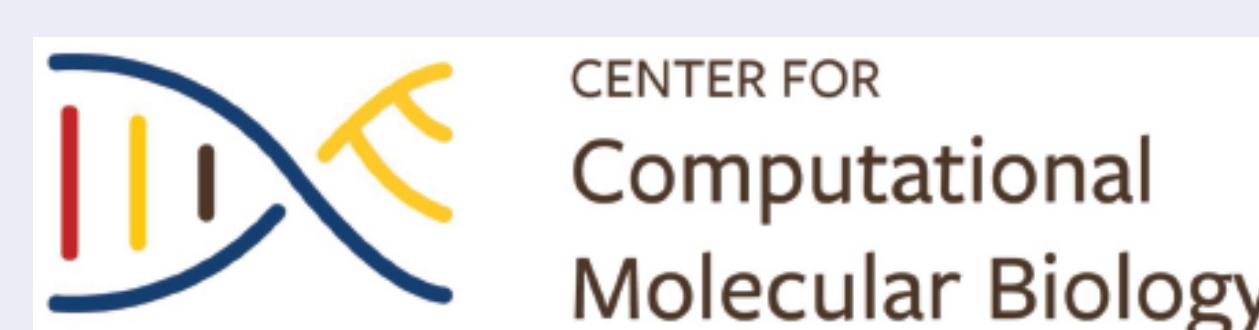


scMultiNODE: Temporal Single-Cell Data Integration across Unaligned Modalities



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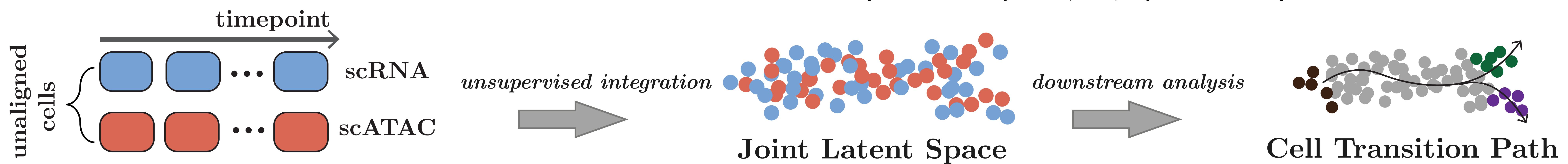
Codes & Paper

github.com/rsinghlab/scMultiNODE

Introduction

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



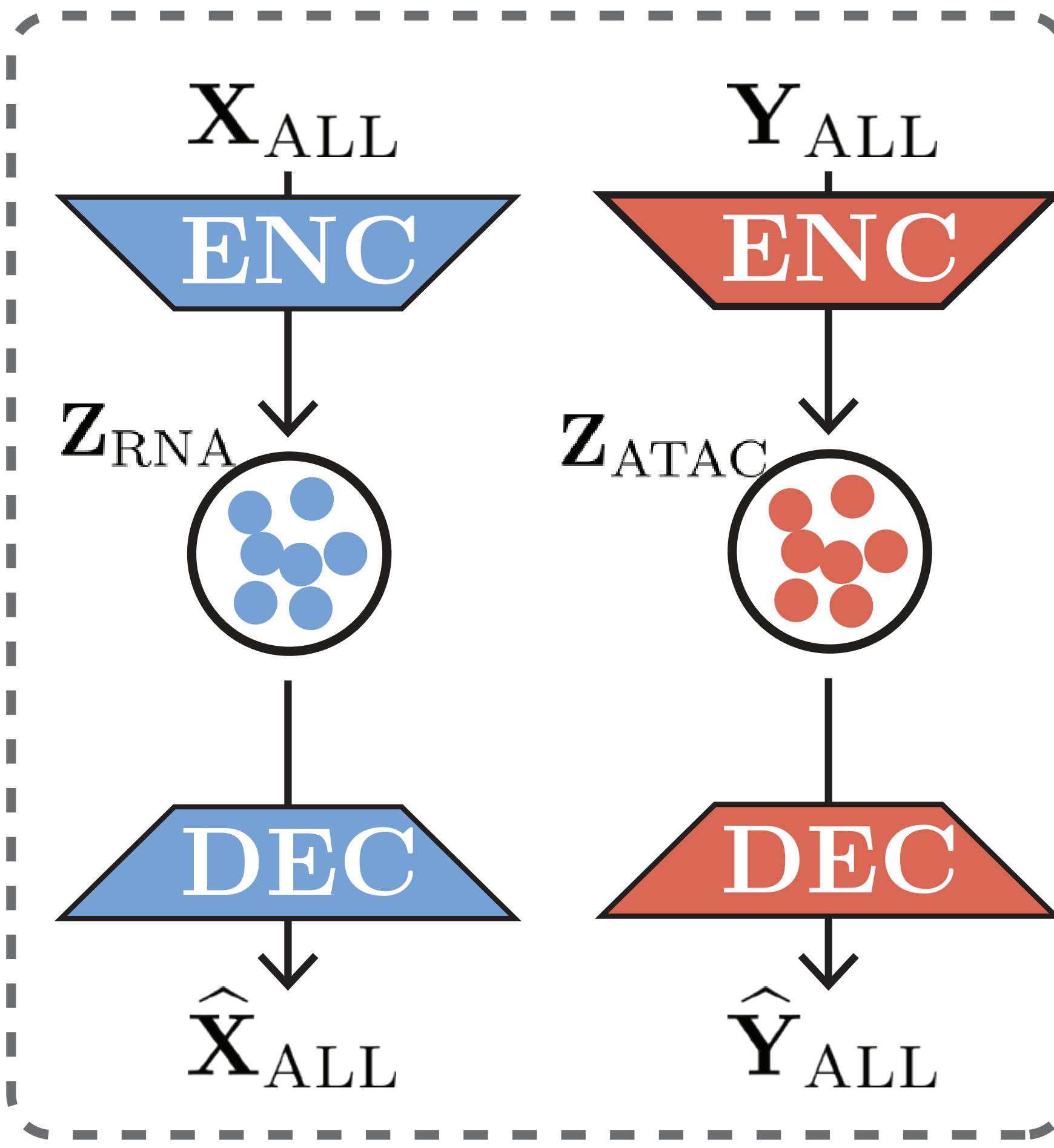
Method: single-cell Multi-Modal Neural Ordinary Differential Equation (scMultiNODE)

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 $t \in \mathcal{T}_{\text{ATAC}} \subset \{0, 1, \dots\}$

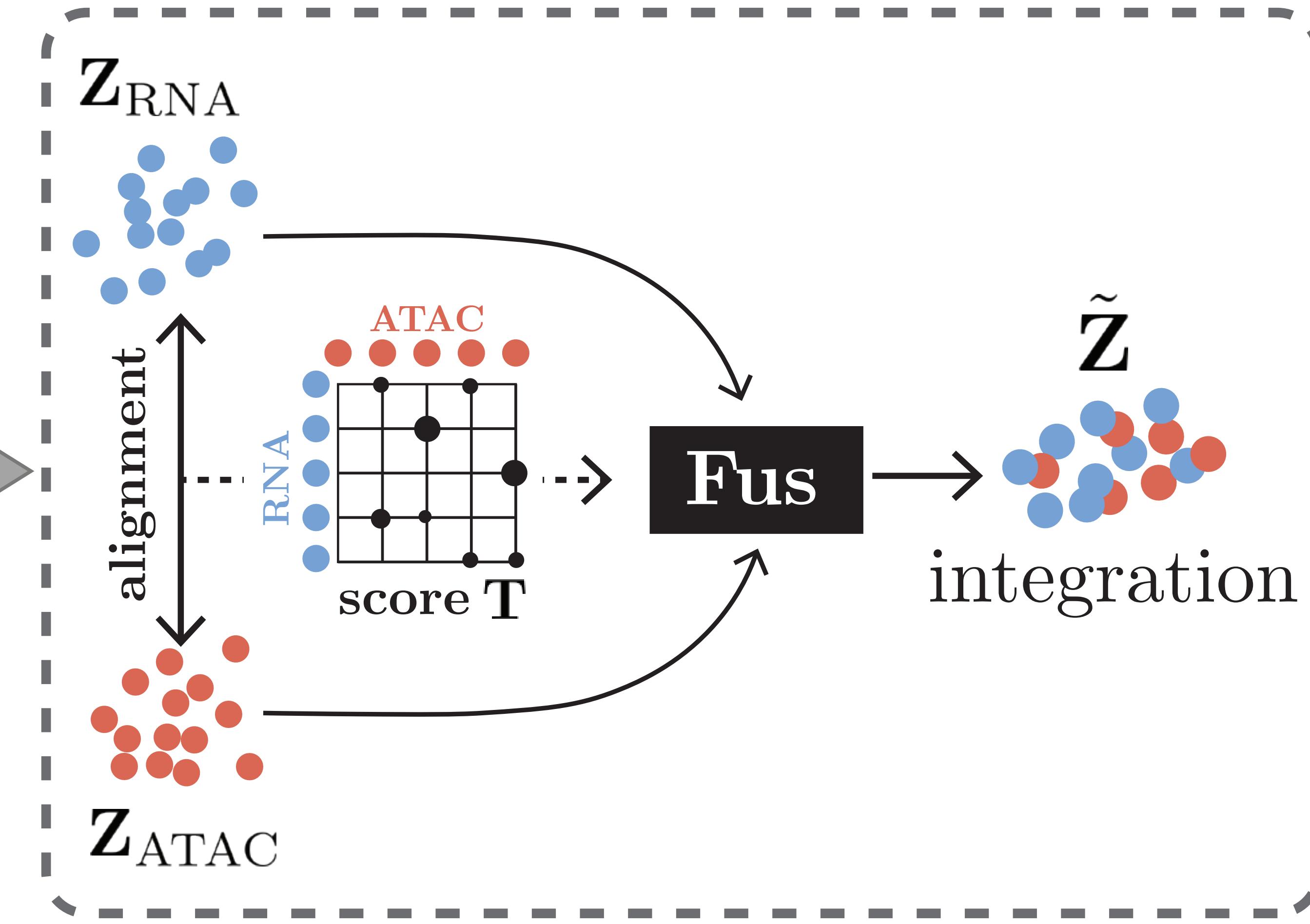
Stage I:

Pre-train separate AEs to compress high-dim. and sparse single-cell data



Stage II:

Align modalities with GW Optimal Transport

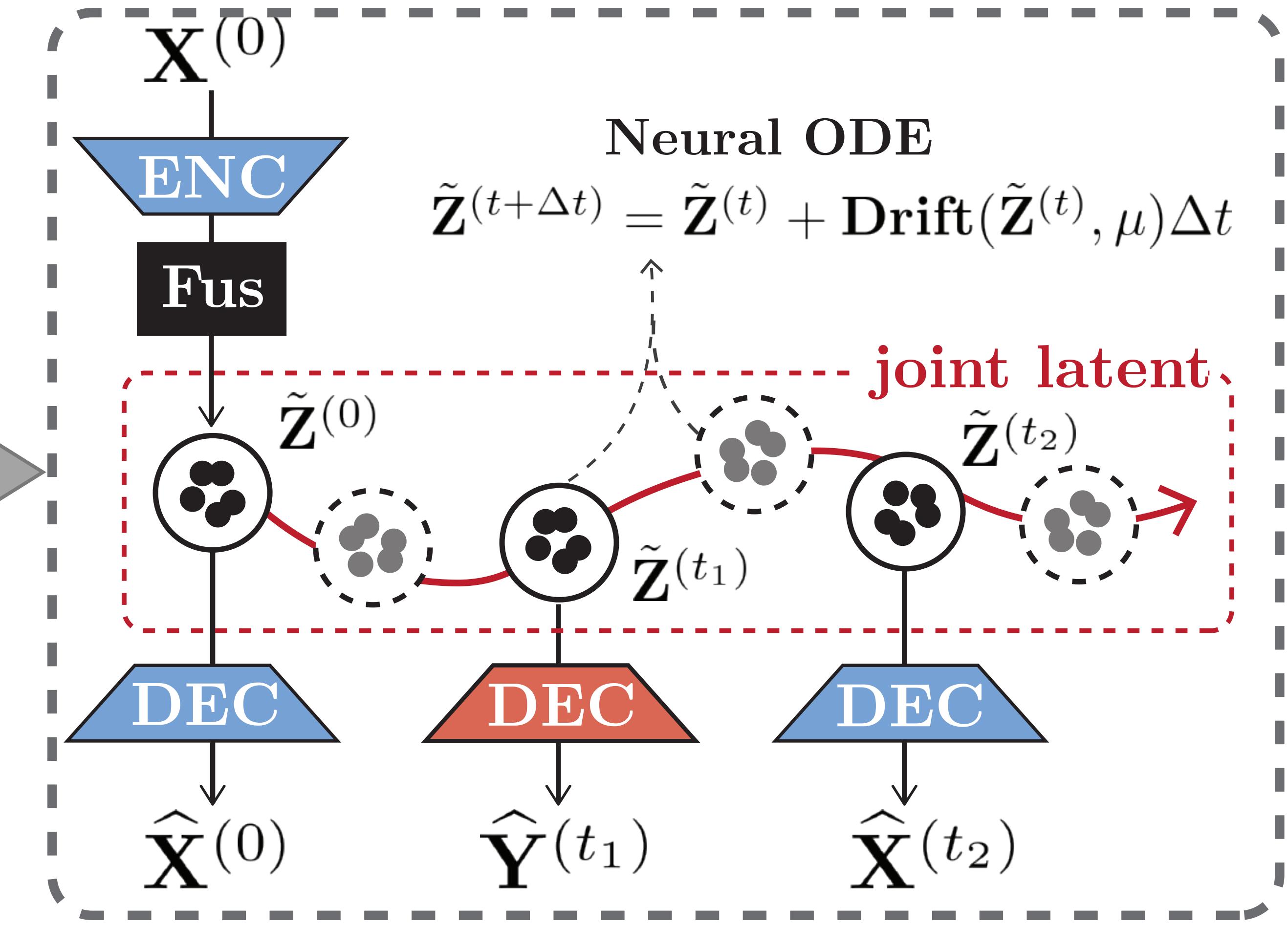


Advantage

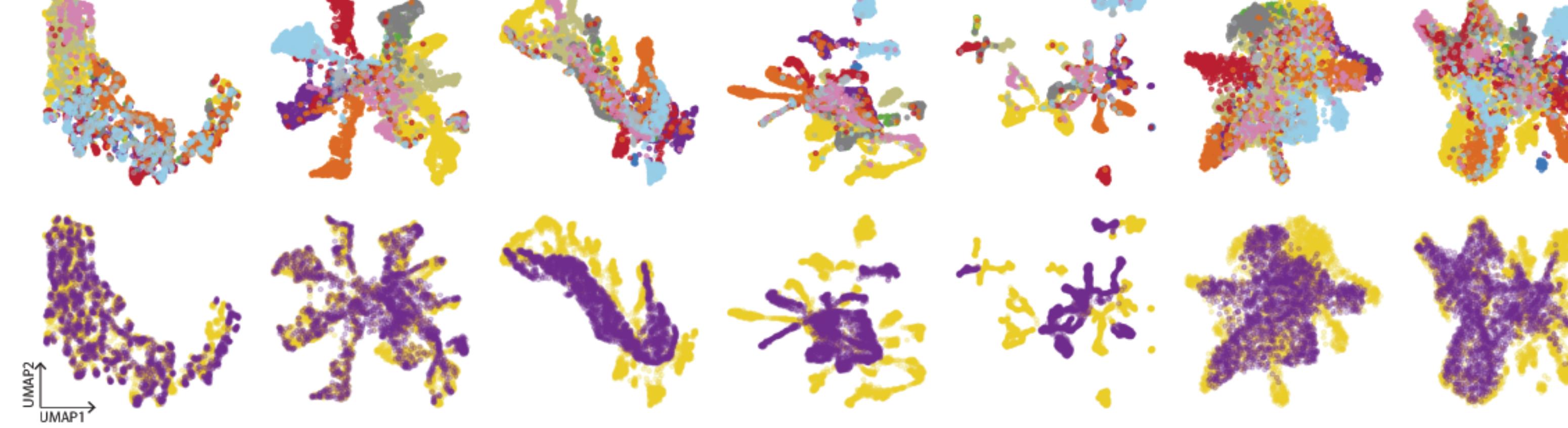
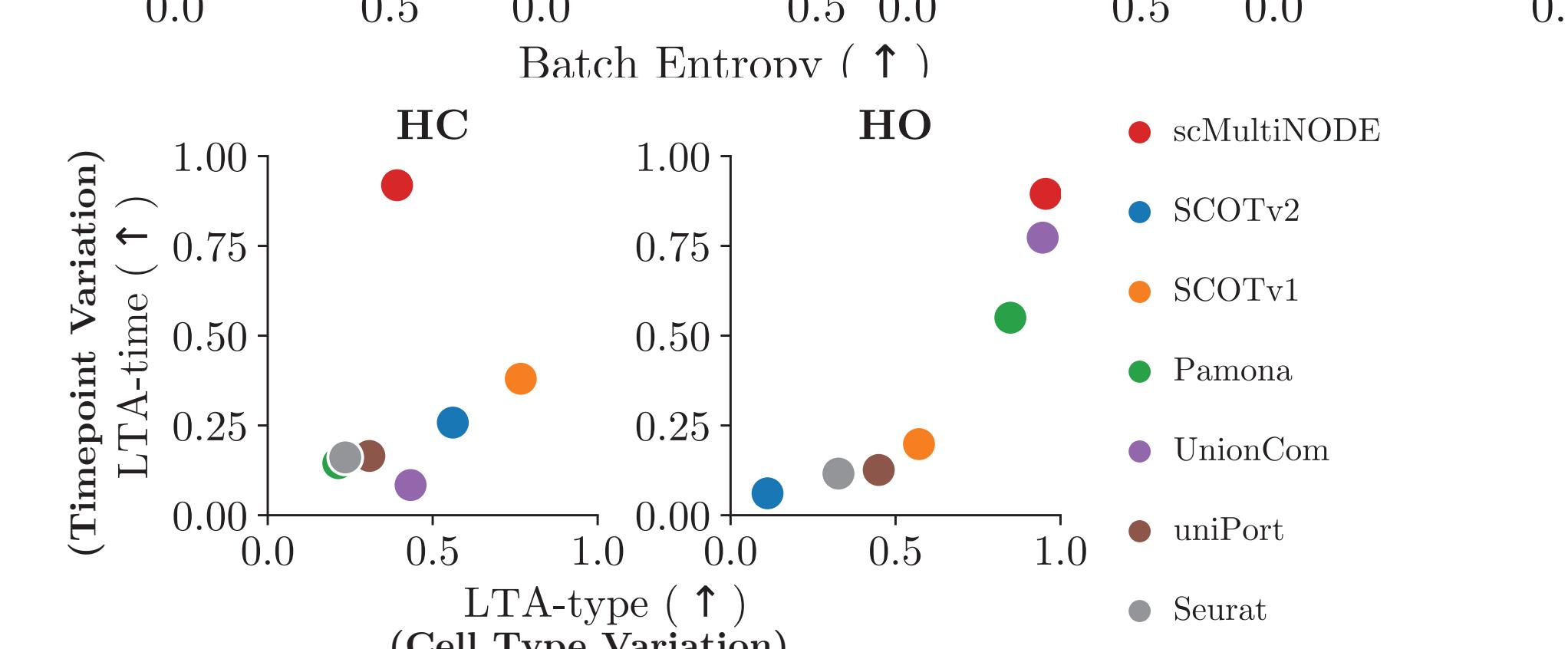
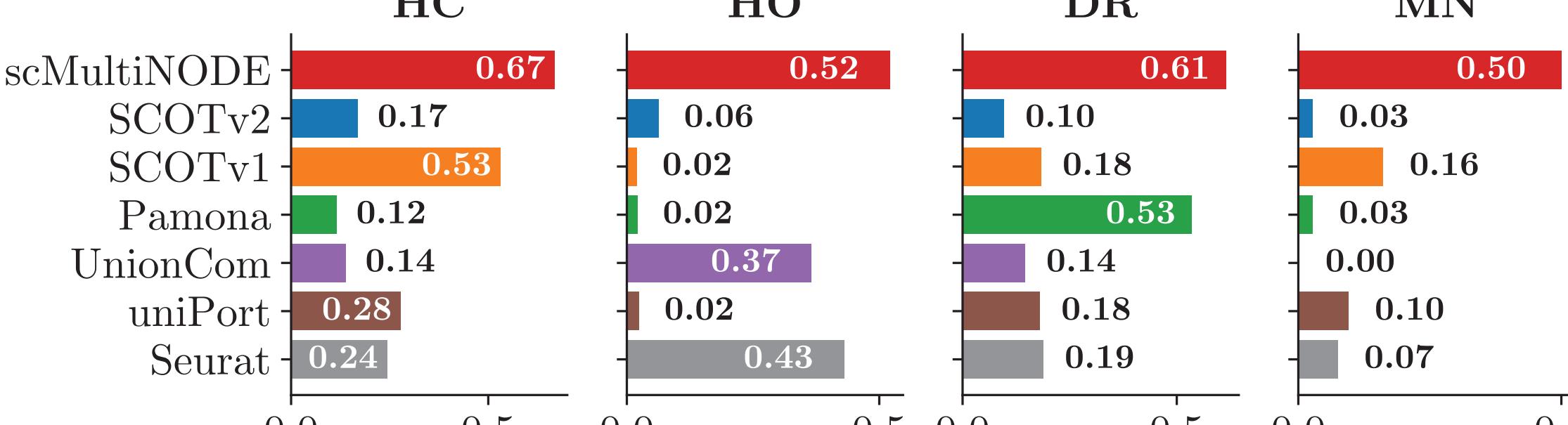
- Quantization GW enables efficient alignment across large-scale multi-modal data
- Integrations capture both cell type variations and developmental dynamics

Stage III:

Incorporate cellular dynamics with Neural ODE



scMultiNODE Captures Cell Type Variations & Cellular Dynamics in Integration



Understanding Cell State Transition

