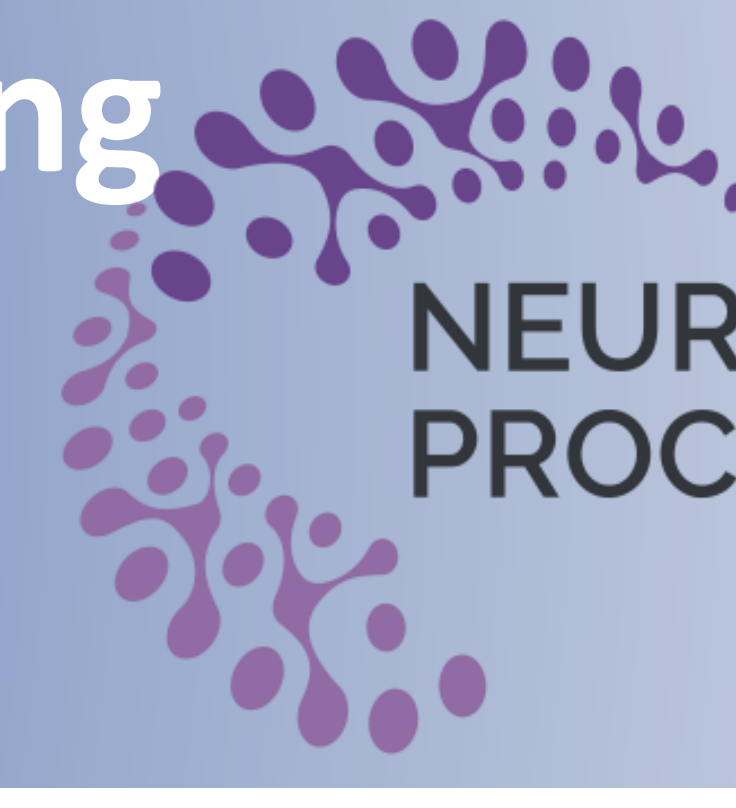




# Joint Velocity-Growth Flow Matching for Single-Cell Dynamics Modeling

Dongyi Wang, Yuanwei Jiang, Zhenyi Zhang, Xiang Gu, Peijie Zhou, Jian Sun  
School of Mathematics and Statistics, Xi'an Jiaotong University, China  
School of Mathematical Sciences, Peking University, Beijing, China



NEURAL INFORMATION  
PROCESSING SYSTEMS

## Background & Motivation

Single-cell RNA seq yields **unpaired** and **unbalanced** data.

**Simulation-based models** (e.g., TIGON, DeepRUOT)

■ Growth rate 😊

■ Scalability 😞

**Simulation-free models** (e.g., OT-CFM, SF2M)

■ Growth rate 😞

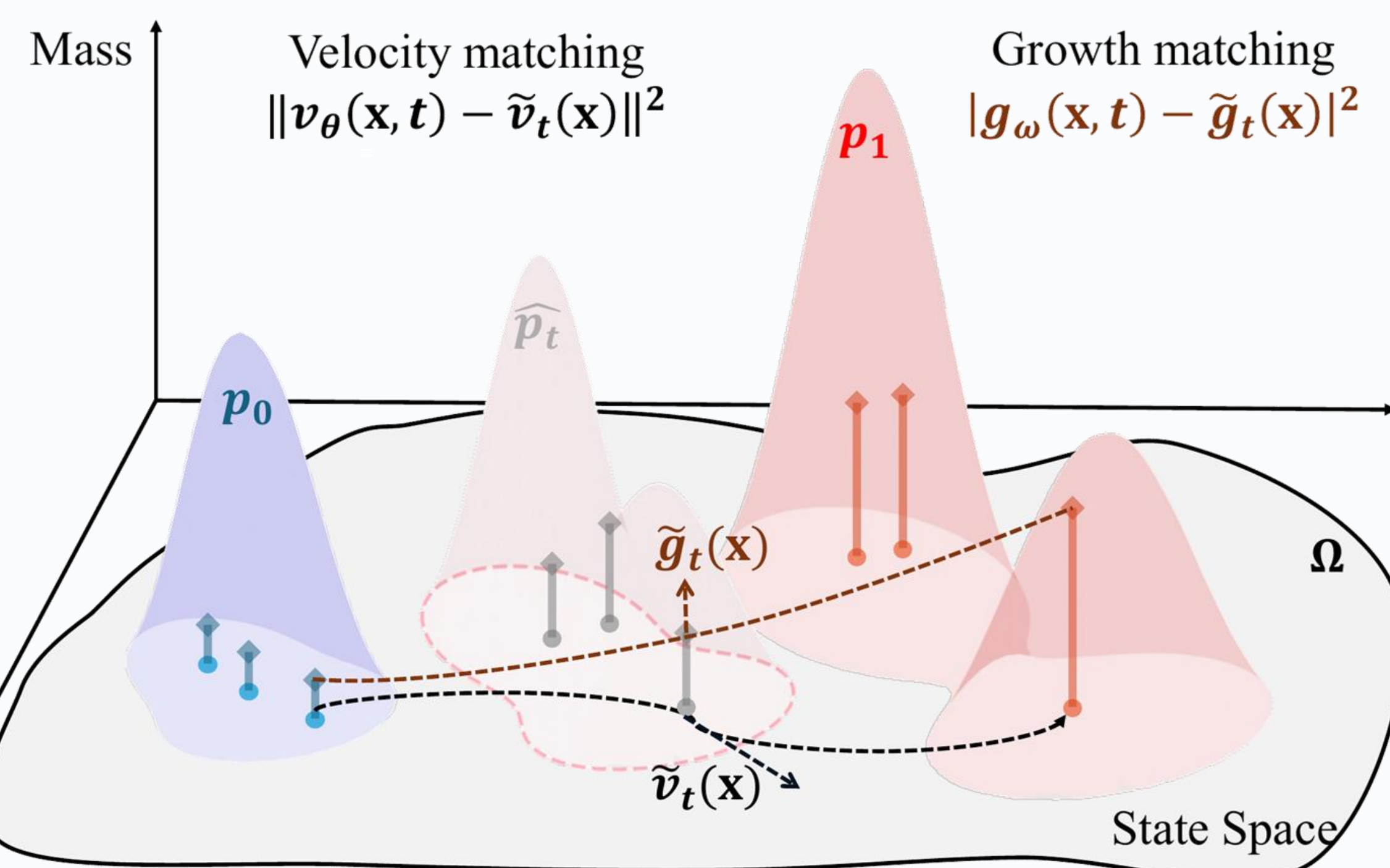
■ Scalability 😊

### Our approach:

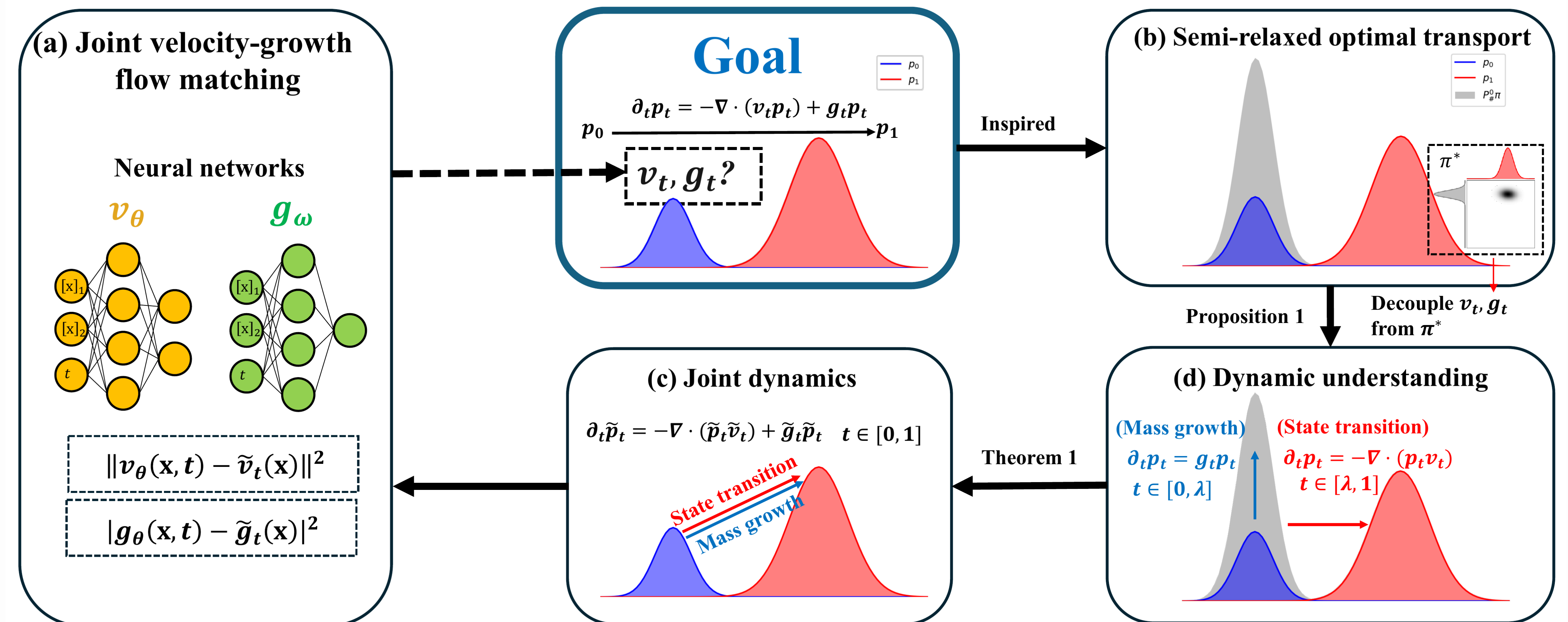
VGFM jointly learns the **state transition** and **mass growth** of single-cell evolution by **flow matching**.

■ Growth rate 😊

■ Scalability 😊



## Our Approach: Velocity-Growth Flow Matching via SROT

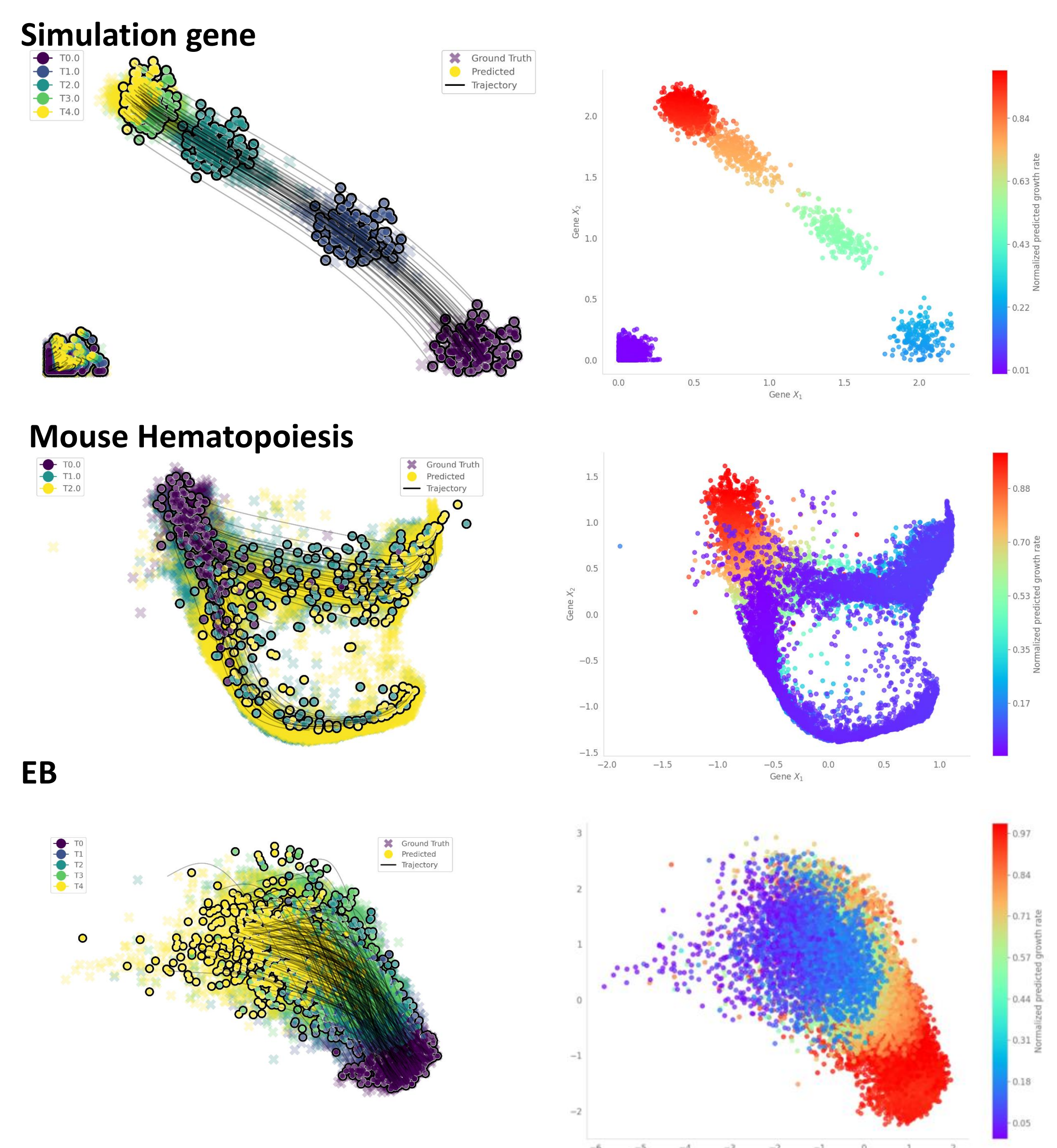


1. Dynamic understanding of semi-relaxed OT (SROT) ( $v, g$  can be decoupled from SROT plan)
2. Build a novel dynamic process between unbalanced distributions based on dynamic SROT
3. Regress  $\tilde{v}, \tilde{g}$  using neural networks  $\left\|v_{\theta}(\mathbf{x}_t, t) - (\mathbf{x}_1^j - \mathbf{x}_0^i)\right\|^2 + |g_{\omega}(\mathbf{x}_t, t) - \log([\pi^{0 \rightarrow 1} \mathbf{1}_m]_i)|^2$

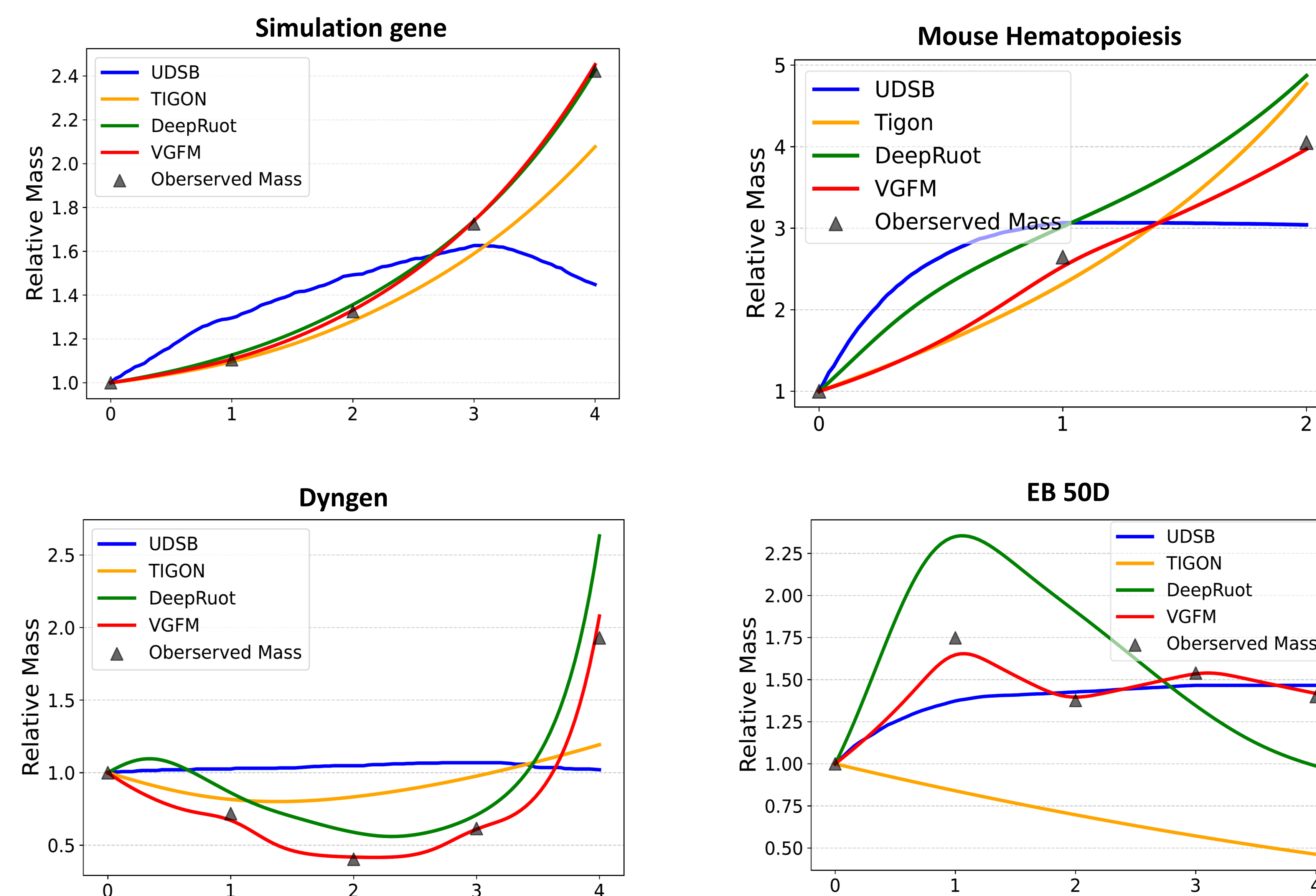
$$\mathcal{L}(\theta, \omega) = \underbrace{\mathcal{L}_{\text{VGFM}}(\theta, \omega)}_{\text{Flow matching loss}} + \underbrace{\mathcal{L}_{\text{OT}}(\theta, \omega)}_{\text{Distribution fitting loss}}$$

## Experiments

### Trajectory and growth reconstruction



### Mass matching



### Wasserstein-1 distance and Relative mass error

Method	Simulation Gene (2D)		Dyngen (5D)		Gaussian (1000D)	
	$\mathcal{W}_1$	RME	$\mathcal{W}_1$	RME	$\mathcal{W}_1$	RME
OT-CFM* [22]	0.302	—	3.926	—	10.126	—
OT-MFM* [38]	0.311	—	3.976	—	11.008	—
UDSB [57]	0.665	0.192	1.914	0.658	N/C	N/C
TIGON [23]	0.099	0.065	1.029	0.542	N/C	N/C
DeepRUOT [26]	0.068	0.016	0.474	0.199	N/C	N/C
<b>VGFM</b>	<b>0.046</b>	<b>0.006</b>	<b>0.420</b>	<b>0.053</b>	<b>3.010</b>	<b>0.037</b>

### Training and analysis on 2k gene space

