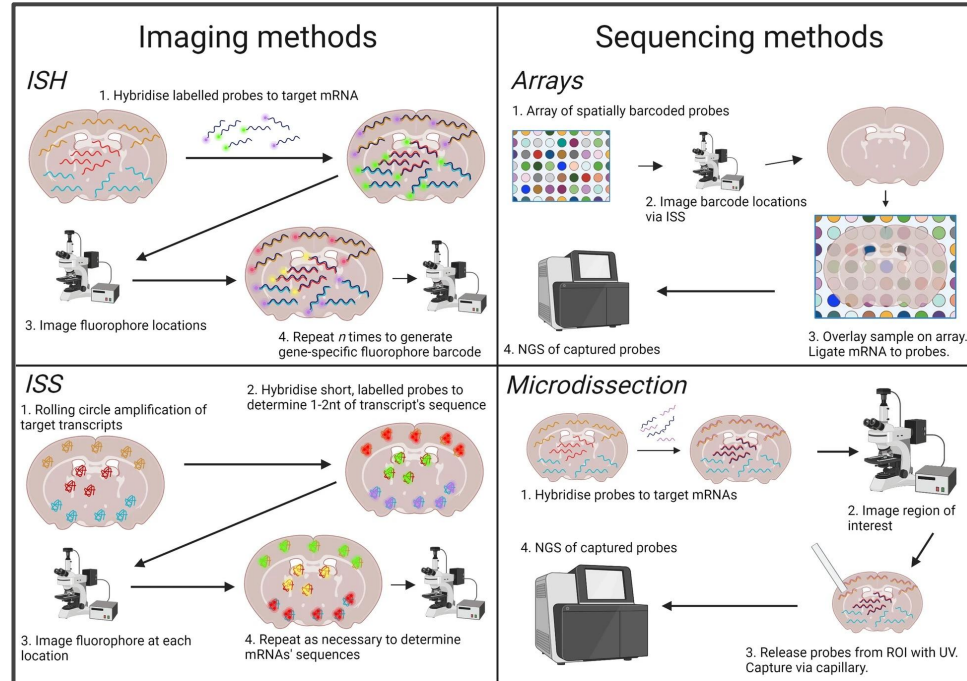


Identification of regionally variant genes

Orhan Hosten-Mittermaier

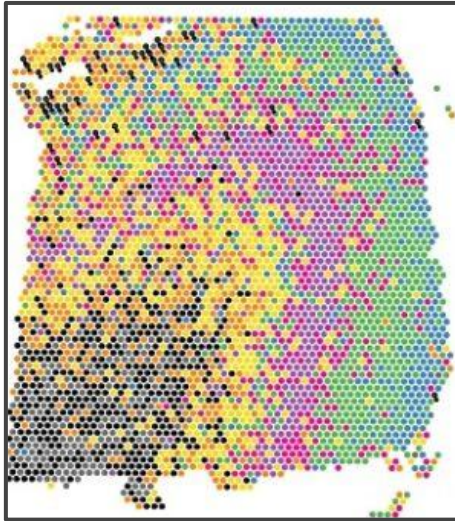
Spatial Transcriptomics Enables Profiling of Cells in Space

Goal: understand spatial relationships of mRNA expression

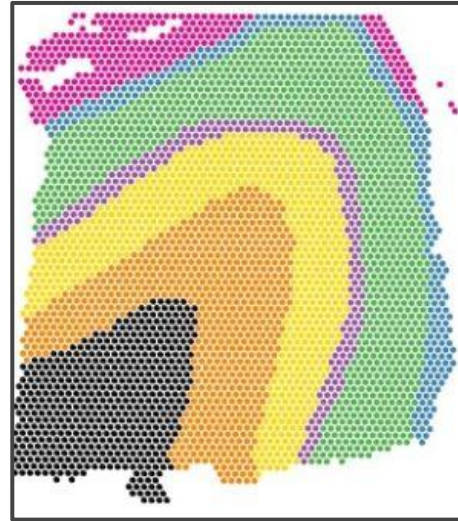


Spatial Transcriptomics Enables Profiling of Cells in Space

Cell type clustering

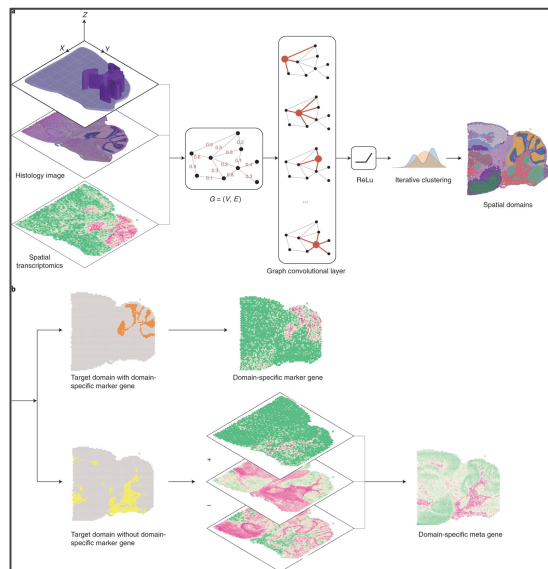


Regions in space



How are regions assigned?

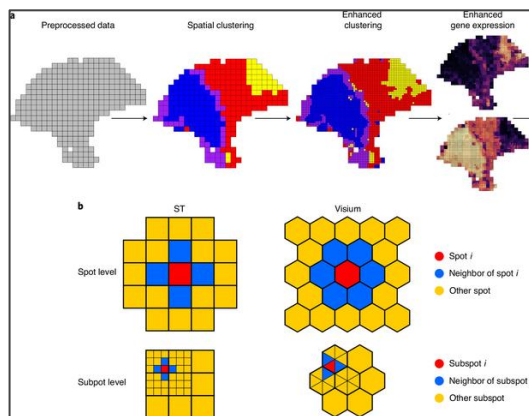
Neural Network



STAGATE, SpaGCN, GASTON

Hu, et al.

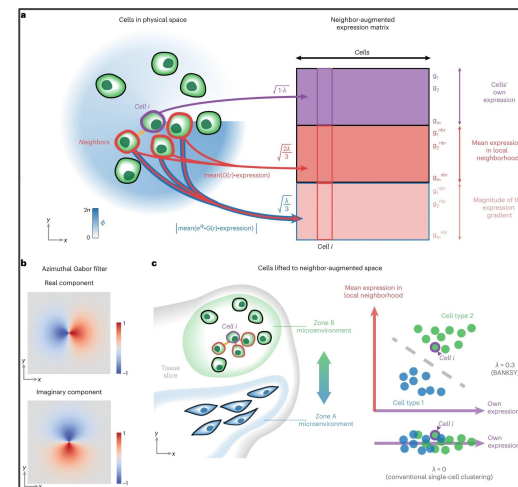
HMMRF



BayesSpace, Giotto

Zhao, et al.

Spatial Smoothing



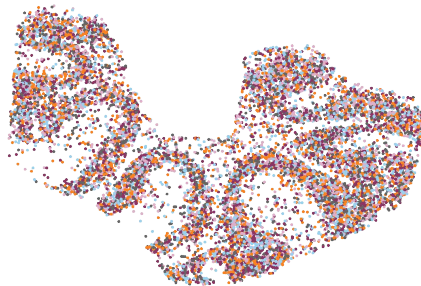
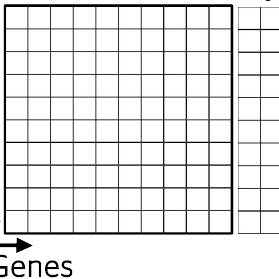
BANKSY, Concordex

Singhal, et. al.

Concordex

Input

Spots/Cells
↑
Genes



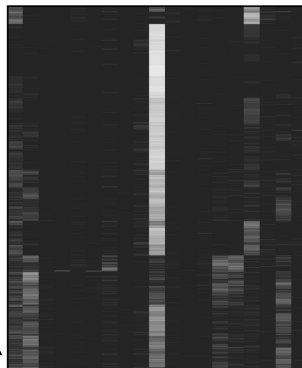
- Cell type 1
- Cell type 2
- Cell type 3
- Cell type 4
- Cell type 5
- Cell type 6
- Cell type 7
- Cell type 8



1. kNN Graph

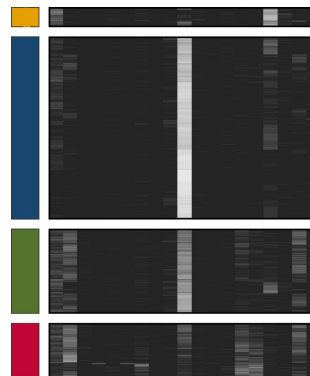


Spots/Cells
↑
Annotations

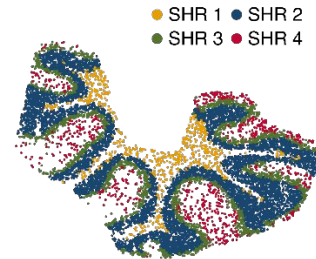


2. Neighborhood Consolidation Matrix

Fraction



3. Region Clustering



Guiding Research Questions

- A. Are there region specific genes?
 - a. genes expressed differentially across regions (“regional DE genes”)
- B. Are there region specific DE genes w/in a cell type?
 - a. Genes expressed differentially in a cell type between regions (“cell type-regional DE genes”)
- C. How can we leverage spatial information to gain more insight?

The Dataset

Technology: Slide-seq V2

Tissue: Mouse Cerebellum

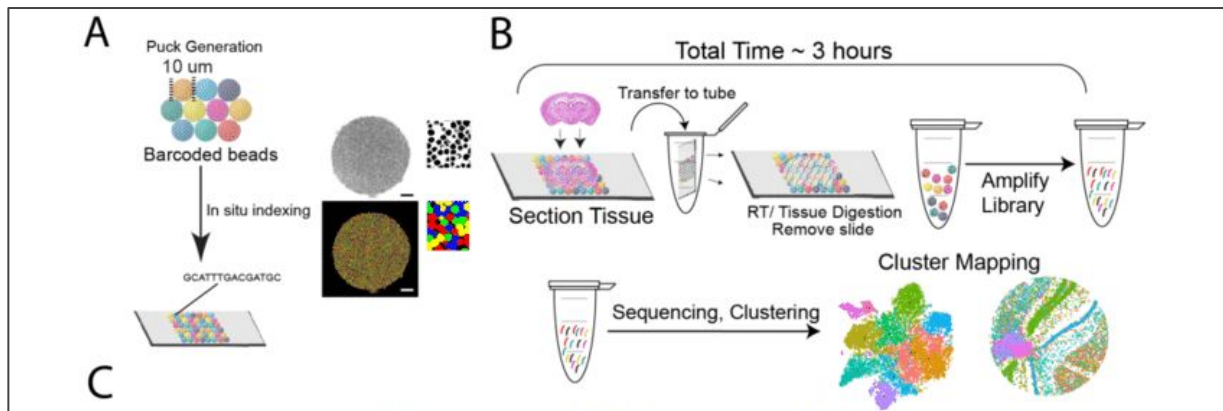
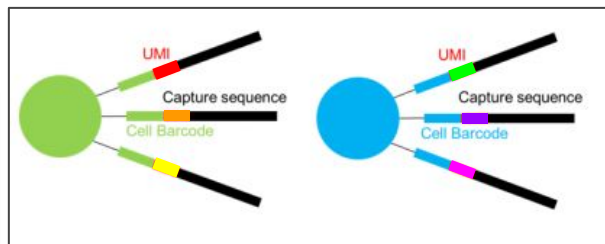


- | | |
|---------------|--------------------|
| ● Astrocytes | ● Lugaro |
| ● Bergmann | ● MLI1 |
| ● Candelabrum | ● MLI2 |
| ● Choroid | ● Macrophages |
| ● Endothelial | ● Microglia |
| ● Ependymal | ● Oligodendrocytes |
| ● Fibroblast | ● Polydendrocytes |
| ● Globular | ● Purkinje |
| ● Golgi | ● UBCs |
| ● Granule | |

The Dataset

Technology: Slide-seq V2

Tissue: Mouse Cerebellum



The Dataset

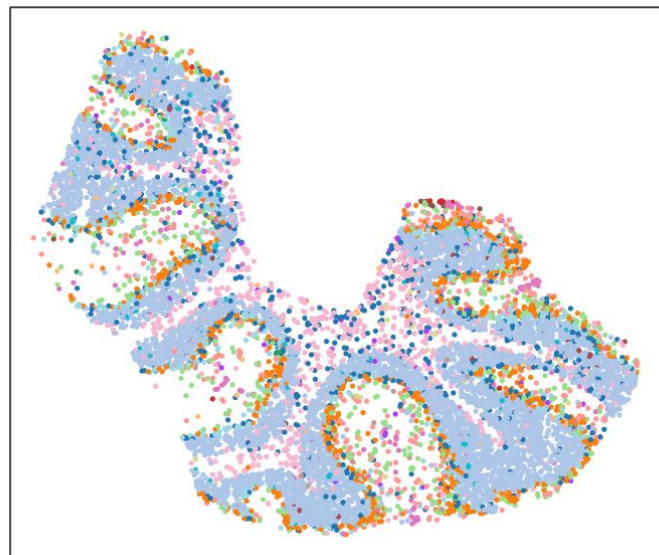
Technology: Slide-seq V2

Tissue: Mouse Cerebellum

cells captured: **9,985**

genes found: **23,096**

cell types identified: **19**



- | | |
|---------------|--------------------|
| ● Astrocytes | ● Lugaro |
| ● Bergmann | ● MLI1 |
| ● Candelabrum | ● MLI2 |
| ● Choroid | ● Macrophages |
| ● Endothelial | ● Microglia |
| ● Ependymal | ● Oligodendrocytes |
| ● Fibroblast | ● Polydendrocytes |
| ● Globular | ● Purkinje |
| ● Golgi | ● UBCs |
| ● Granule | |

The Dataset

Technology: Slide-seq V2

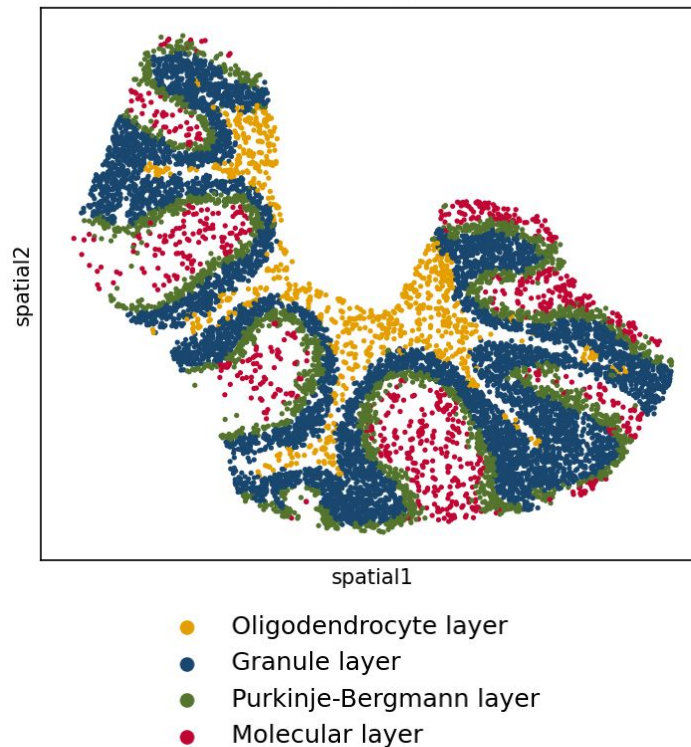
Tissue: Mouse Cerebellum

cells captured: **9,985**

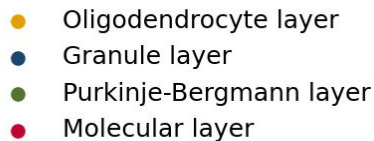
genes found: **23,096**

cell types identified: **19**

Region assignments by
concordex



Assigned regions correspond to functional regions



Pre-processing

Filtering:

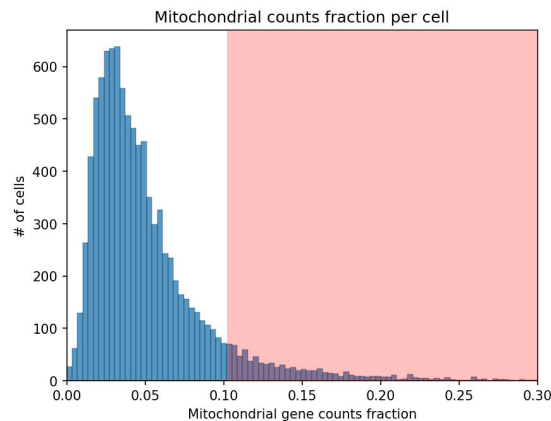
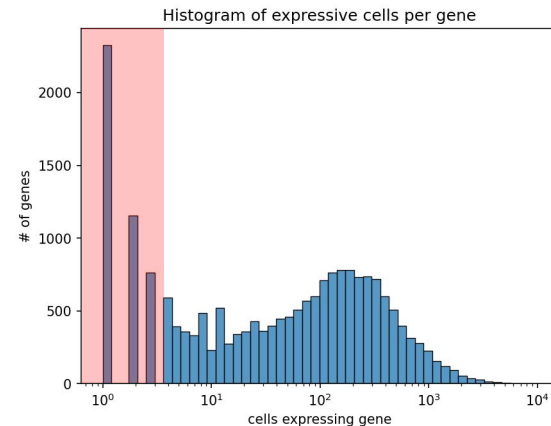
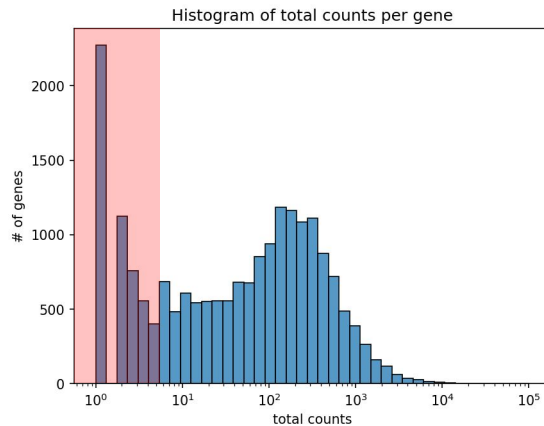
- total counts per gene > 50
- cells expressing gene > 25
- mitochondrial gene expression fraction < 0.1

Genes: **23,096** → **10,293**

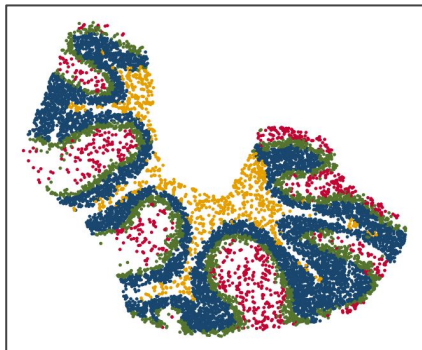
Cells: **9,985** → **9,051**

Normalization:

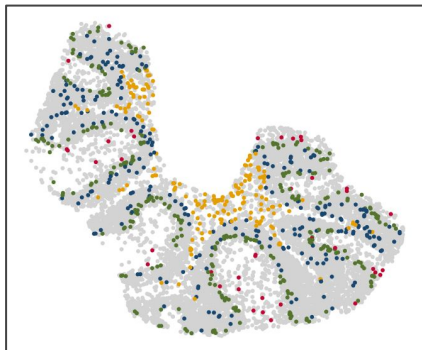
- By total counts across each cell
- log1p



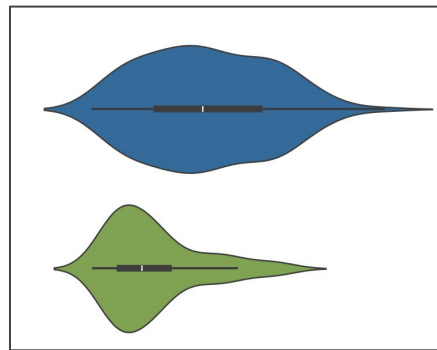
Identifying DE genes



- Oligodendrocyte layer
- Granule layer
- Purkinje-Bergmann layer
- Molecular layer



1. Isolate a cell type



2. Compare expression

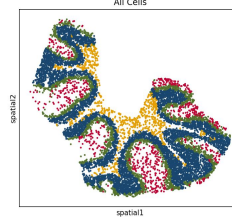
Gene	Cell Type	Regions	p-value
...
...
...
...

3. Tabulate results

204 significant comparisons
124 unique genes

Interpretation of significant results

- Oligodendrocyte layer
- Granule layer
- Purkinje-Bergmann layer
- Molecular layer



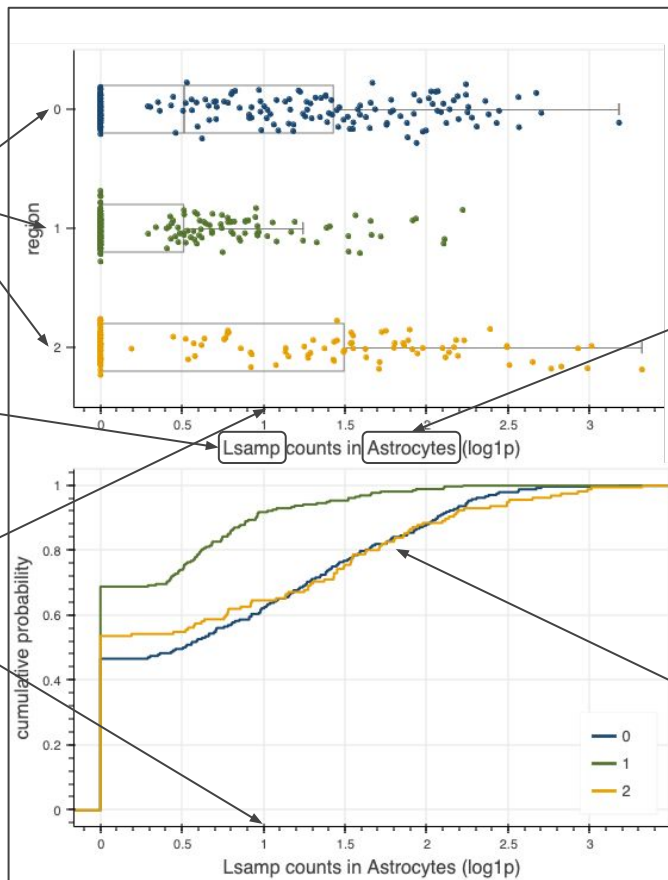
Regions included in plot if part of a pairwise stat-sig relationship

Gene

Aligned axes

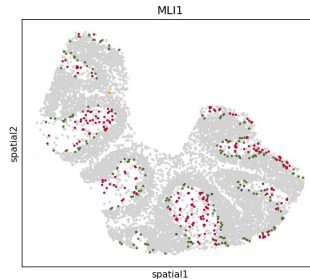
Cell type

Region colors are consistent

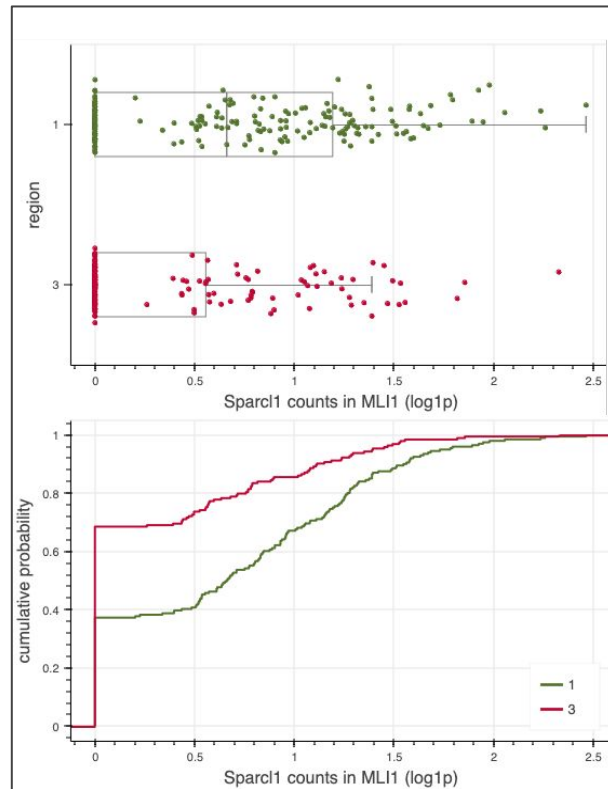
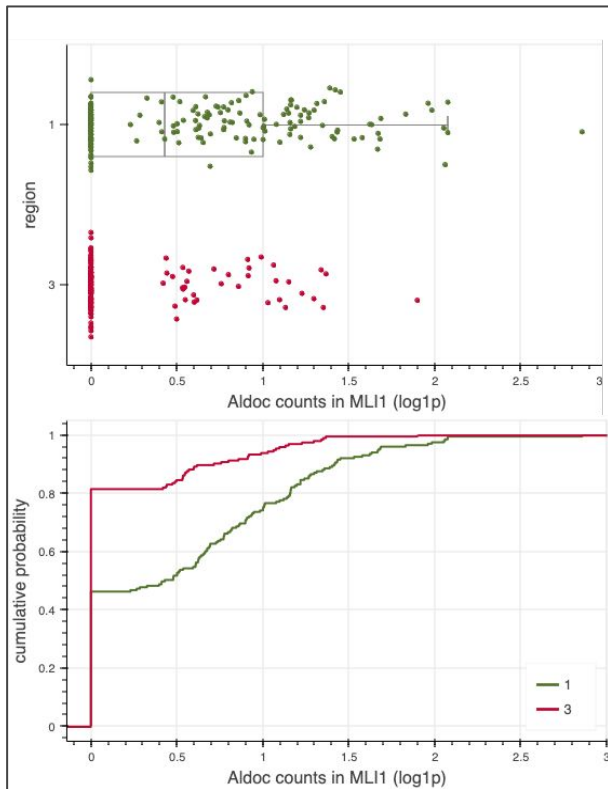


MLI1s are more active in Purkinje-Bergmann layer

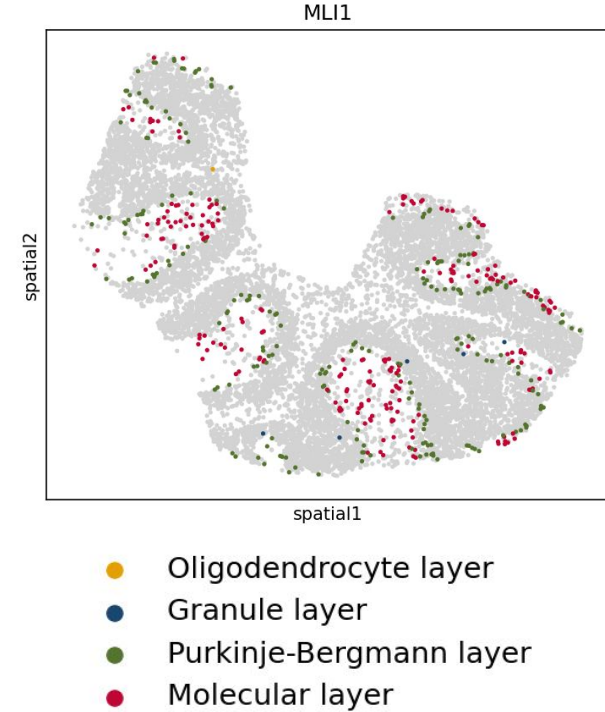
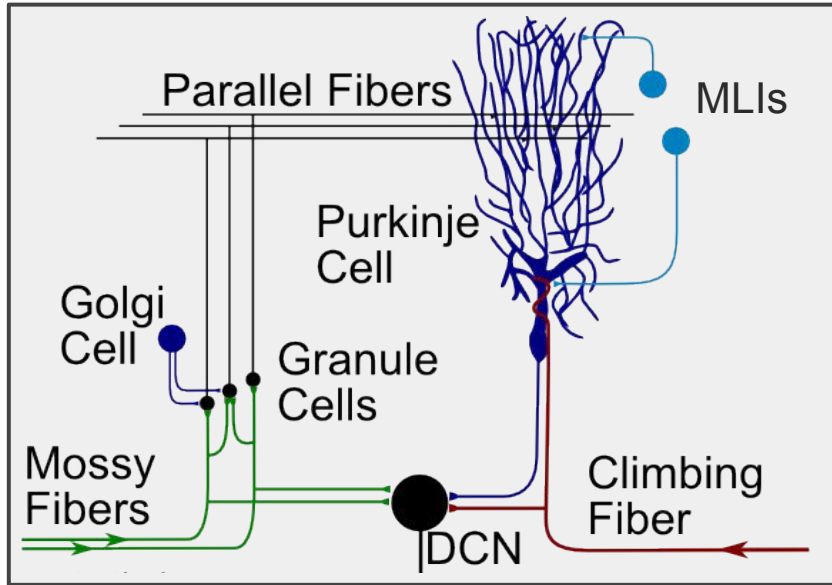
- Oligodendrocyte layer
- Granule layer
- Purkinje-Bergmann layer
- Molecular layer



Cell type: MLI1

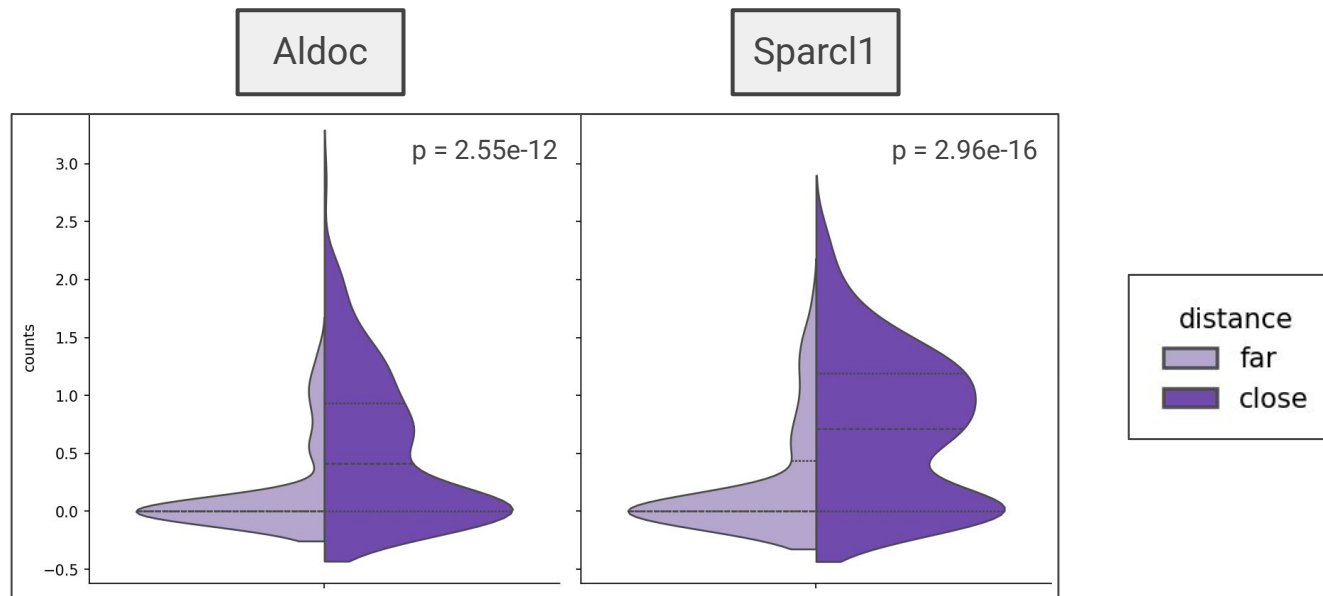


MLI1s are more active in Purkinje-Bergmann layer



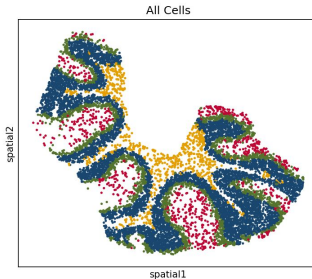
MLI1 activity levels depend on proximity to granules

Cell type: MLI1

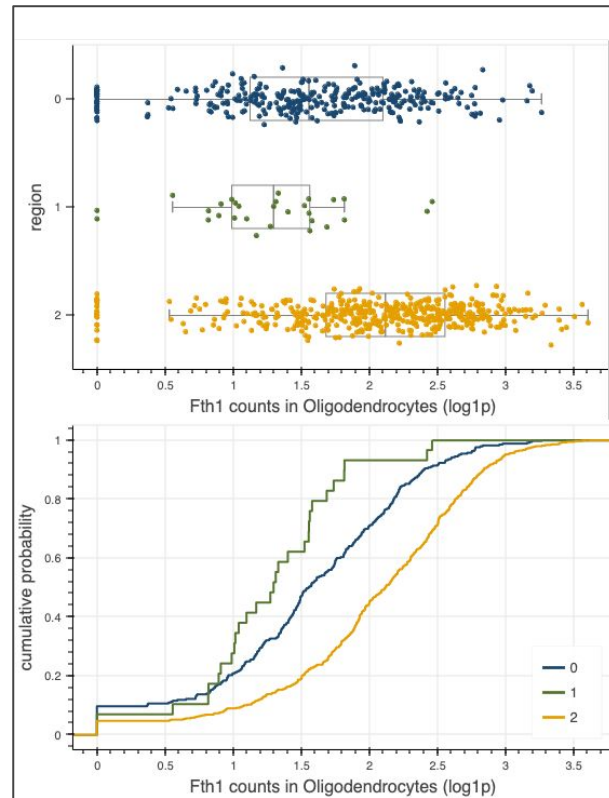
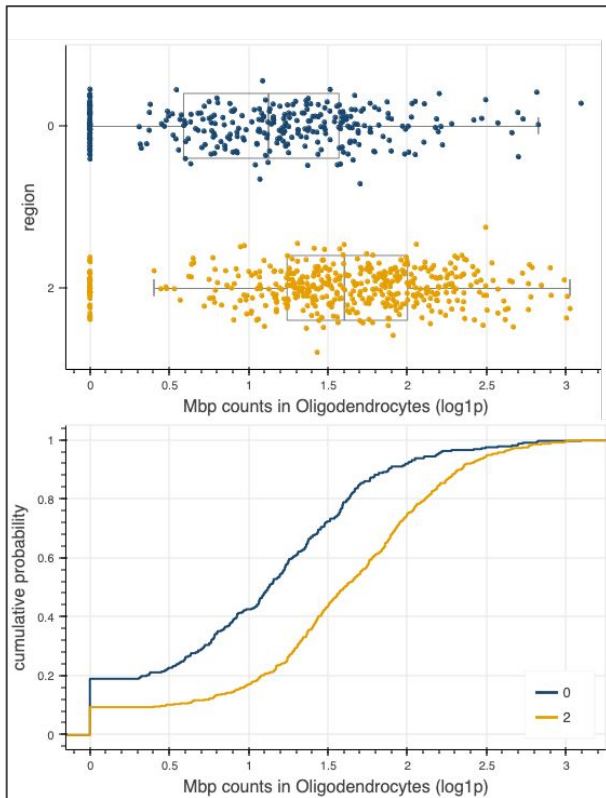


The oligodendrocyte layer has a regionally upregulated myelination function

- Oligodendrocyte layer
- Granule layer
- Purkinje-Bergmann layer
- Molecular layer

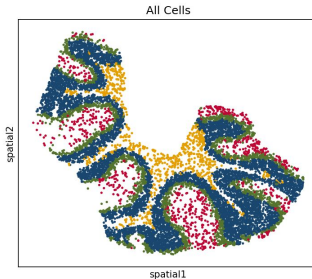


Cell type:
Oligodendrocytes

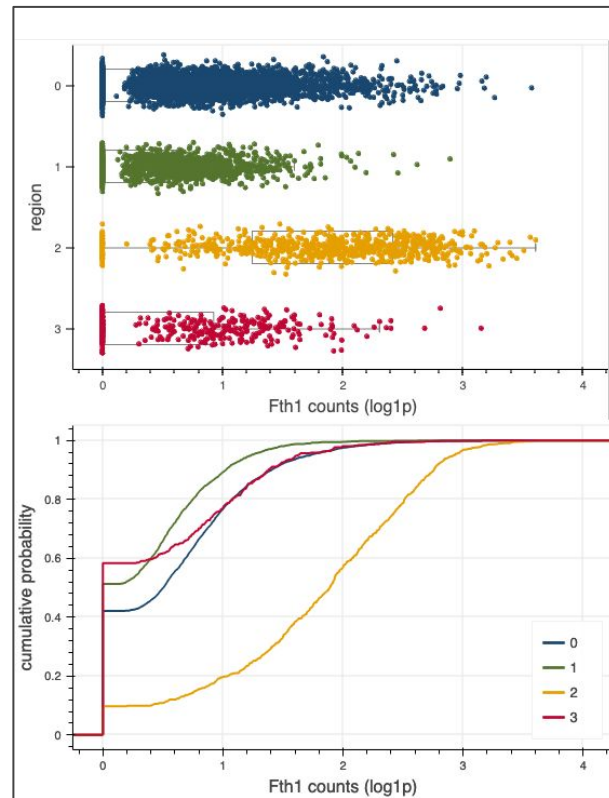
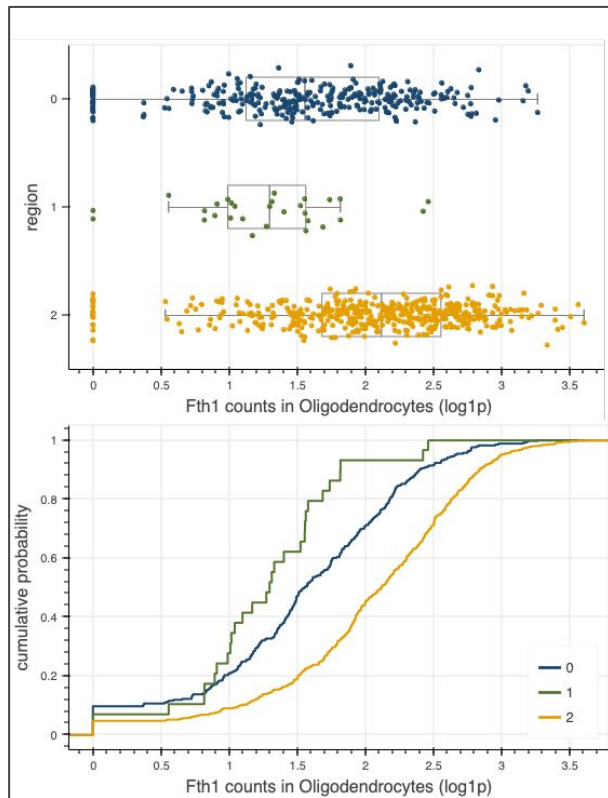


Iron storage regulation may be important for all cells in the oligodendrocyte layer

- Oligodendrocyte layer
- Granule layer
- Purkinje-Bergmann layer
- Molecular layer

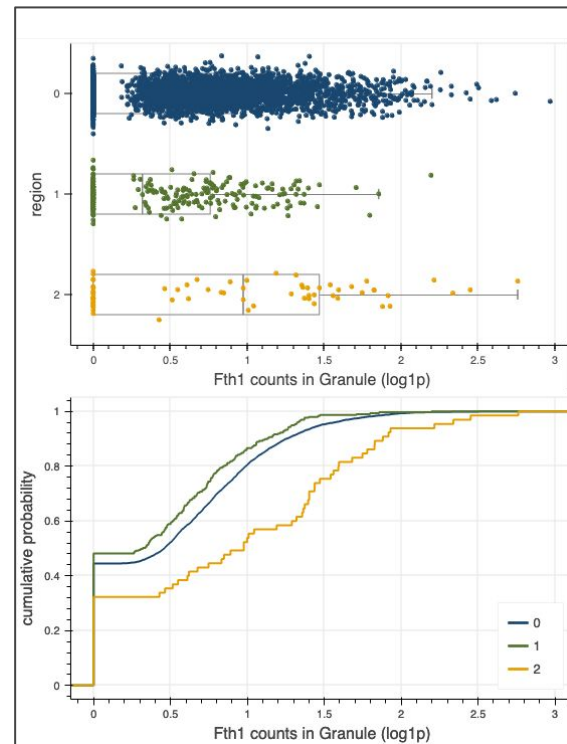
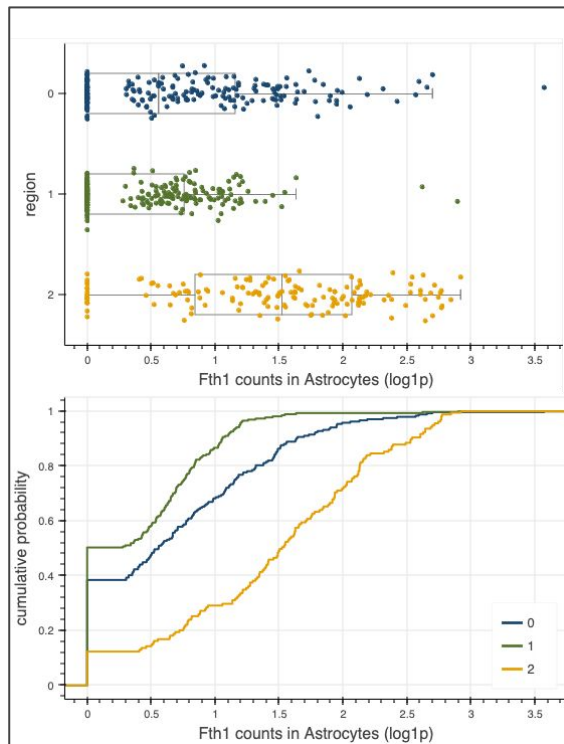
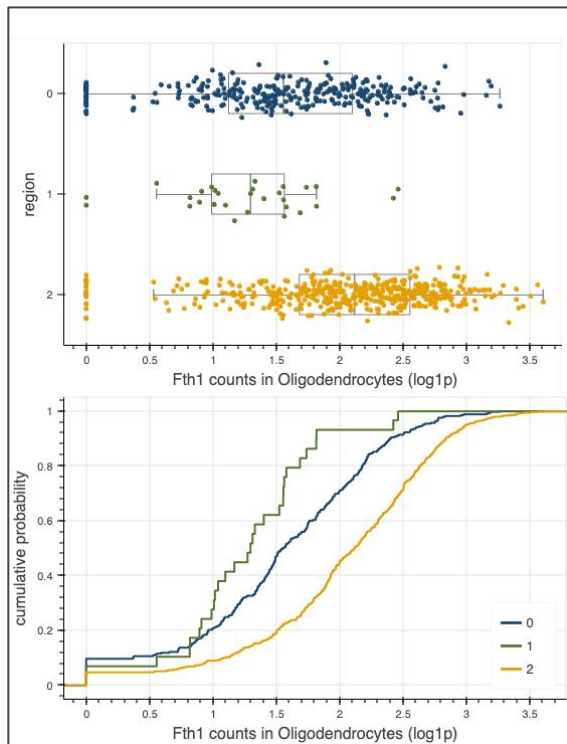
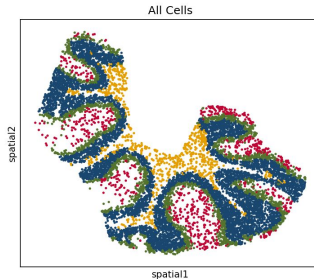


Cell type:
Oligodendrocytes



Iron storage regulation may be important for all cells in the oligodendrocyte layer

- Oligodendrocyte layer
- Granule layer
- Purkinje-Bergmann layer
- Molecular layer



Conclusions

- A. Regional differences between cells of the same type suggest differences in cell state
- B. Examining regional gene expression can be used to gain further insight into region-specific functionality
- C. Cell type clustering alone is insufficient to detect regional DE genes shared by multiple cell types

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Thank you :-)