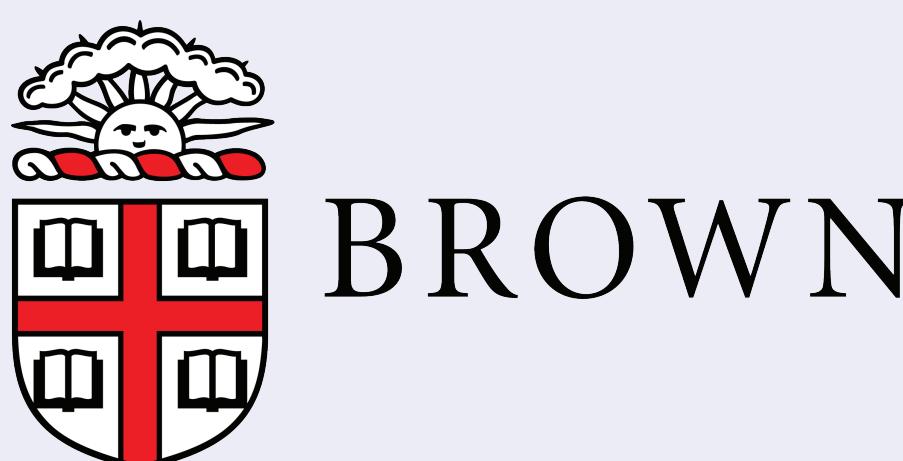


# scMultiNODE: Temporal Single-Cell Data Integration across Unaligned Modalities



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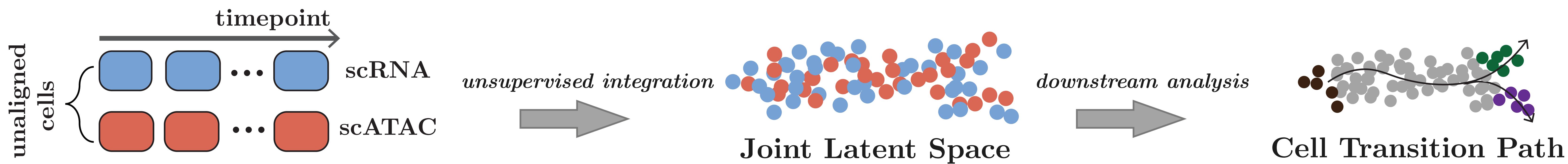


Codes & Paper

[github.com/rsinghlab/scMultiNODE](https://github.com/rsinghlab/scMultiNODE)

## Problem

- Temporal scRNA-seq data are only profiled at discrete and sparsely spaced timepoints due to laborious and expensive lab experiments
- Obtaining different sequencing assays on the same cells across developmental stages is technically challenging



## Goal

- Integrate unaligned cell profiles from two modalities: gene expression and chromatin accessibility
- Retain both **cell type variations & cellular dynamics** during integration

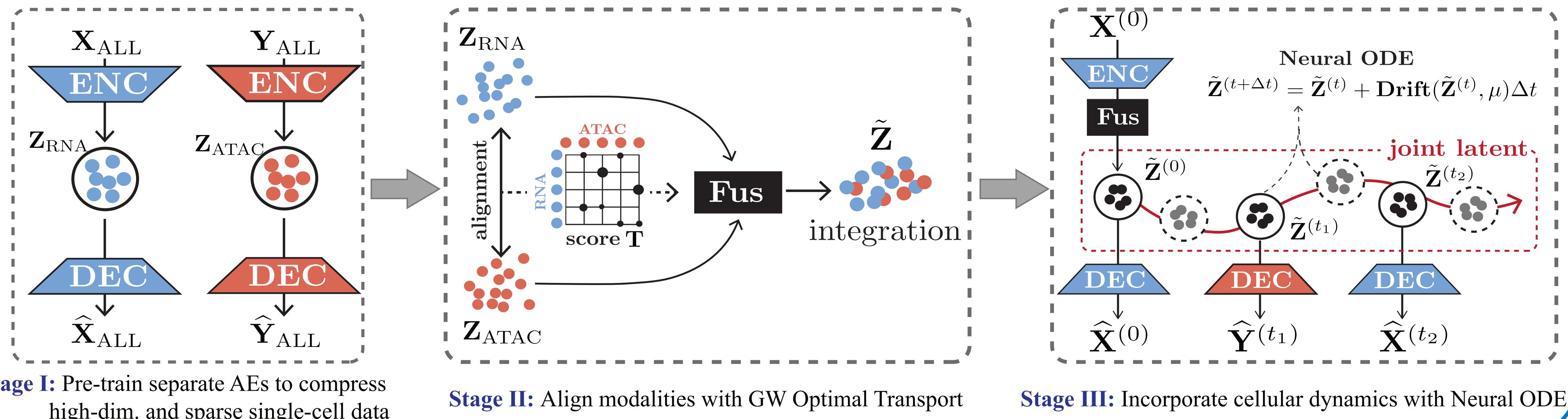
## Method: single-cell Multi-Modal Neural Ordinary Differential Equation (scMultiNODE)

### Input (e.g., scRNA-seq + scATAC-seq)

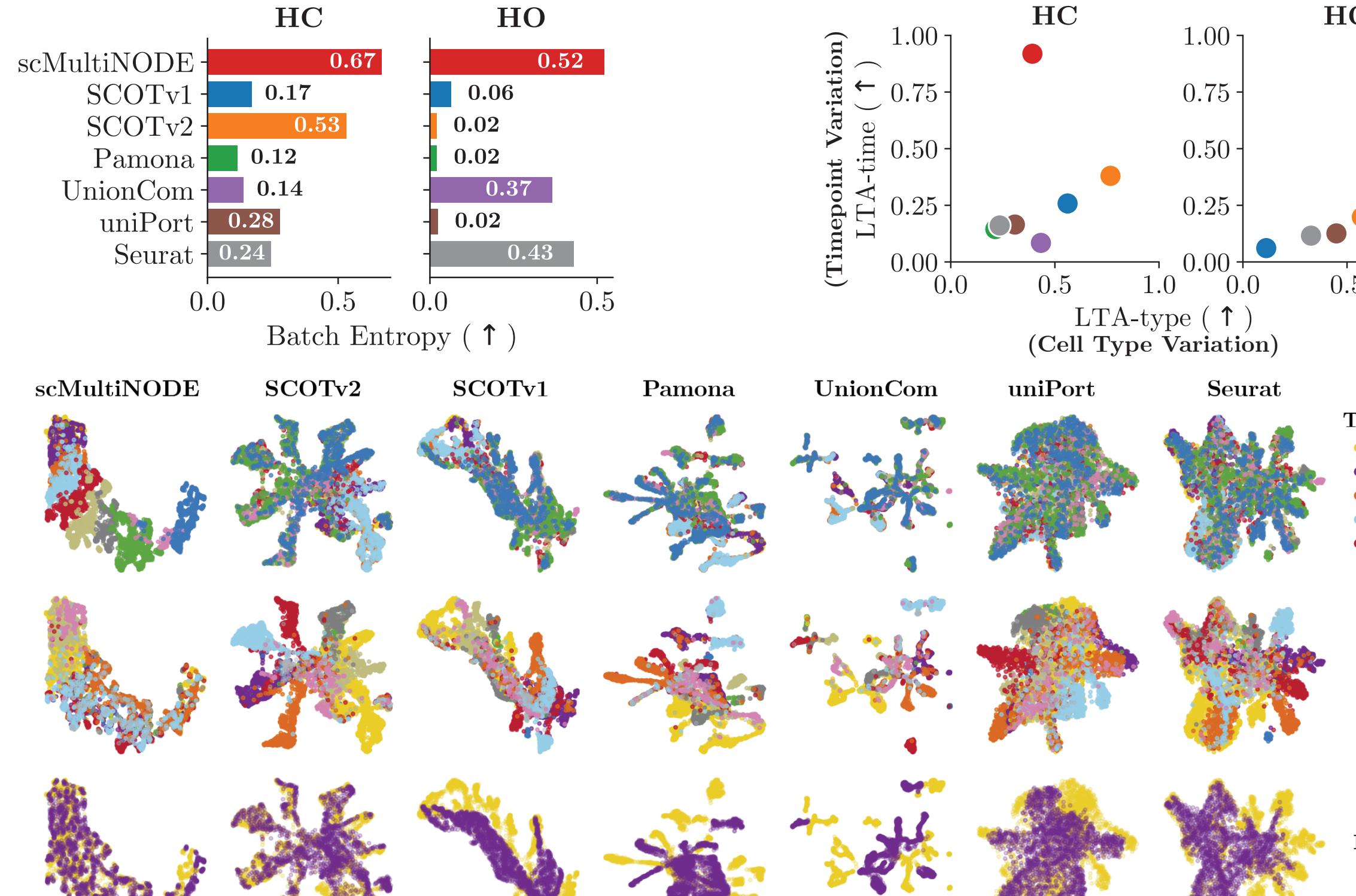
- Gene expression  $\mathbf{X}^{(t)}$  at measured timepoints  $t \in \mathcal{T}_{\text{RNA}} \subset \{0, 1, \dots\}$
- Chromatin accessibility  $\mathbf{Y}^{(t)}$  at measured timepoints  $t \in \mathcal{T}_{\text{ATAC}} \subset \{0, 1, \dots\}$

### Advantage

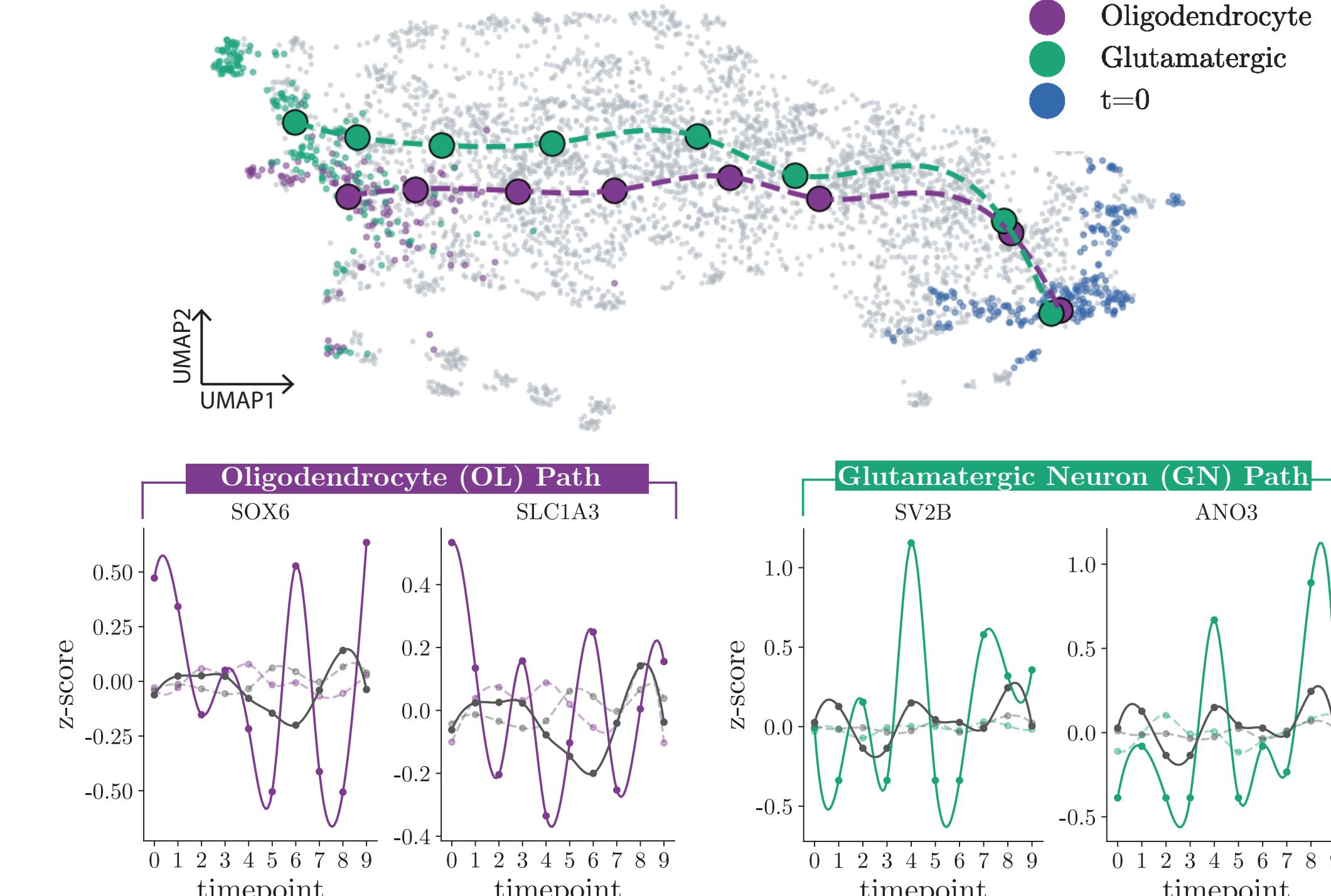
- Quantization GW enables efficient alignment across large-scale multi-modal data
- Integrations capture both cell type variations and developmental dynamics



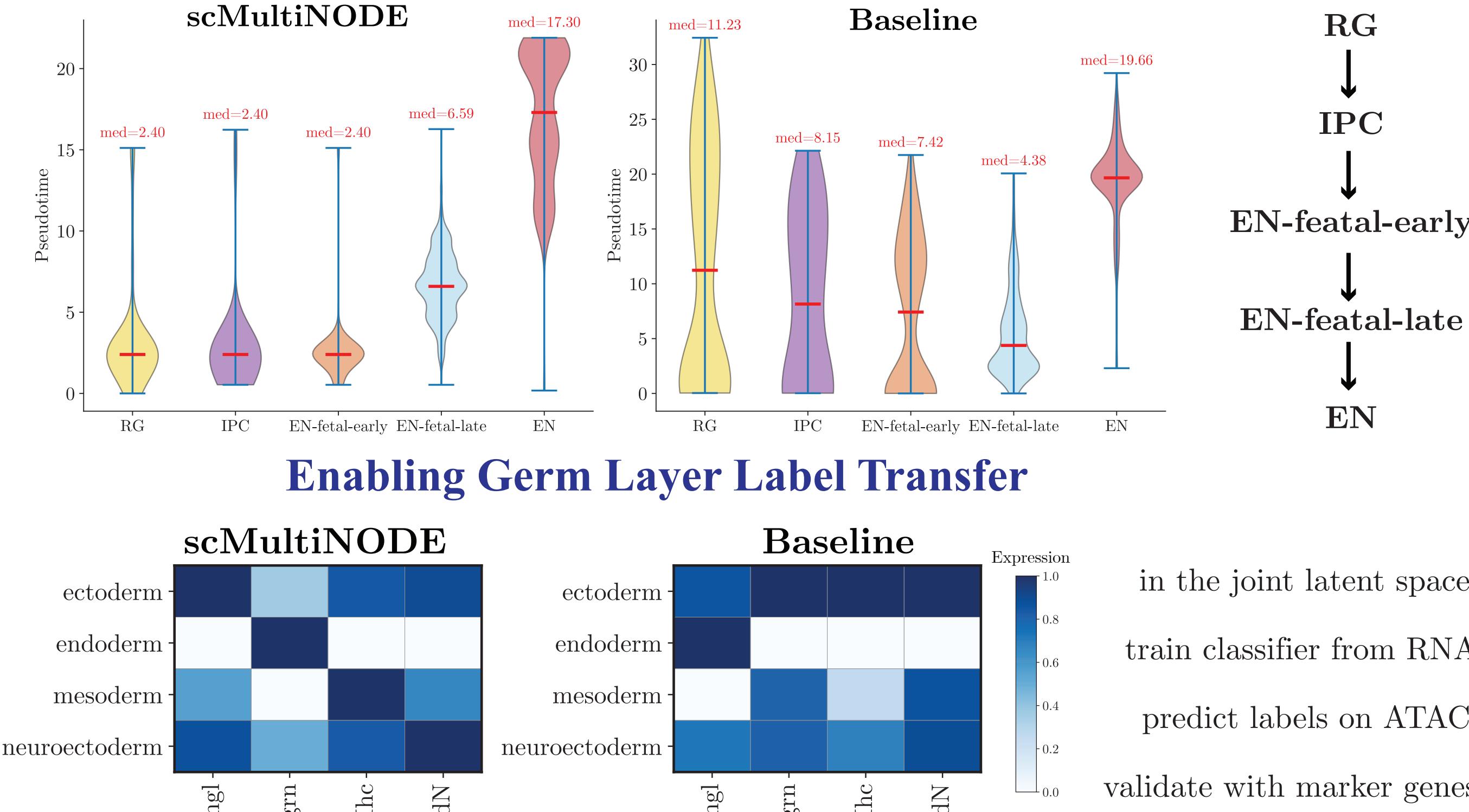
## scMultiNODE Captures Cell Type Variations & Cellular Dynamics in Integration



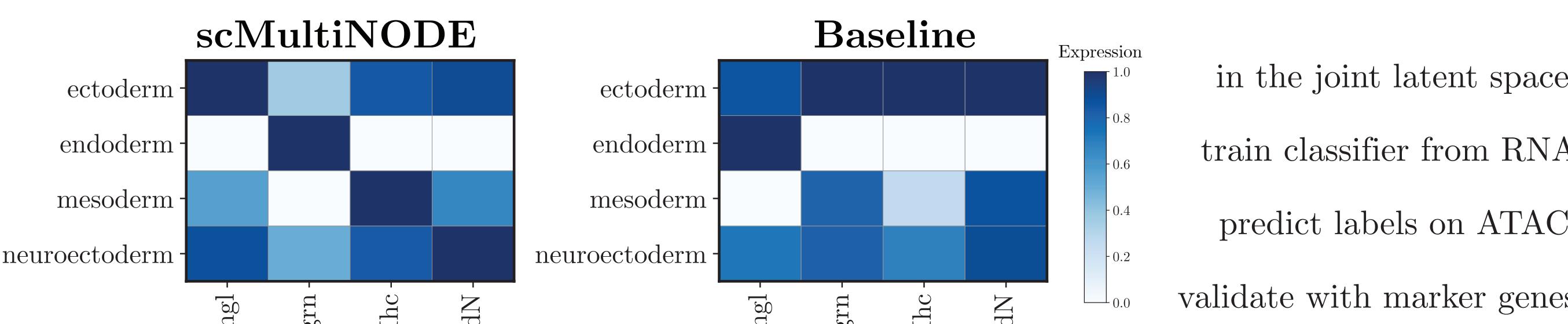
## Understanding Cell State Transition



## Improving Pseudotime Estimation



## Enabling Germ Layer Label Transfer



in the joint latent space  
train classifier from RNA  
predict labels on ATAC  
validate with marker genes