# VeTra: a tool for trajectory inference based on RNA velocity

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Supplementary Materials

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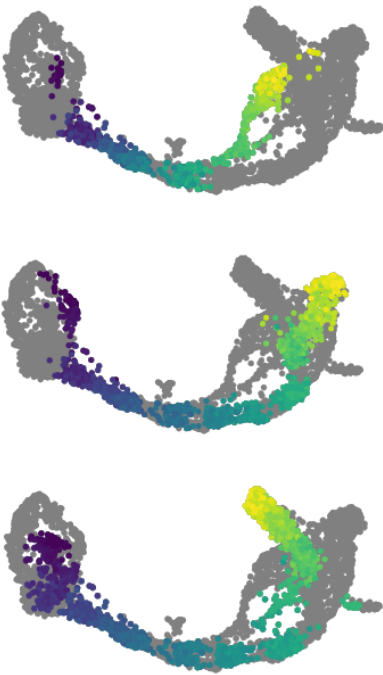
kyoung.won@bric.ku.dk) and JK (junil.kim@bric.ku.dk).

A. Pancera data

B. Hippocampus data

C. Chromaffin data
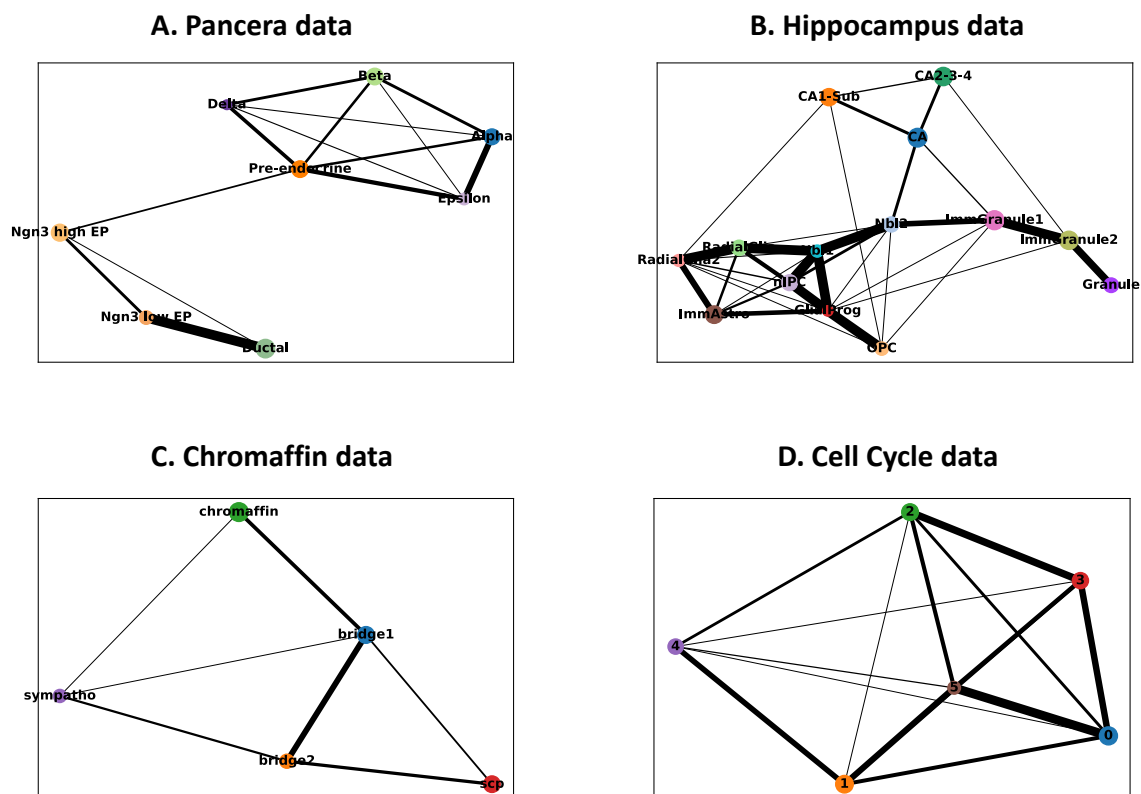
D. Cell Cycle data

Supplementary Fig. 1. The TI results from PAGA for various scRNAseq datasets
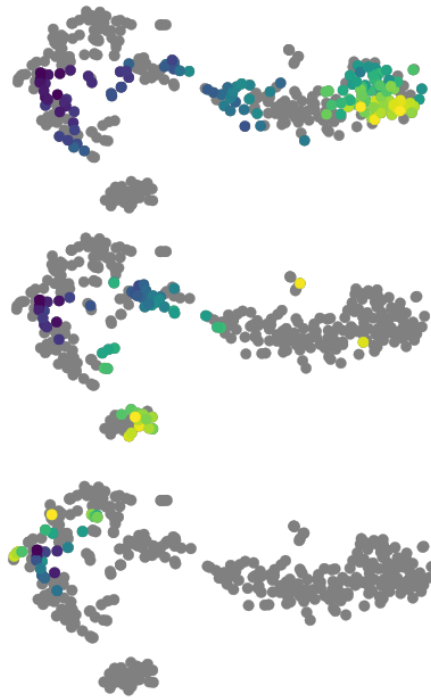
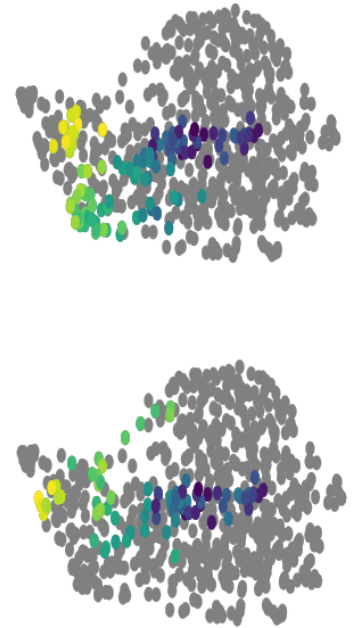# Cellpath performance on real datasets

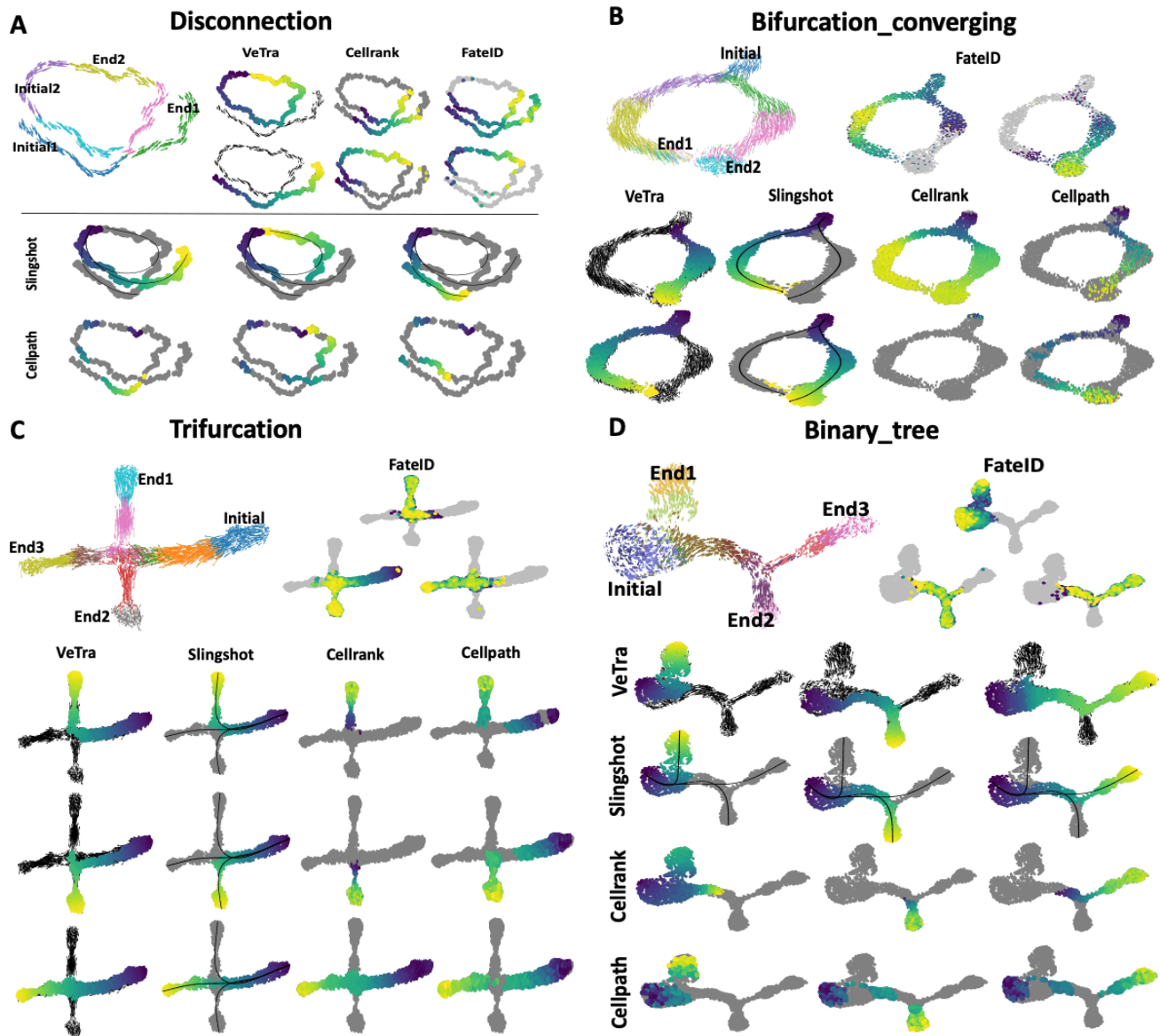## A. Hippocampus development

B. Pancreatic development

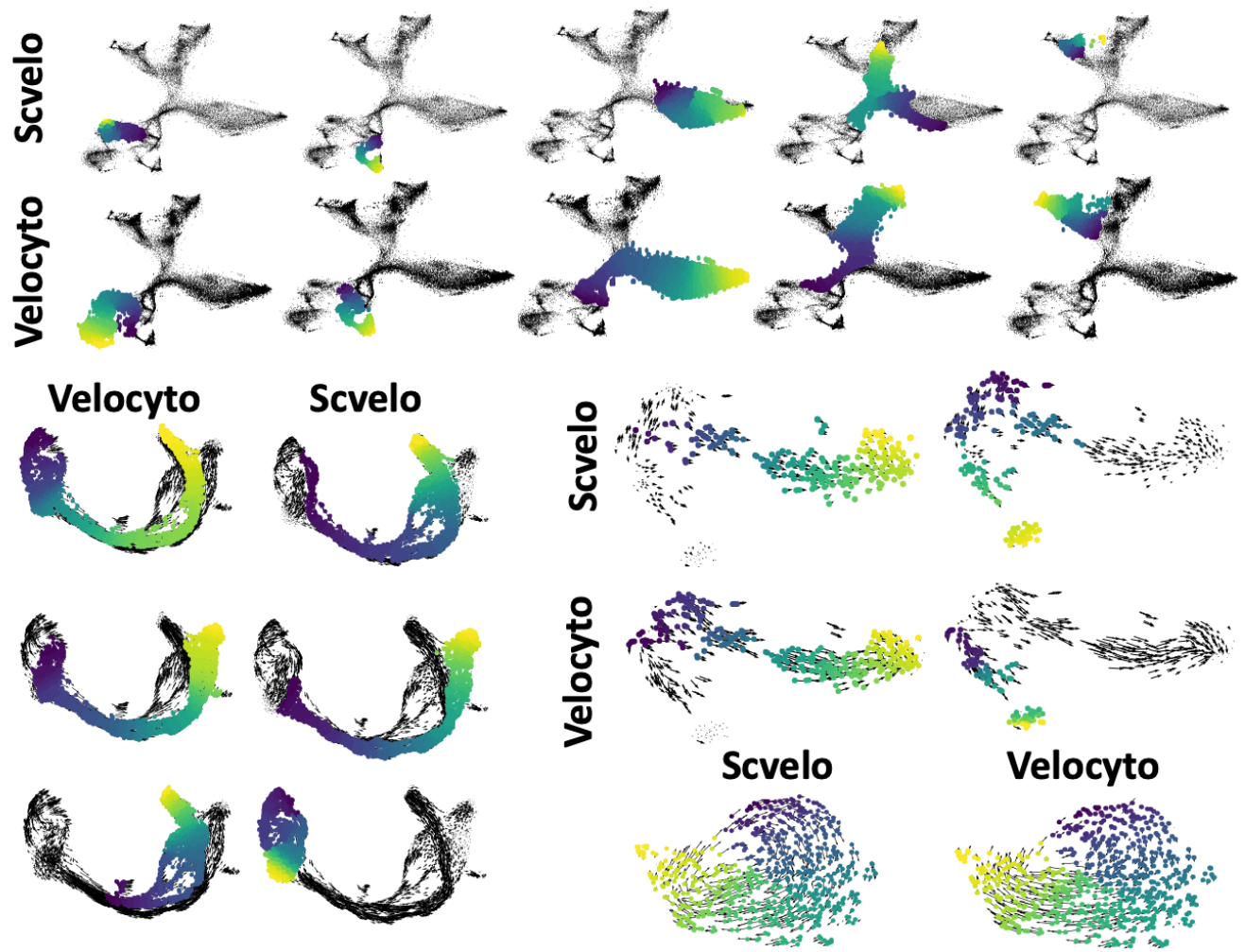## C. Chromaffin development

D. Cell cycle

Supplementary Fig. 2. The TI results from CellPath for various scRNAseq datasets

Supplementary Fig. 3. Performance of all TI tools on the 4 types of simulated datasets

Supplementary Fig. 4. VeTra's outputs tested on Velocyto and Scvelo

Supplementary Table 1. Performance assessment using the simulated datasets. The score is $(1 - D) *$ 100, where D is the average value of hamming distances between predicted lineages and the known lineages normalized to the total number of cells.

	Trifurcation	Converging	Binary Tree	Disconnection	Overall
VeTra	91	88	91	99	92
Slingshot	95	95	95	78	91
FateID	72	77	76	67	73
CellRank	71	52	69	63	64
Cellpath	78	56	64	67	66