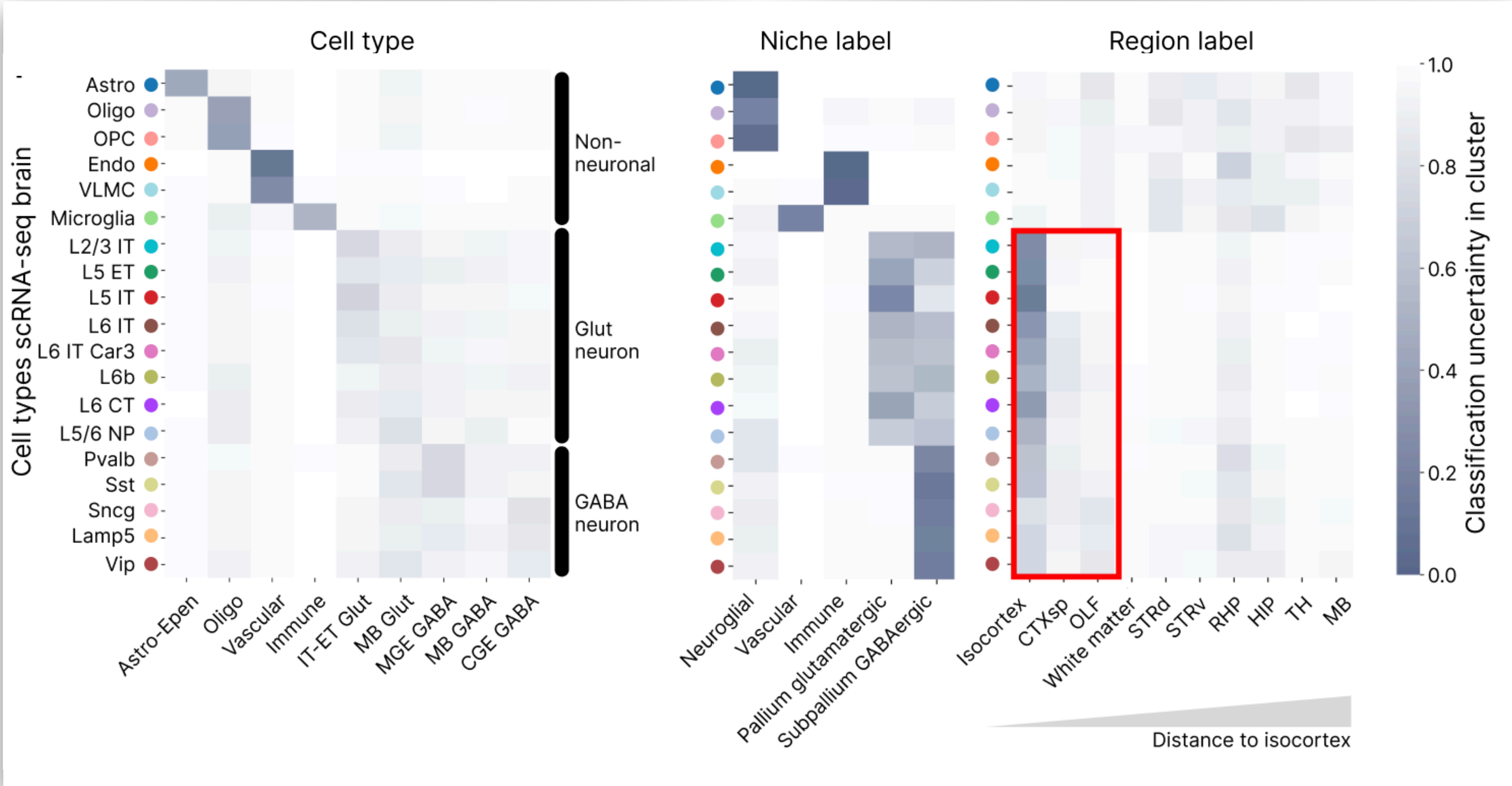
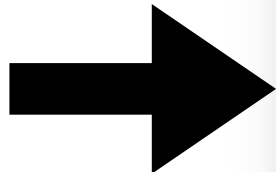
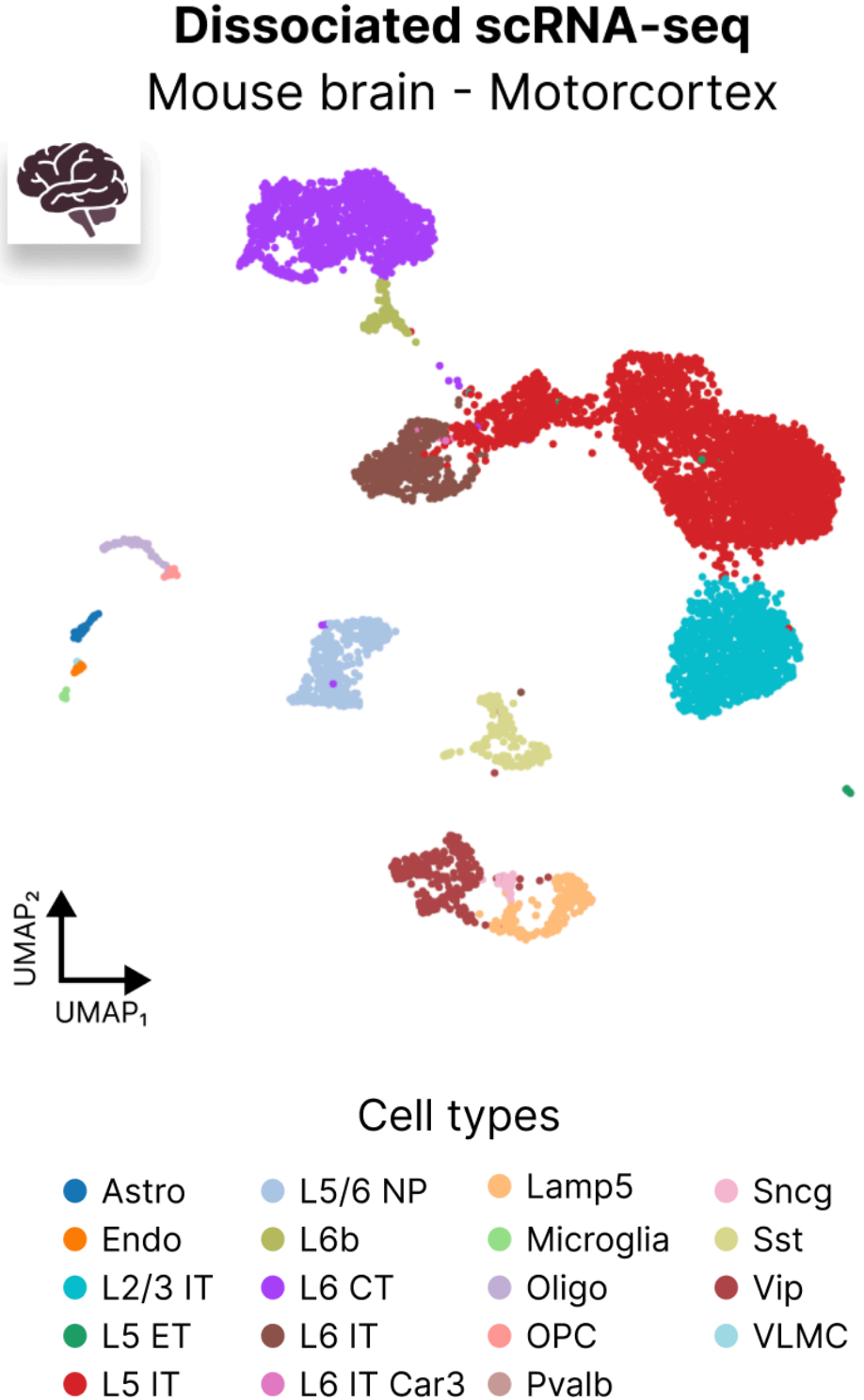


# Nicheformer spatial label transfer



Yao, Z. et al. *Nature* 598 (2021)

# Nicheformer spatial label transfer



Yao, Z. et al. *Nature* **598** (2021)

**Outlook:** Spatial omics will soon **outgrow** dissociated single-cell data when it comes to number of cells. However, we still lack extensive spatial transcriptomics atlases with **diverse panels capturing various disease states**, this will enable us to start **transferring** knowledge generated with the spatial context onto 'traditional' single-cell data.

# COVET for niche identification and reconstruction

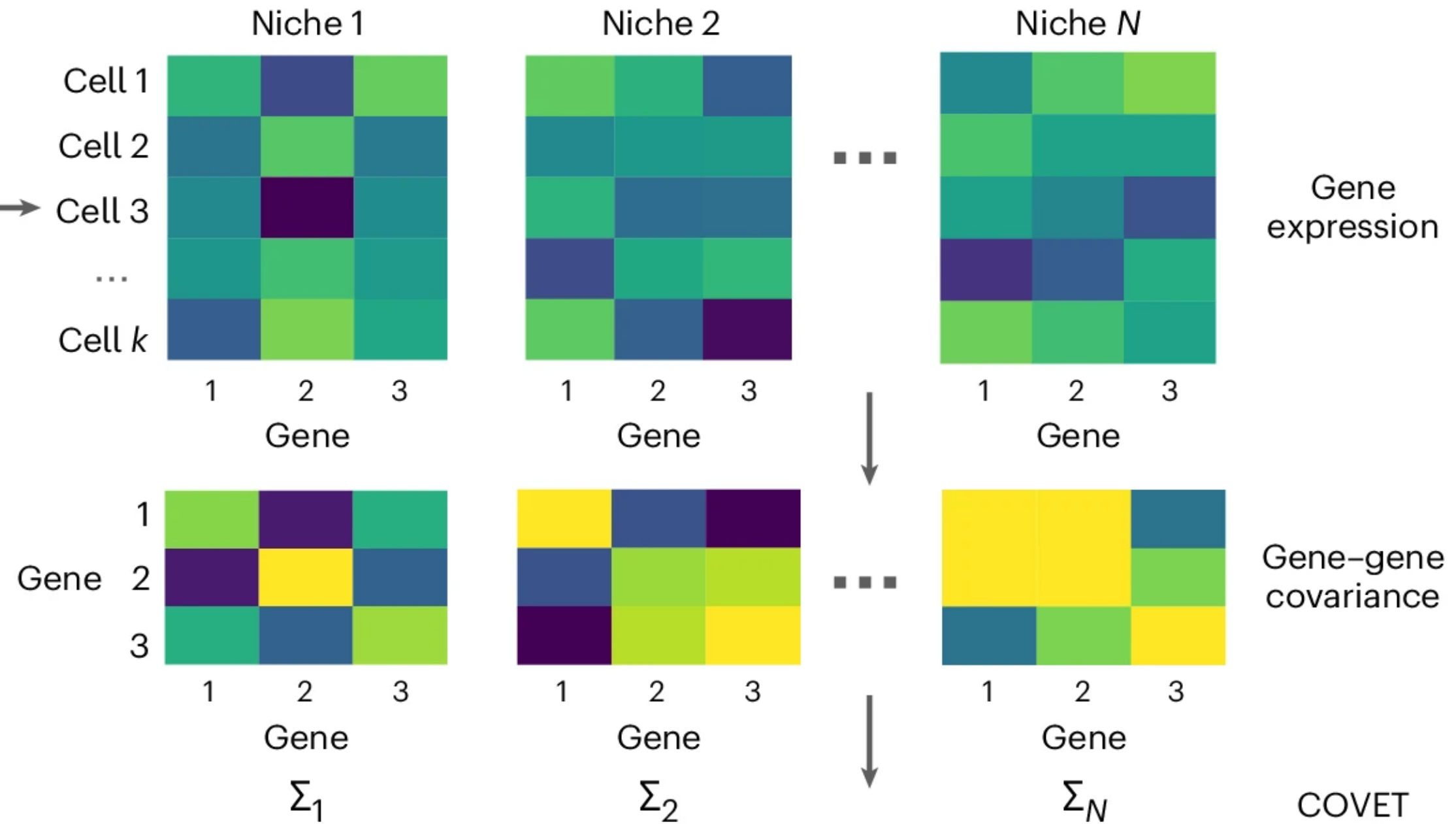
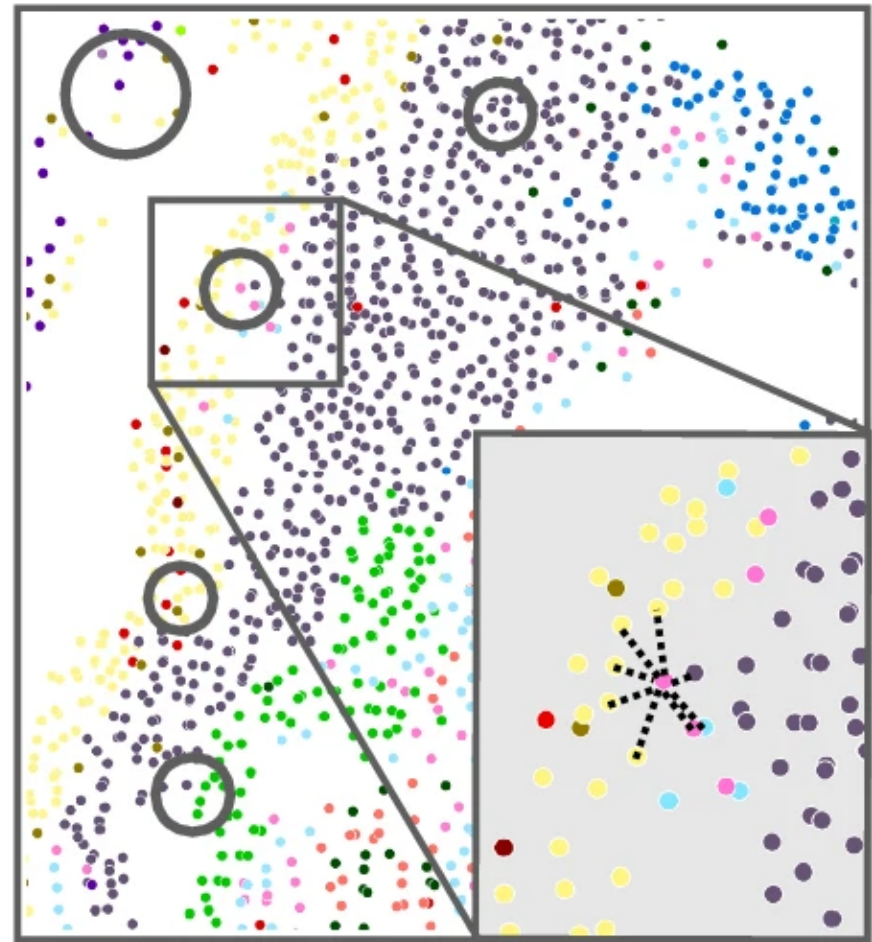
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## The covariance environment defines cellular niches for spatial inference

[Doron Haviv](#), [Ján Remšík](#), [Mohamed Gatie](#), [Catherine Snopkowski](#), [Meril Takizawa](#), [Nathan Pereira](#), [John Bashkin](#), [Stevan Jovanovich](#), [Tal Nawy](#), [Ronan Chaligne](#), [Adrienne Boire](#), [Anna-Katerina Hadjantonakis](#) & [Dana Pe'er](#)

*Nature Biotechnology* (2024) | [Cite this article](#)

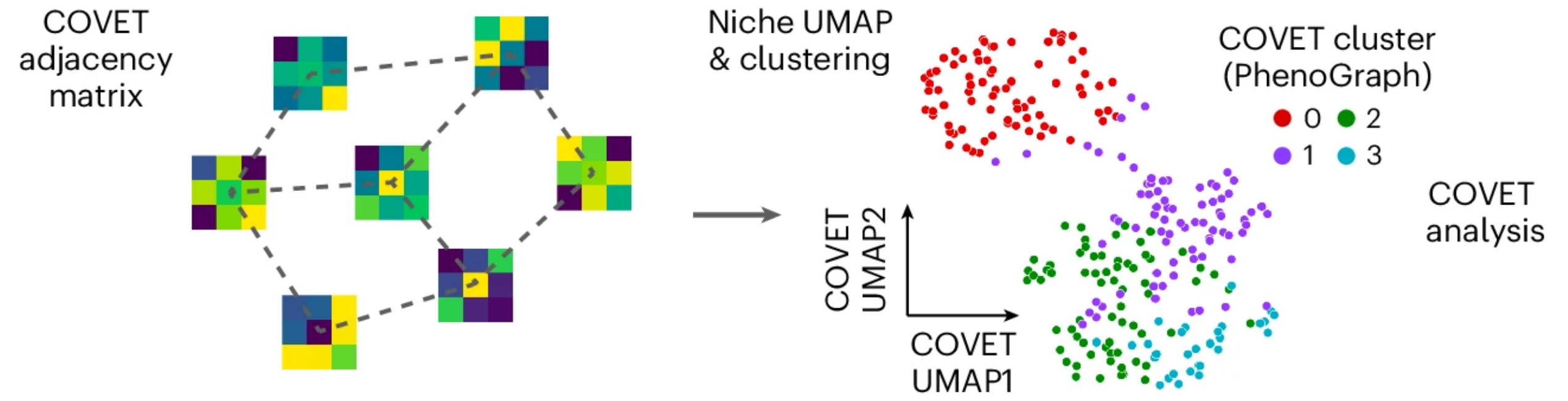
**COVET**: defines niches based on  $k$  spatial nearest neighbours and identifies niche similarities based on OT computed on gene-gene covariances (covariance environment)



Fast approximation of optimal transport (AOT)

$$\Delta(\Sigma_i, \Sigma_j) = OT(\Sigma_i, \Sigma_j) \approx L_2^2(\sqrt{\Sigma_i}, \sqrt{\Sigma_j})$$

Distance between niches



# COVET for niche identification and reconstruction

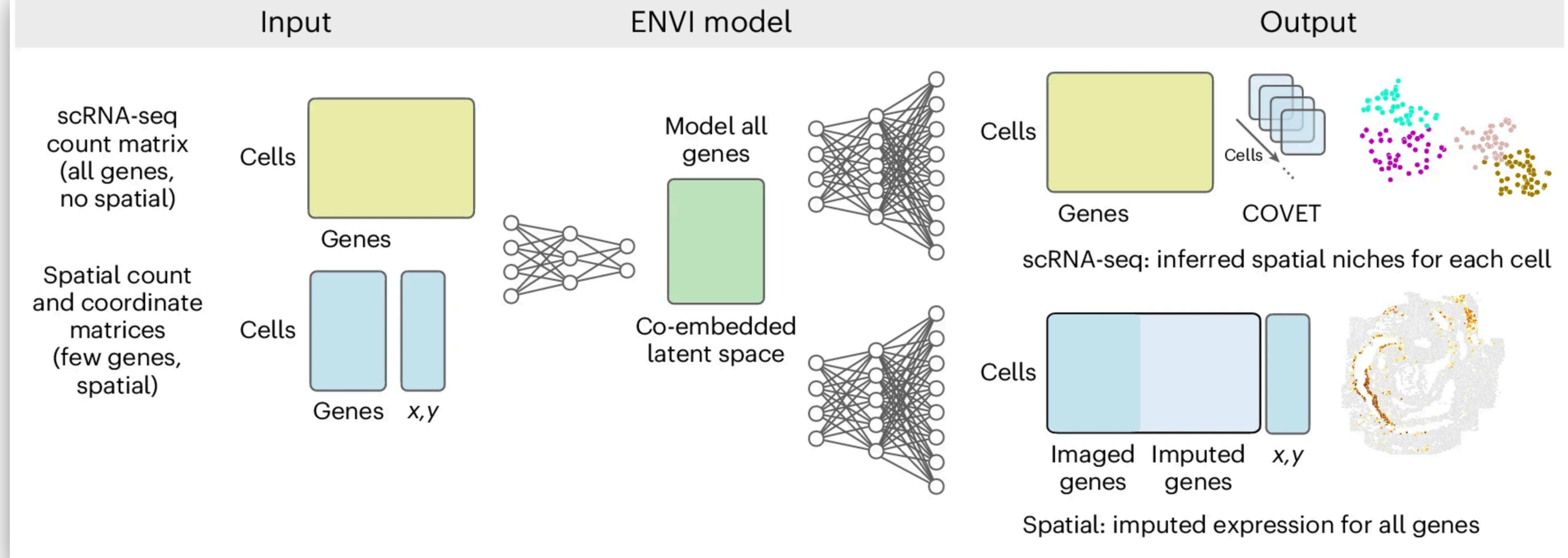
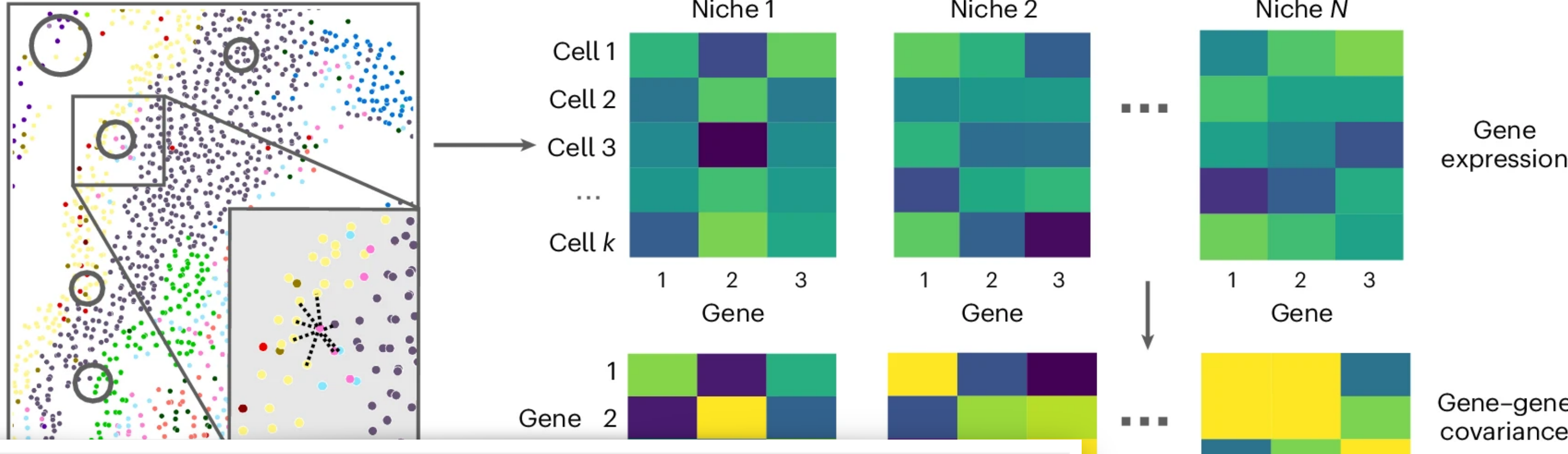
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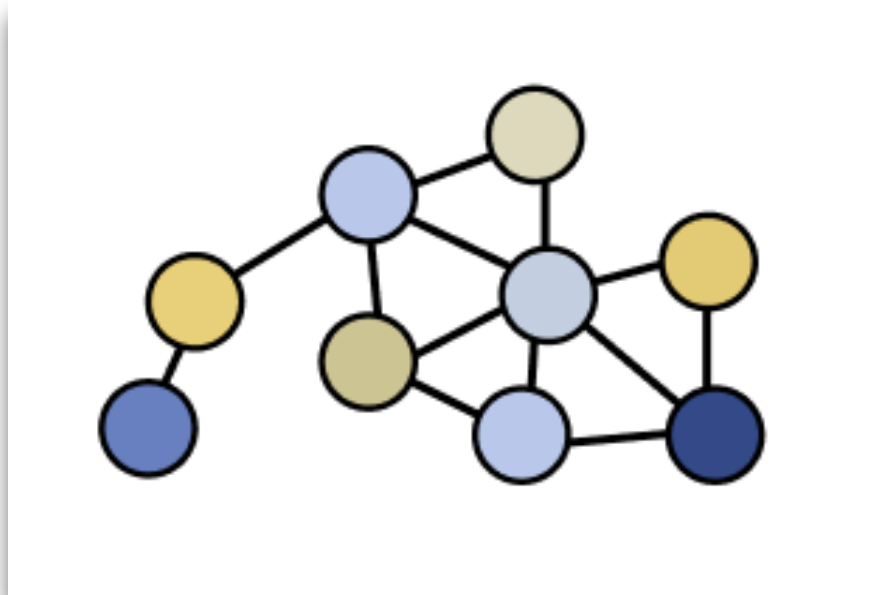
*Nature Biotechnology* (2024) | [Cite this article](#)

**COVET**: defines niches based on k spatial nearest neighbours and identifies niche similarities based on OT computed on gene-gene covariances (covariance environment)



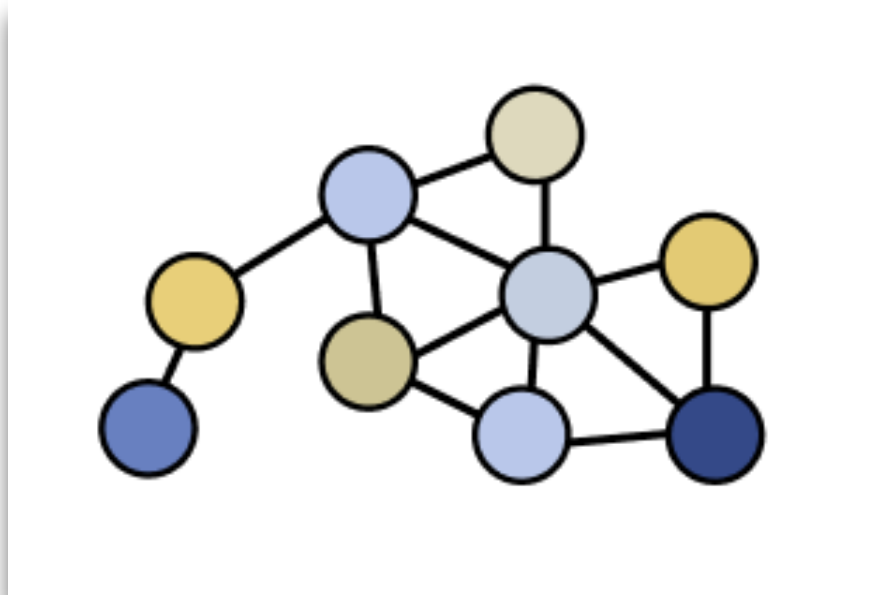
**ENVI**: paired with a conditional autoencoder that simultaneously embeds scRNA-seq and multiplexed spatial transcriptomic data into a unified latent embedding one can transfer niches onto scRNA-seq data

# Summary: What are graphs and niches in spatial comics?

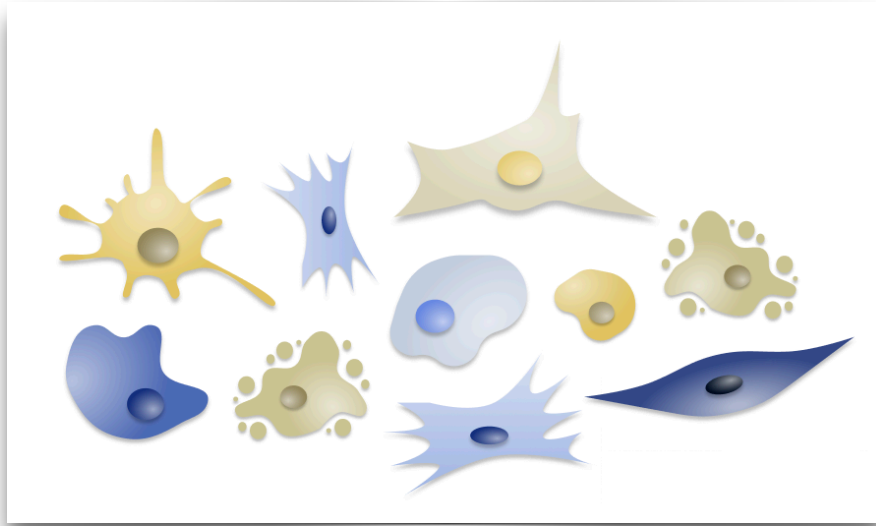


**Graph:** Often defined based on spatial proximity in  $\mu\text{m}$  or pixels

# Summary: What are graphs and niches in spatial comics?



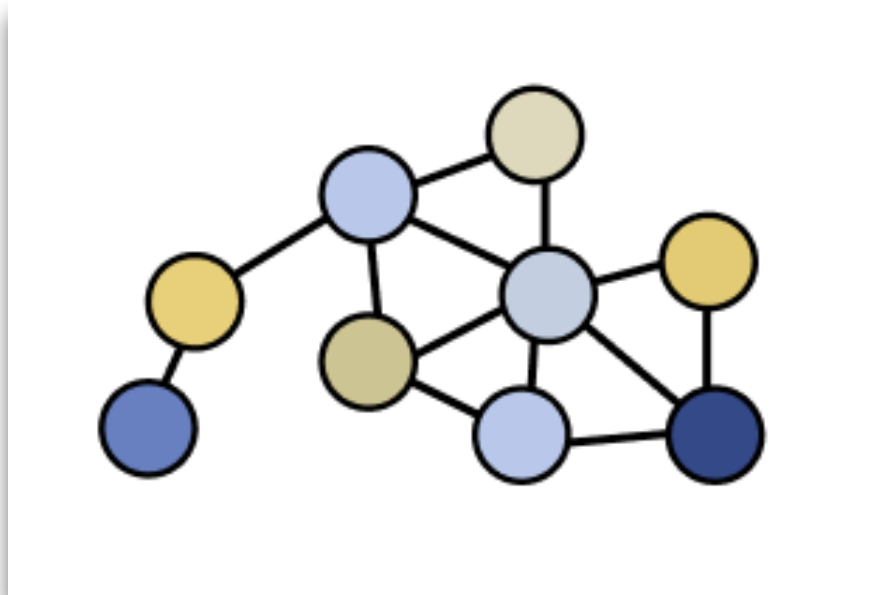
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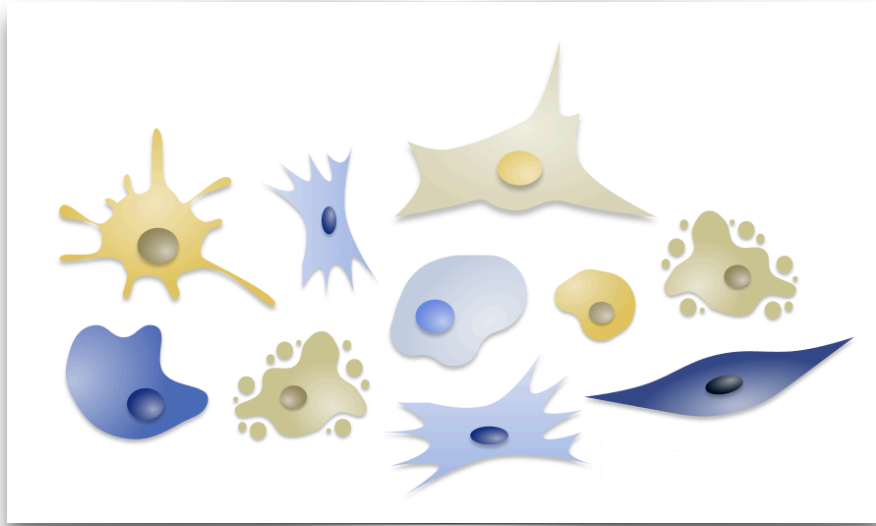
**Niche:** Cellular microenvironment often defined on a close to intermediate length scale



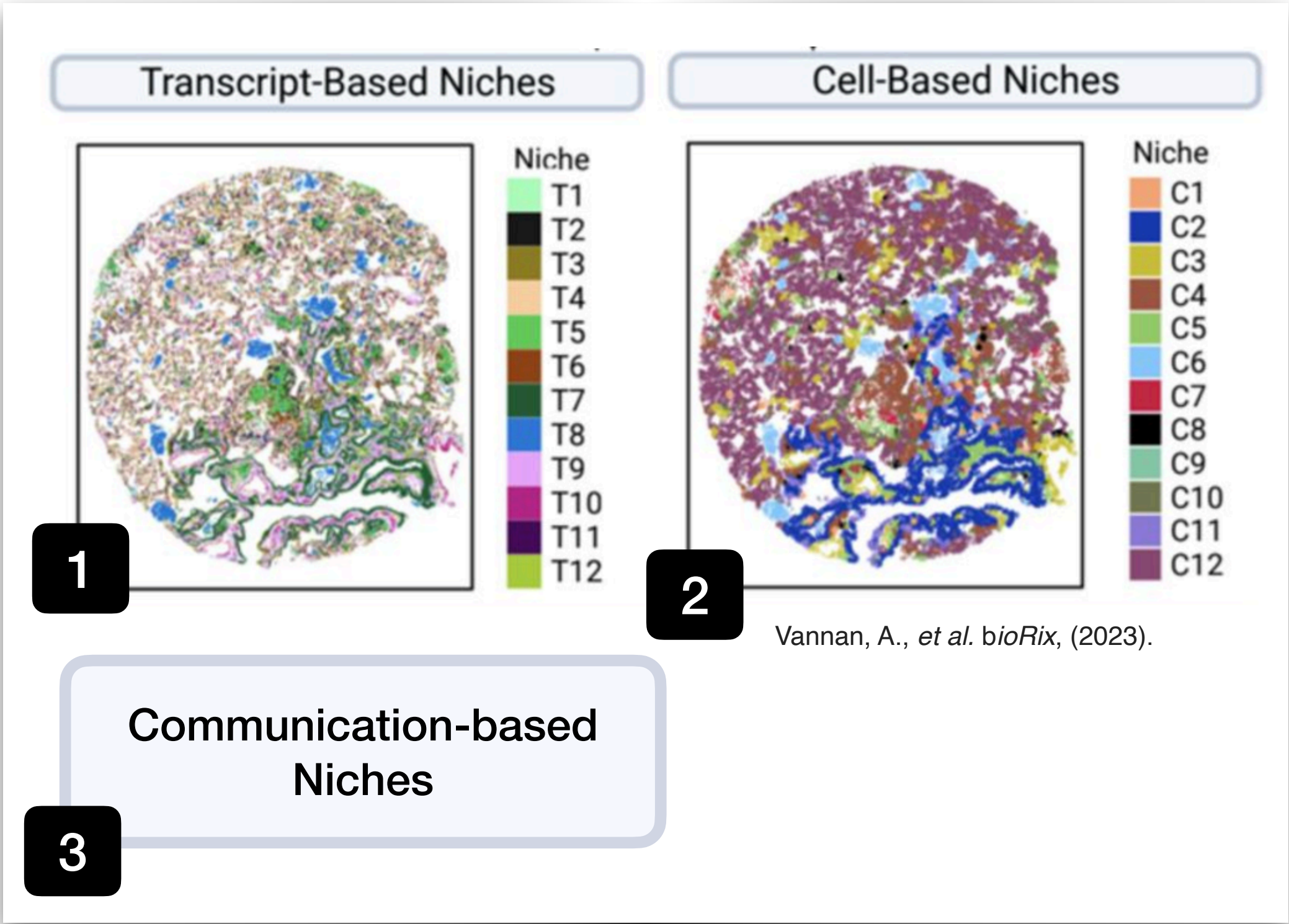
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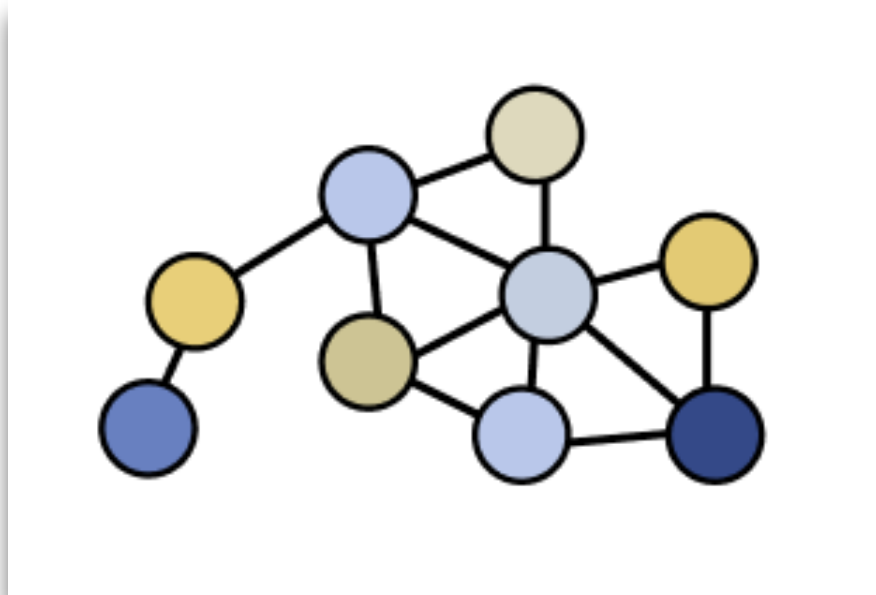


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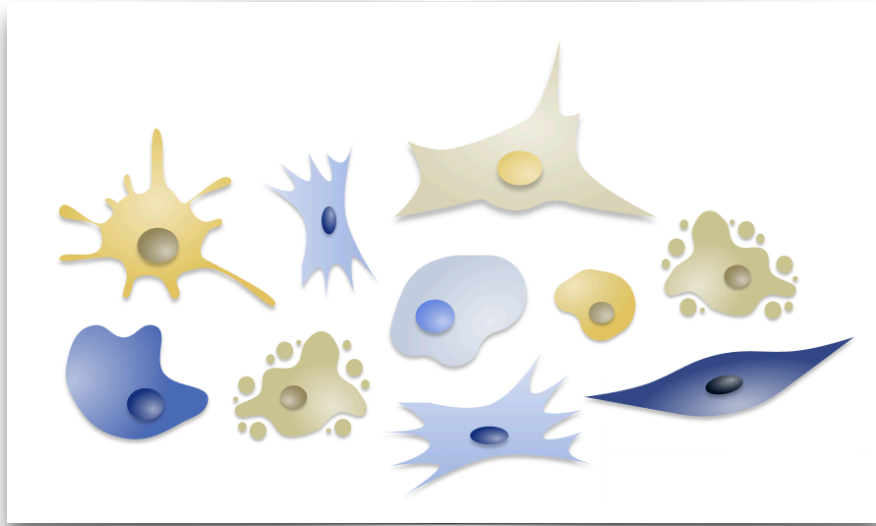


**Niche definitions:** Niches can be defined in various ways, currently there is no «one-fits-all» solution and optimal analysis steps depend on use-case/goal

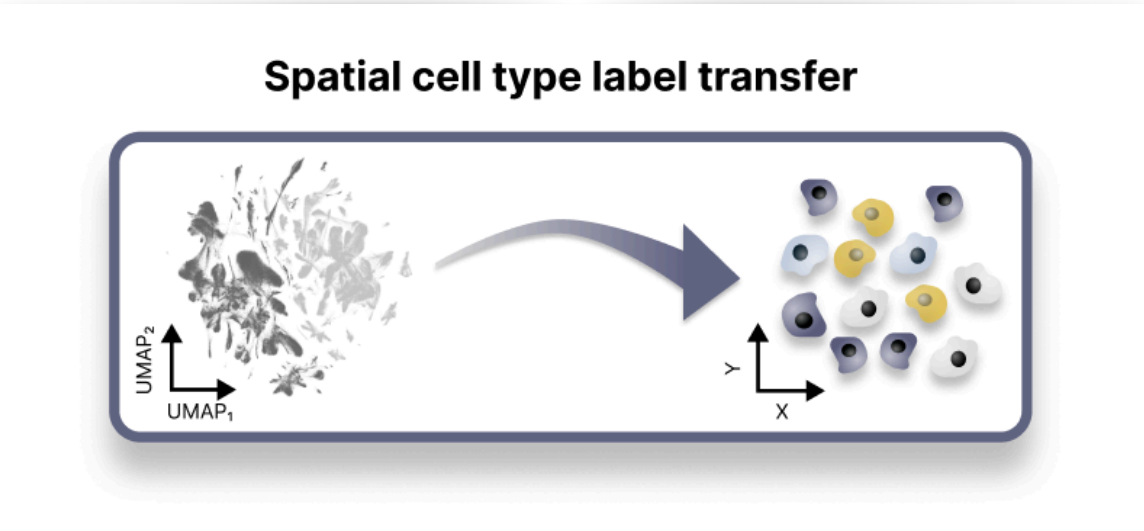
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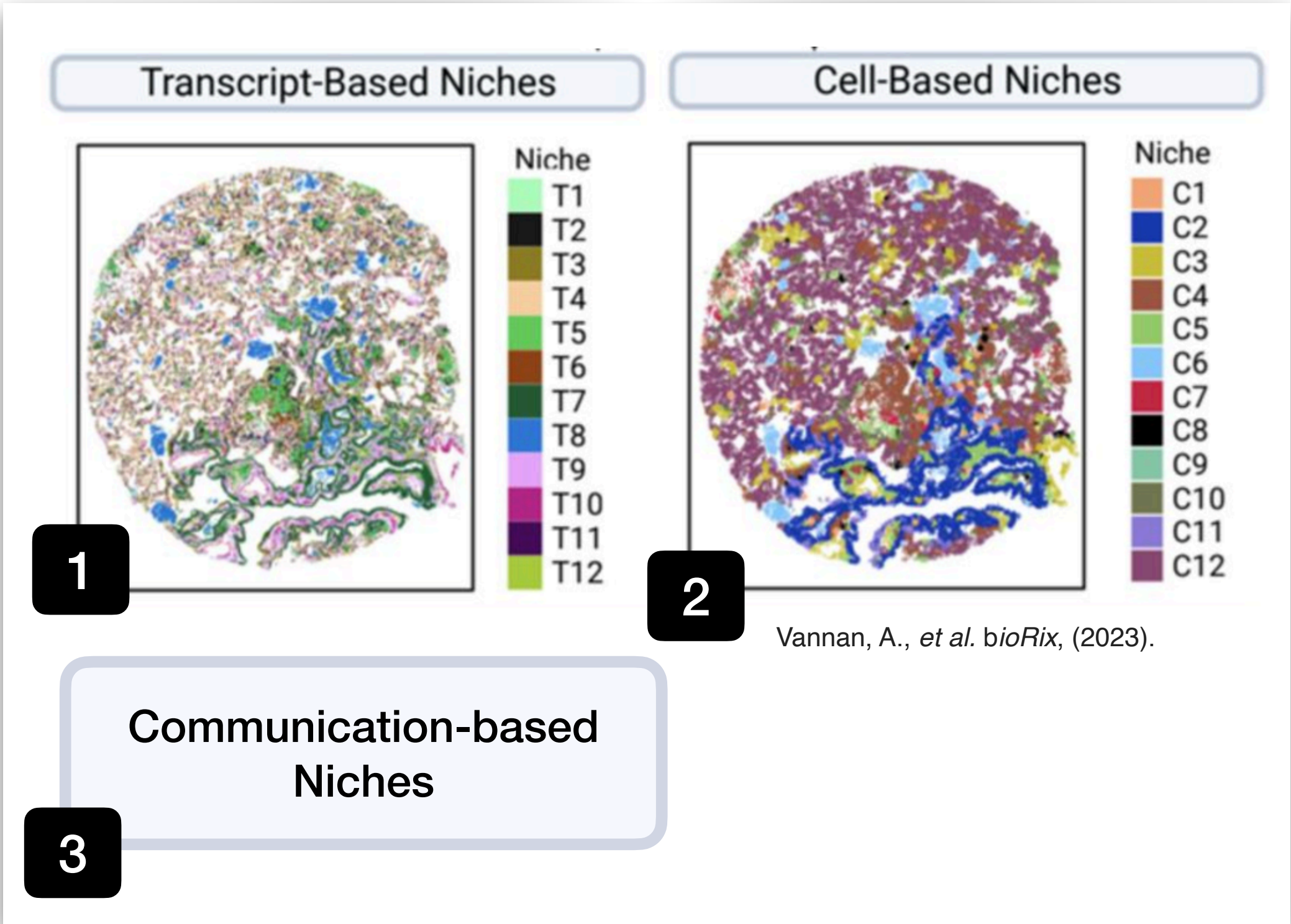
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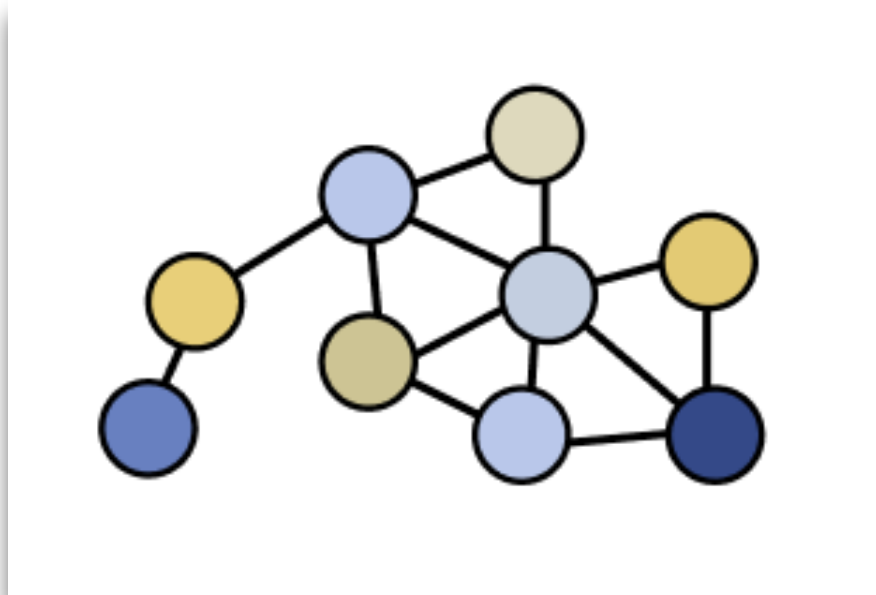


**Niche transfer:** Recent methods aim to enrich dissociated data with knowledge obtained through spatial mics

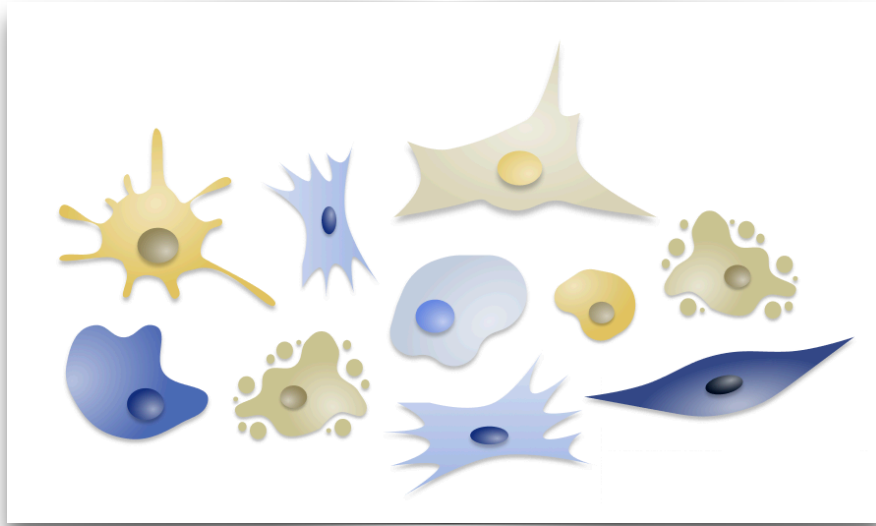


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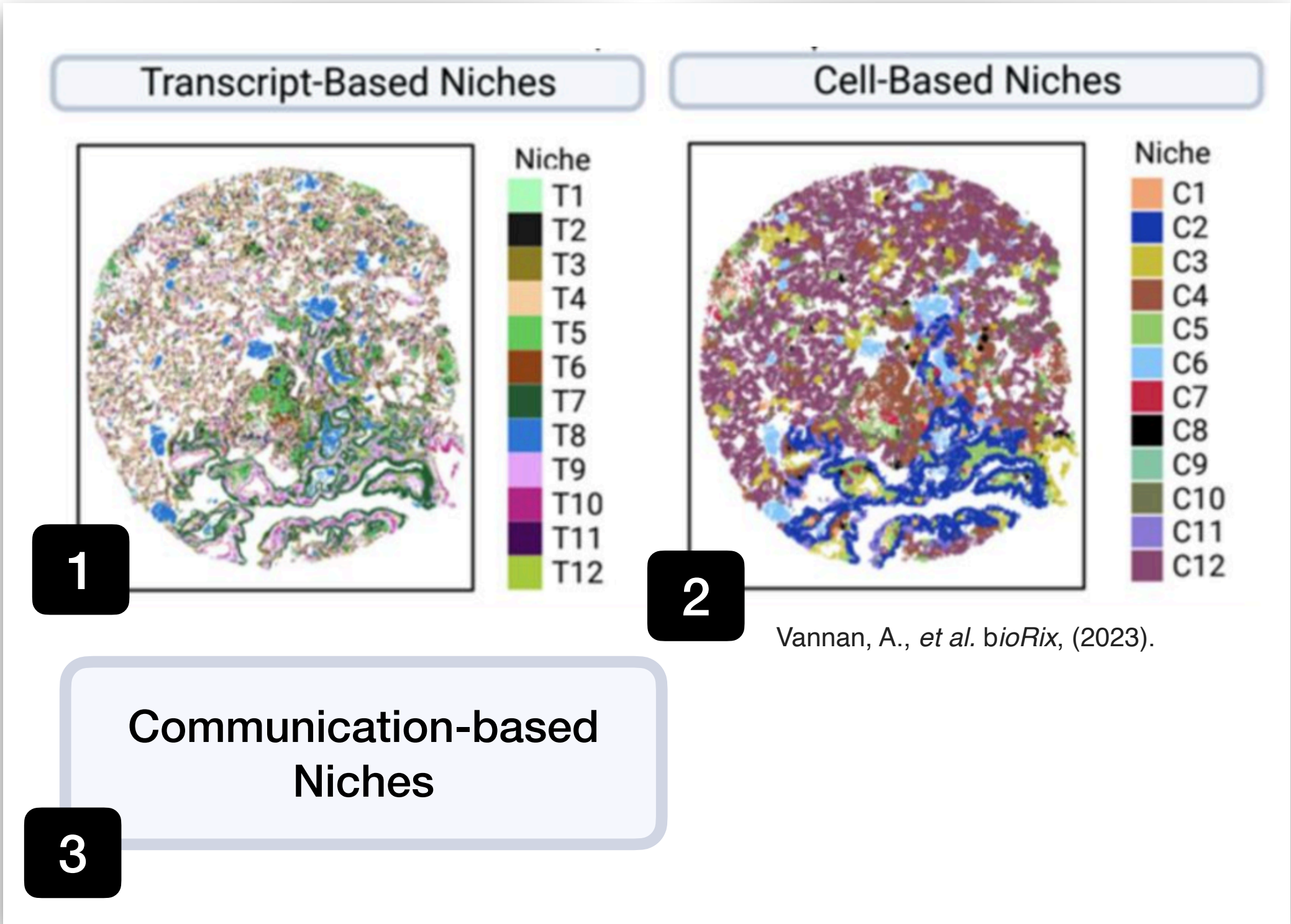
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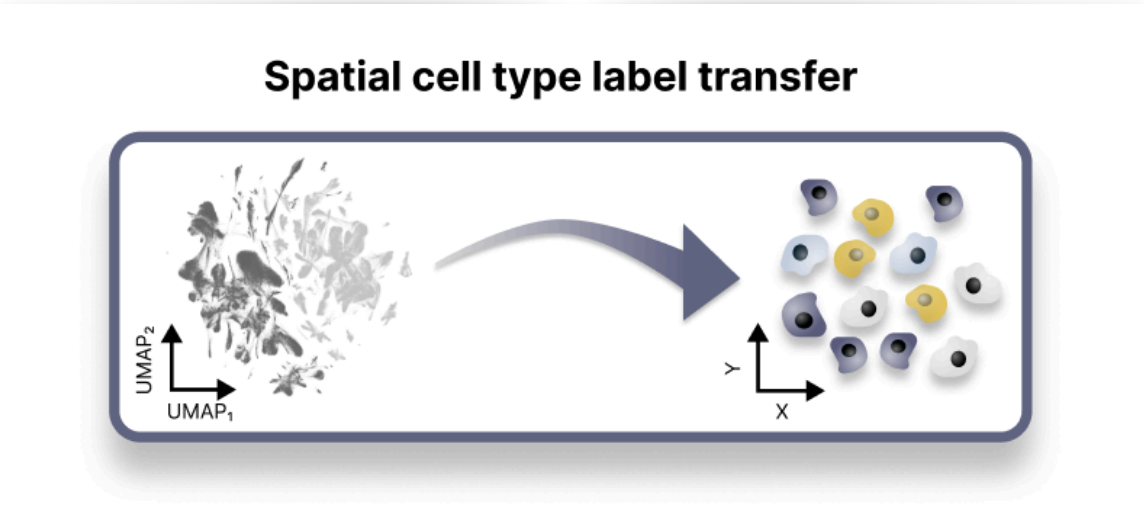
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**Niche transfer:** Recent methods aim to enrich dissociated data with knowledge obtained through spatial mics



**Clinical relevance:** Differences in spatial niches in disease cohorts can be linked to patient sub stratification and is useful for overall survival analysis.

# Acknowledgements



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David Fischer



# Thank you!

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