

scMultiNODE: Temporal Single-Cell Data Integration across Unaligned Modalities



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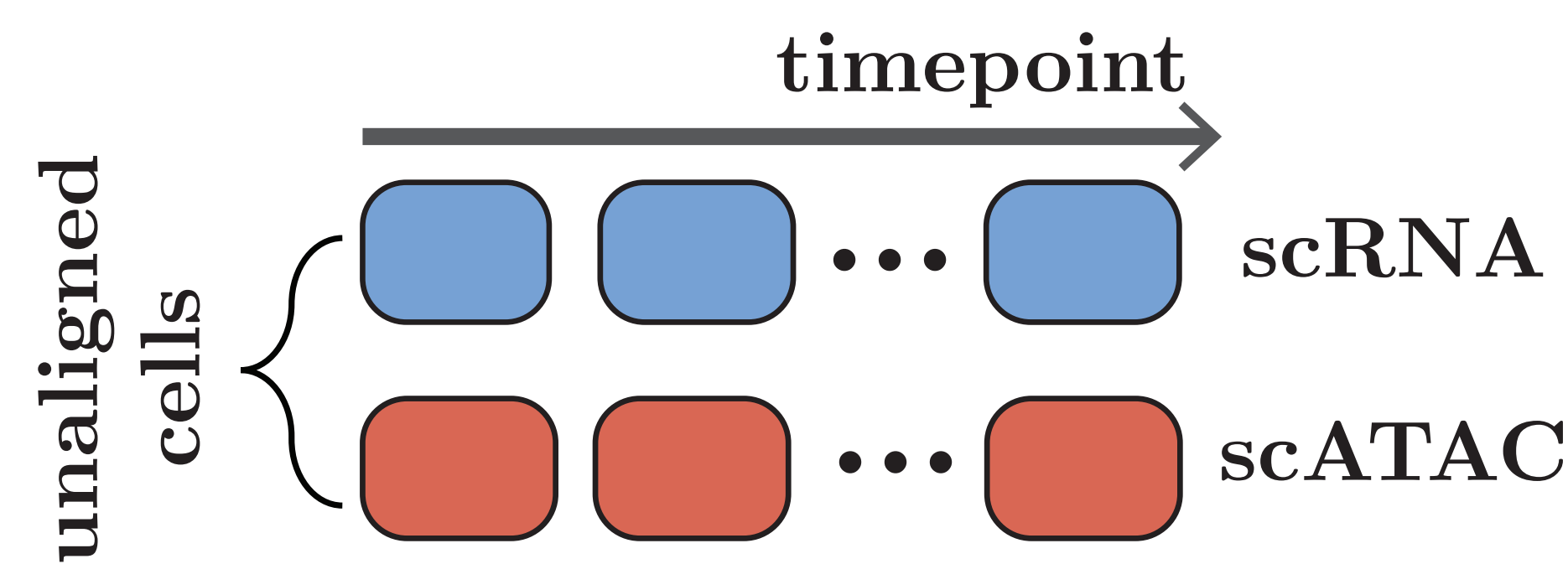


Codes & Paper

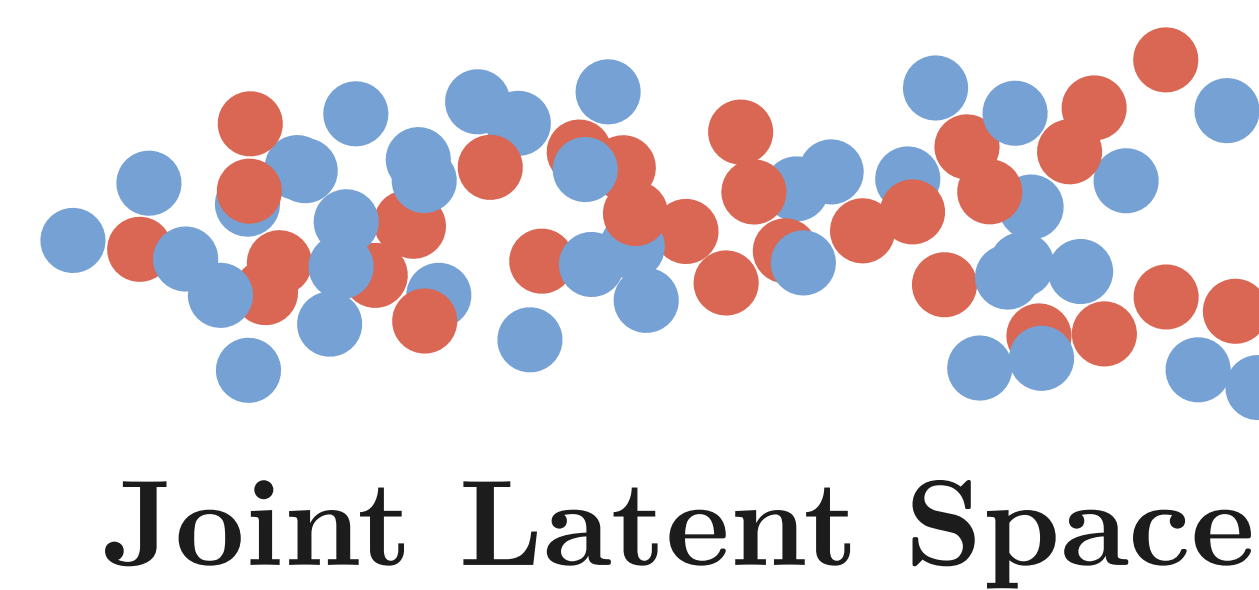
github.com/rsinghlab/scMultiNODE

Problem

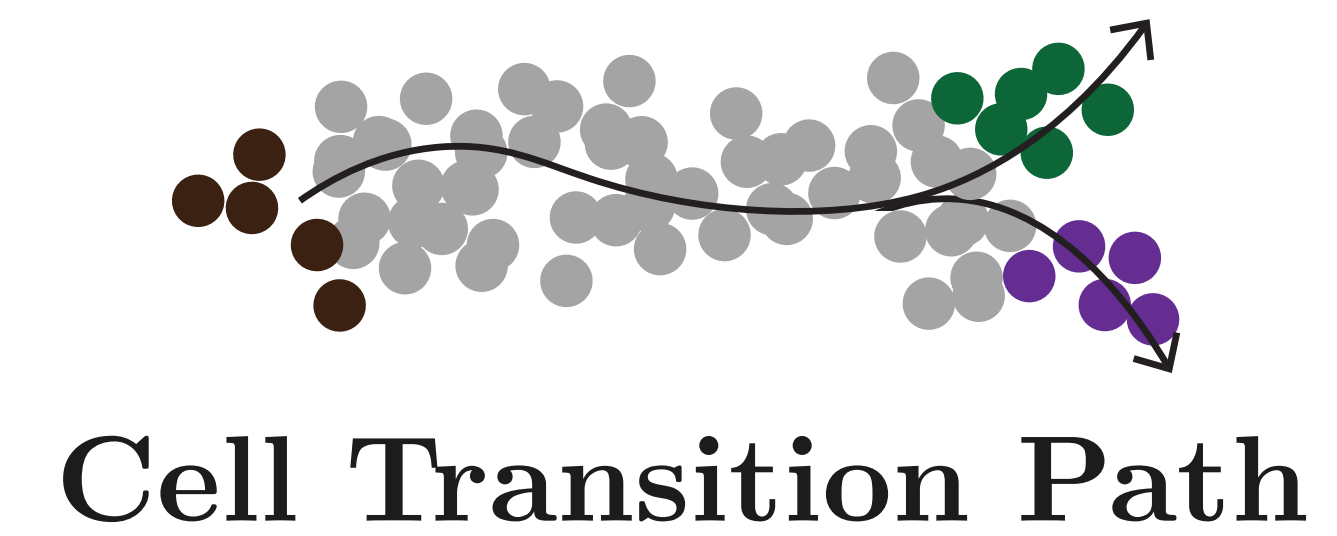
- Temporal scRNA-seq data are only profiled at discrete and sparsely spaced timepoints due to laborious and expensive lab experiments
- Obtaining different sequencing assays on the same cells across developmental stages is technically challenging



unsupervised integration



downstream analysis



Goal

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

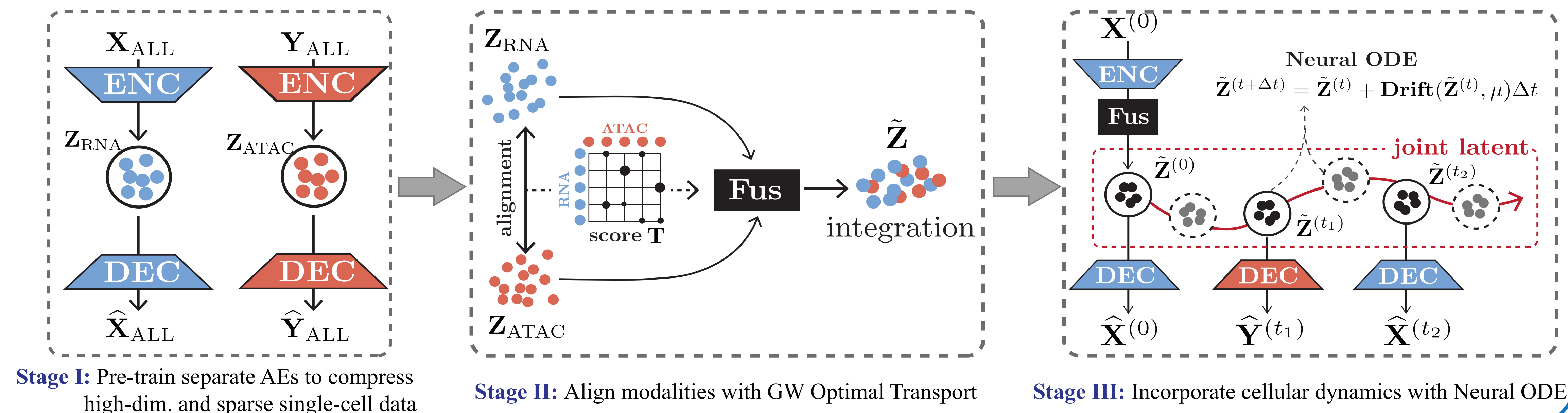
Method: single-cell Multi-Modal Neural Ordinary Differential Equation (scMultiNODE)

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

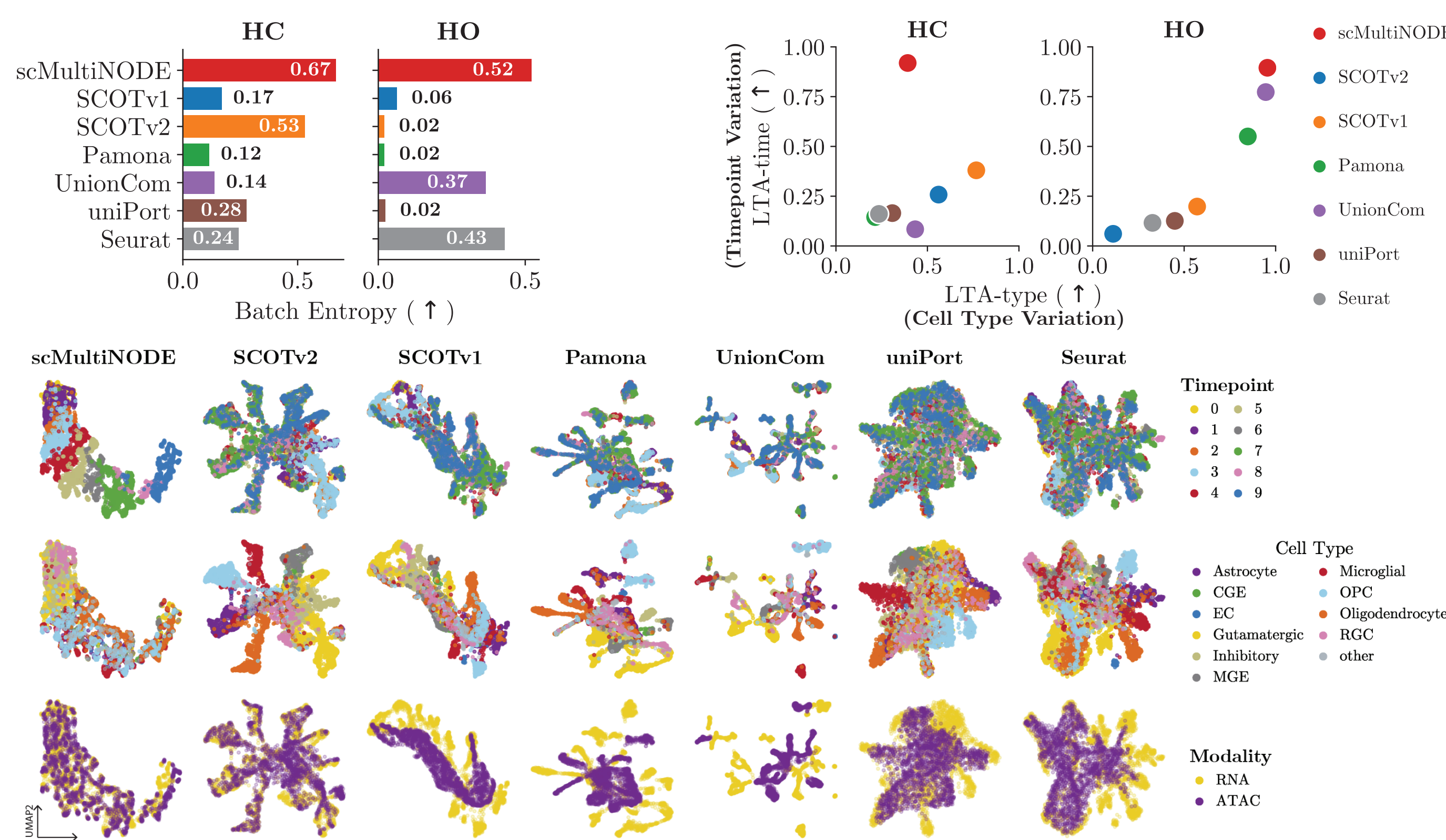
- Gene expression $\mathbf{X}^{(t)}$ at measured timepoints $t \in \mathcal{T}_{\text{RNA}} \subset \{0, 1, \dots\}$
- Chromatin accessibility $\mathbf{Y}^{(t)}$ at measured timepoints $t \in \mathcal{T}_{\text{ATAC}} \subset \{0, 1, \dots\}$

Advantage

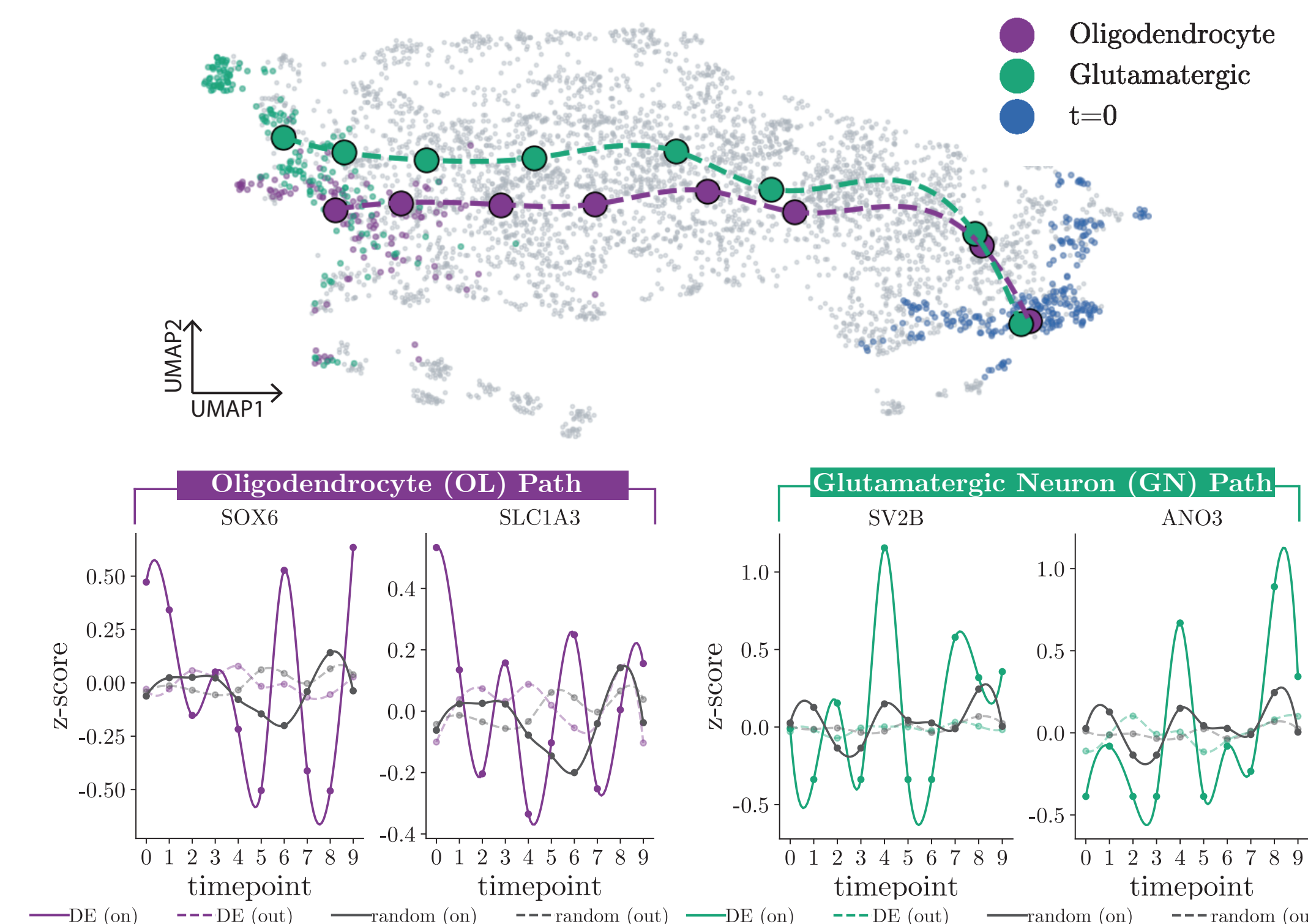
- Quantization GW enables efficient alignment across large-scale multi-modal data
- Integrations capture both cell type variations and developmental dynamics



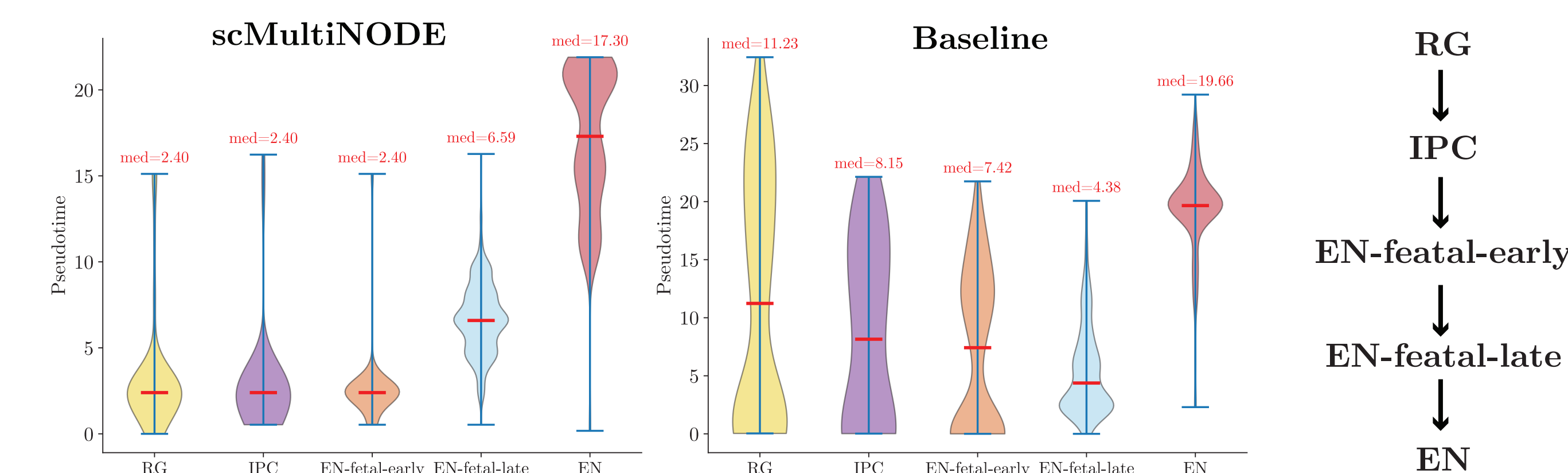
scMultiNODE Captures Cell Type Variations & Cellular Dynamics in Integration



Understanding Cell State Transition



Improving Pseudotime Estimation



Enabling Germ Layer Label Transfer

