

Cell Trajectory
Inference based on
Schrödinger problem
and a mechanistic
stochastic gene
expression model

Clémence FOURNIÉ

3rd year PhD student

Supervisors : Fabien Crauste
and Olivier Gandrillon

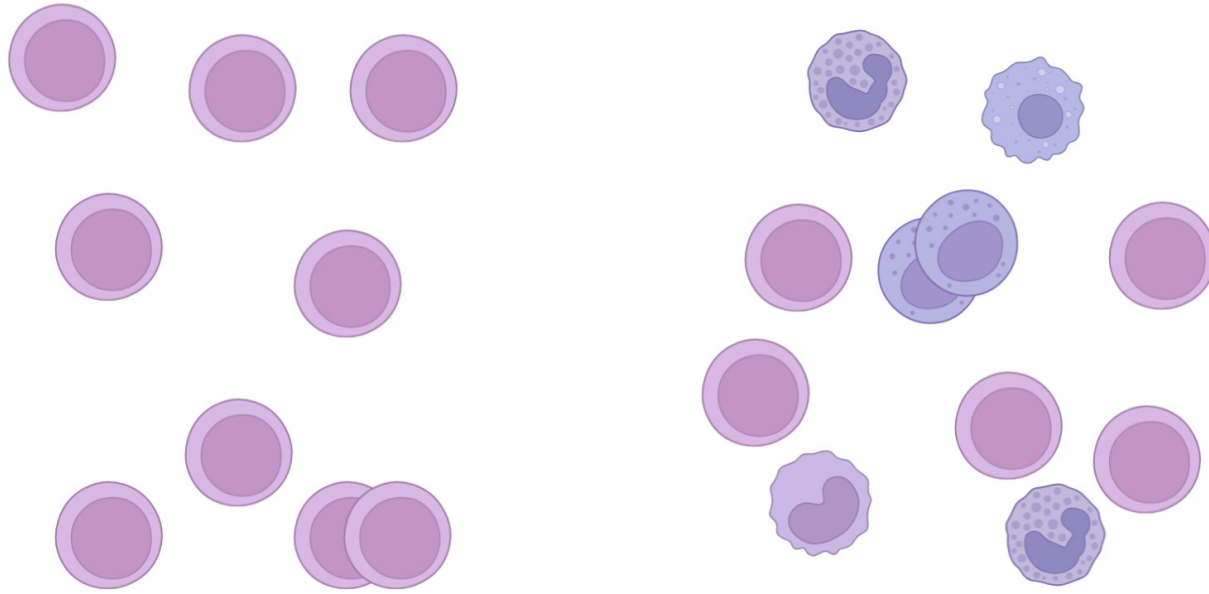
18/03/2026



Cell Trajectory Inference based on Schrödinger problem and a mechanistic stochastic gene expression model

Clémence Fournié, Elias Ventre, Ulysse Herbach, Aymeric Baradat, Olivier Gandrillon, Fabien Crauste, Preprint, 2025.

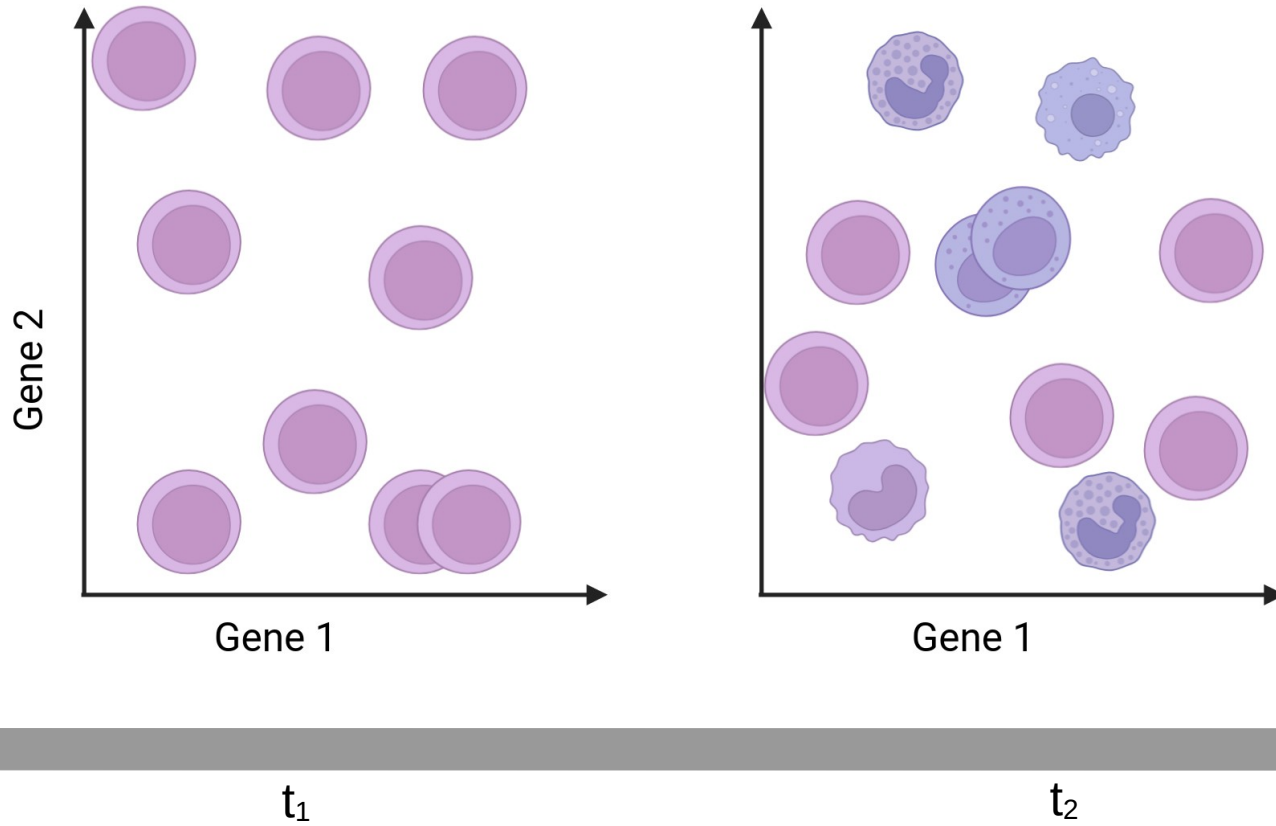
scRNA-seq Data Set



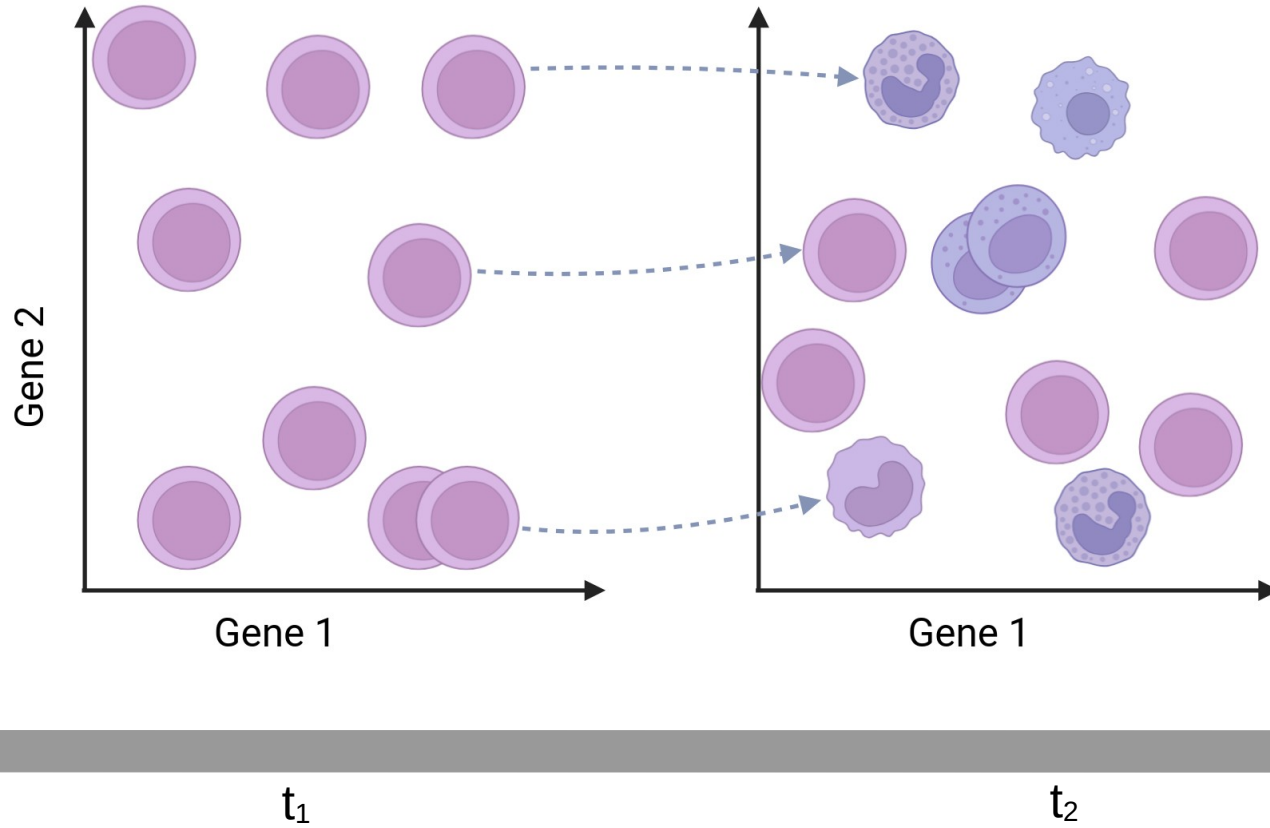
t_1

t_2

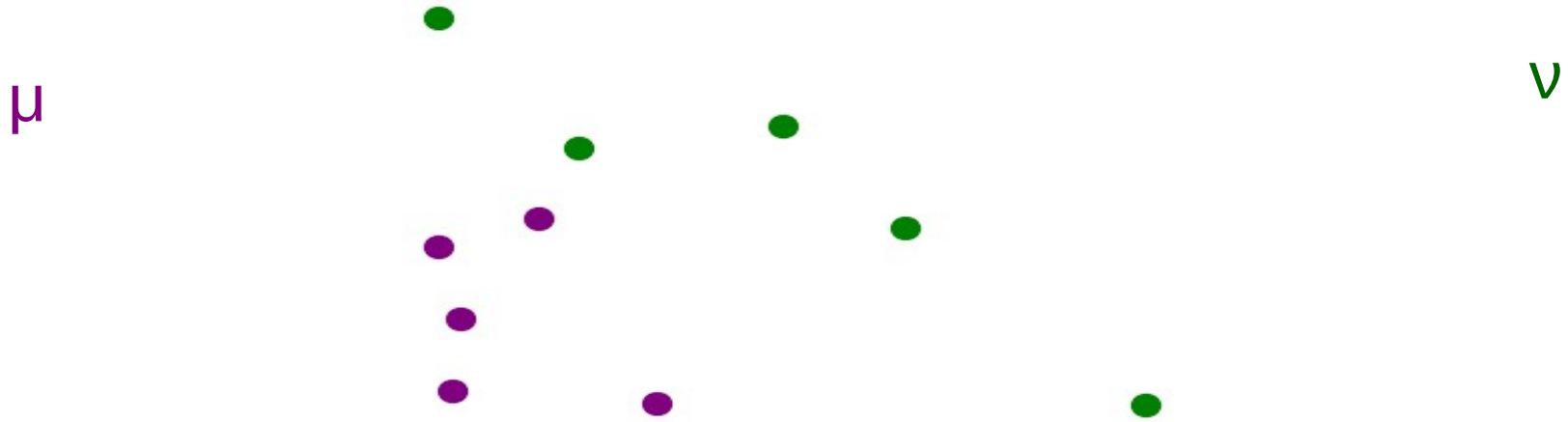
Gene Space



Trajectories Inference

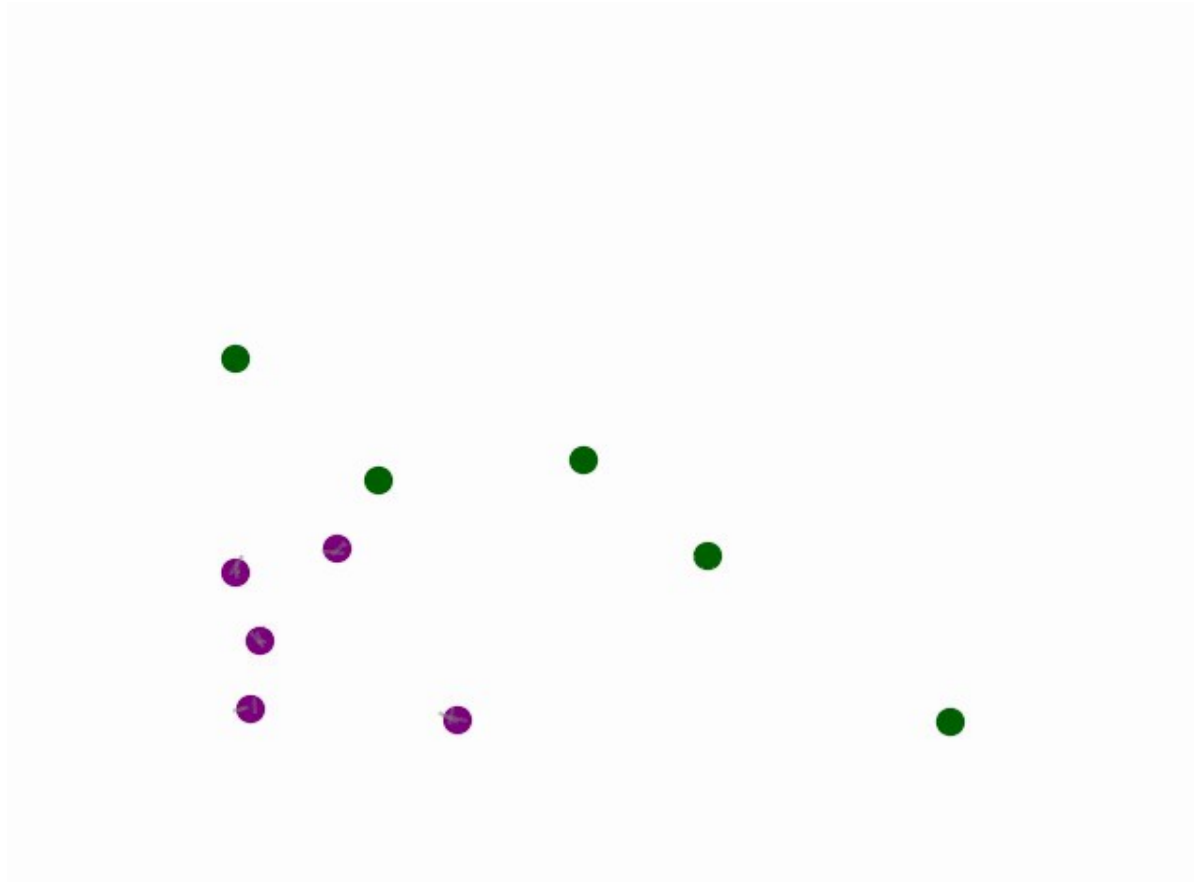


Trajectories Inference - Schrödinger Problem



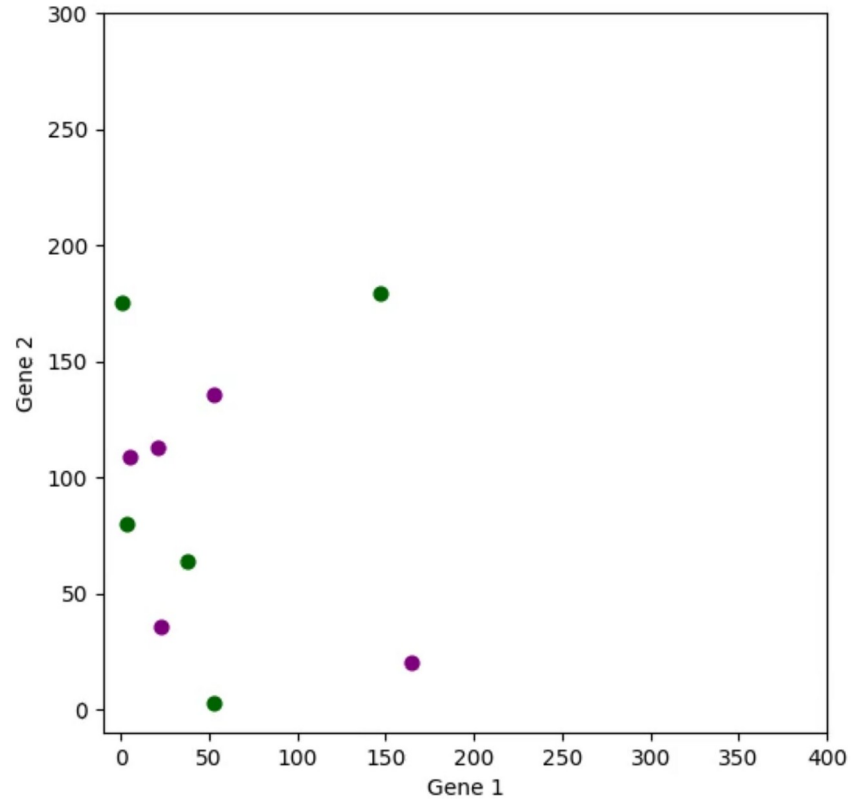
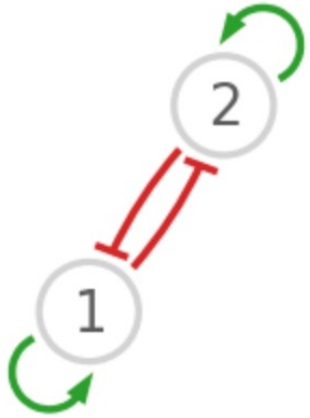
Schrödinger Problem – Diffusive Process

μ



ν

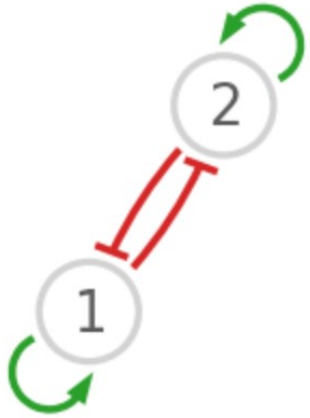
Gene Regulatory Network toggle-switch



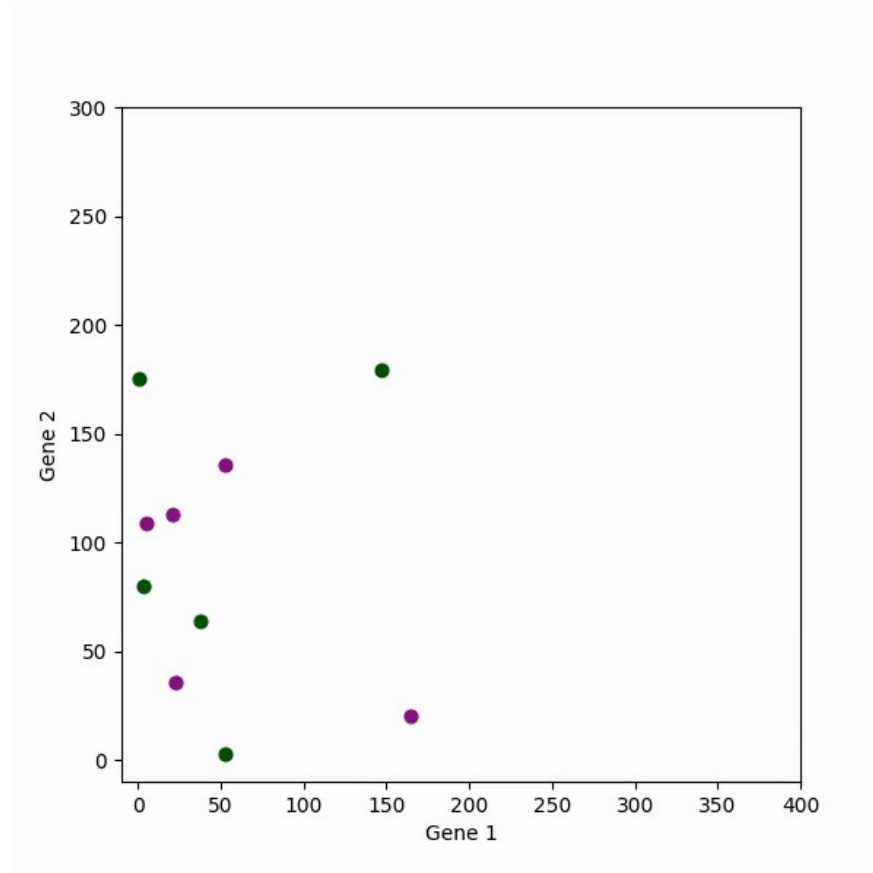
μ

ν

Gene Regulatory Network toggle-switch



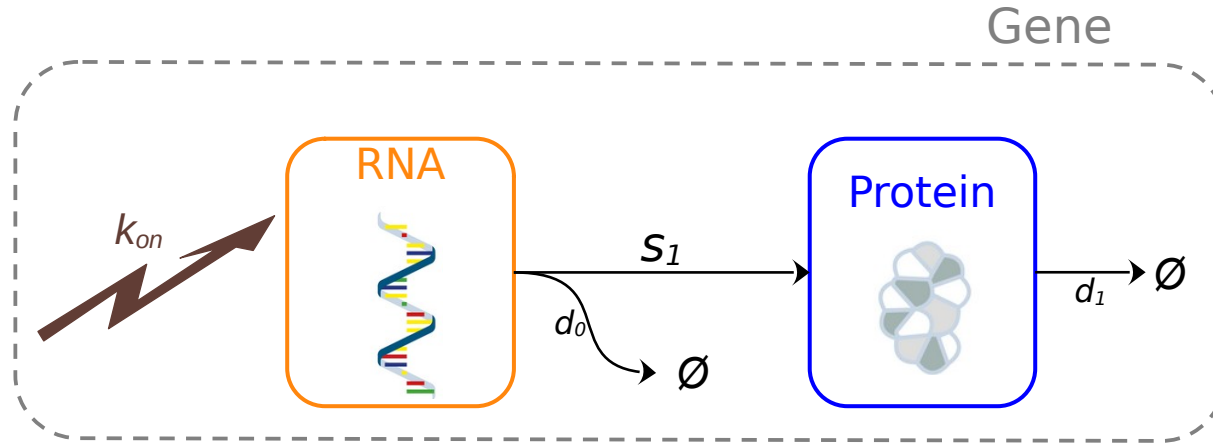
μ



v

Mechanistic Stochastic Gene Expression Model

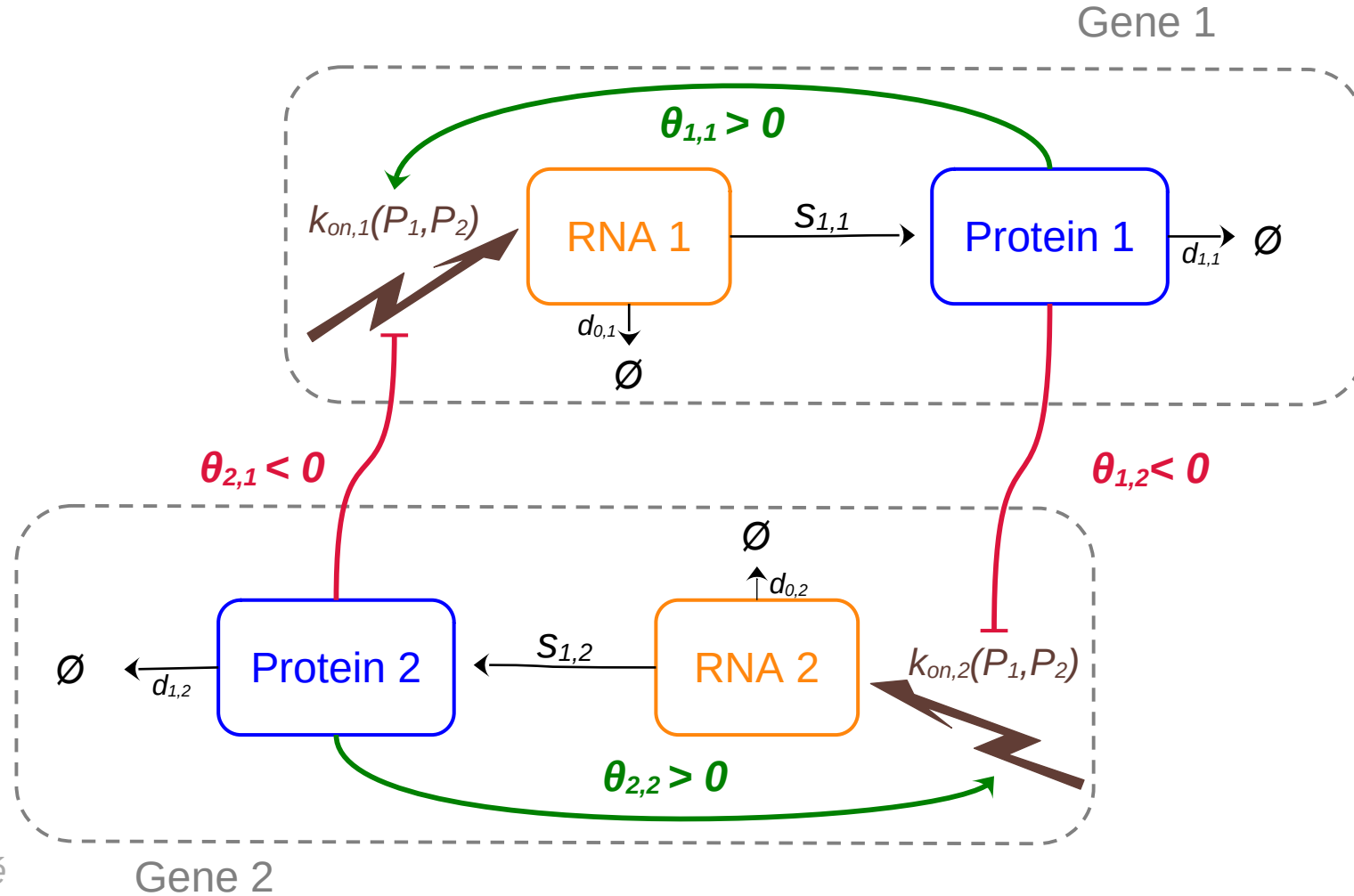
Bursty model



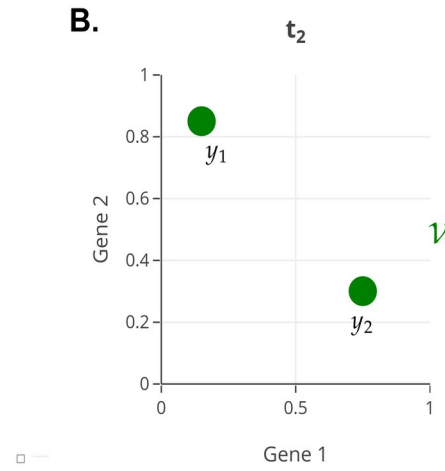
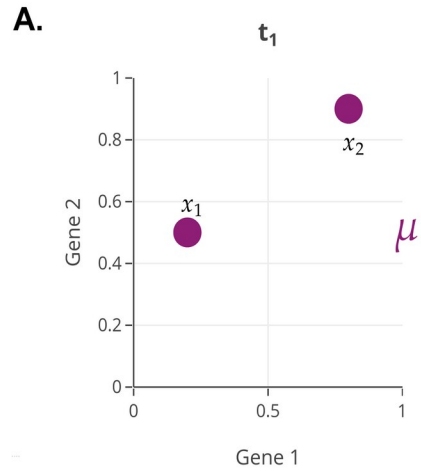
$$k_{on,i}(P_1, \dots, P_G) = \frac{k_{0,i} + k_{1,i} \exp(\beta_i + \sum_{j=1}^G \theta_{ji} P_j)}{1 + \exp(\beta_i + \sum_{j=1}^G \theta_{ji} P_j)}$$

$$\begin{cases} \dot{M}(t) = -d_0 M(t), \\ \dot{P}(t) = s_1 M(t) - d_1 P(t). \end{cases}$$

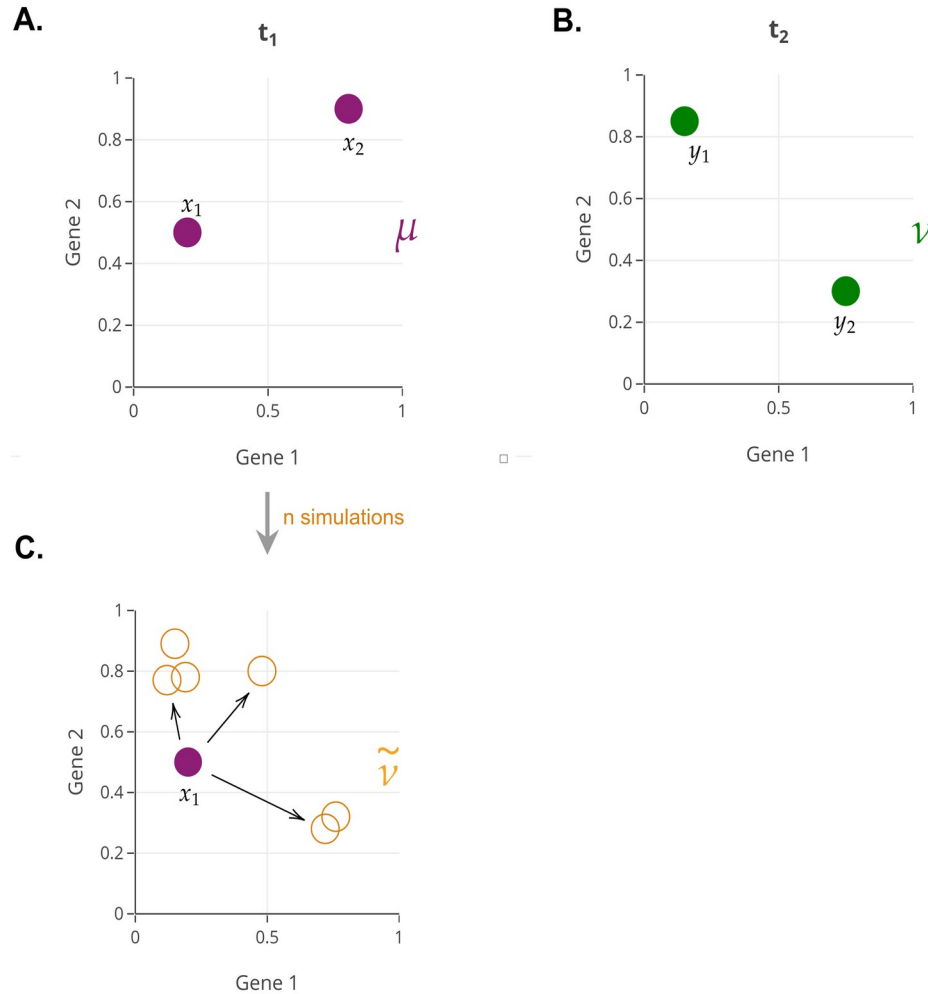
Bursty Model toggle-switch



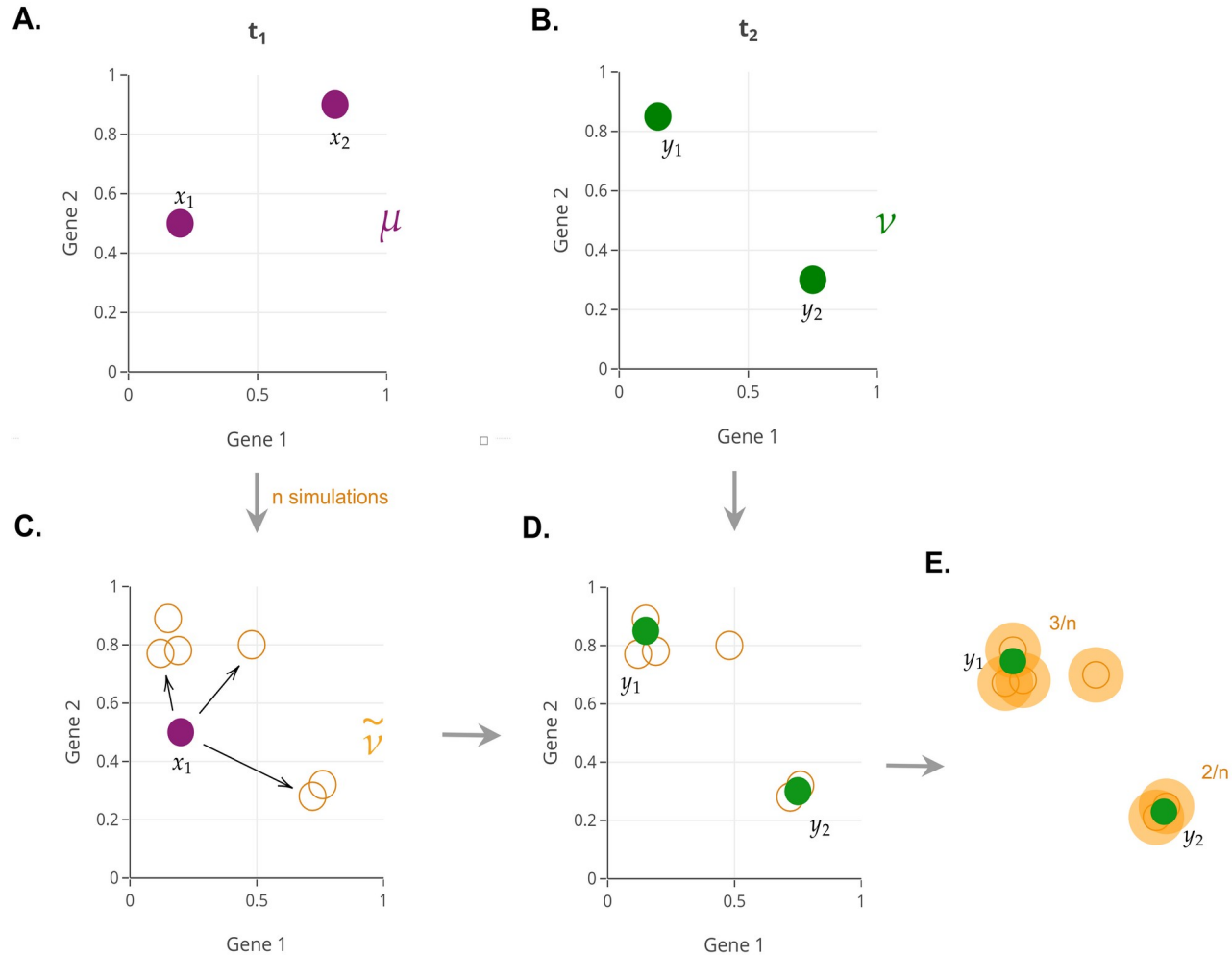
Methods: Approximation of the reference process



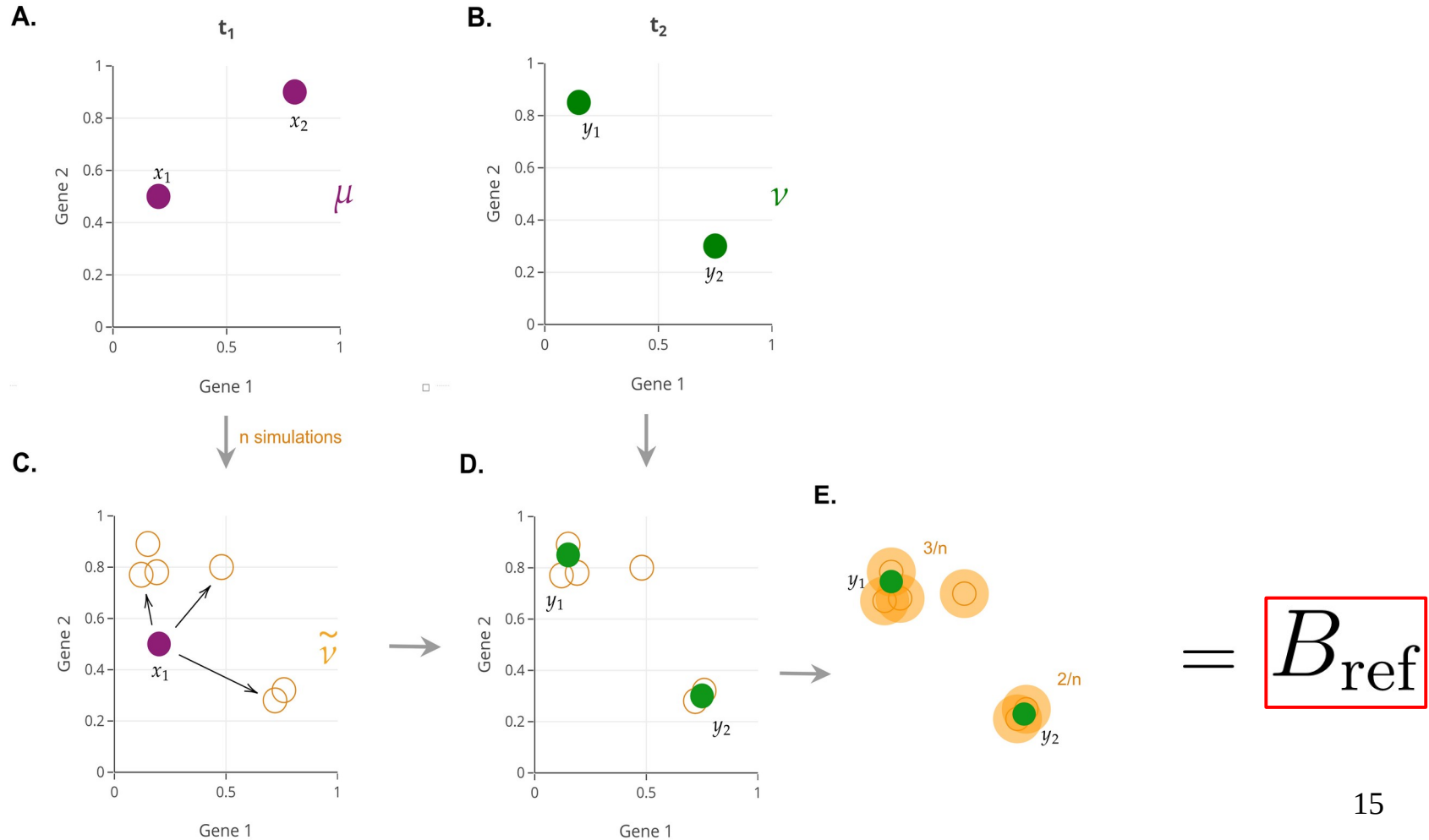
Methods: Approximation of the reference process



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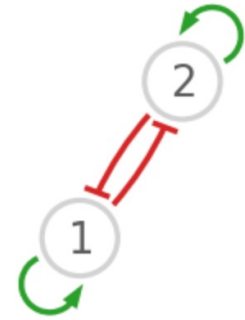
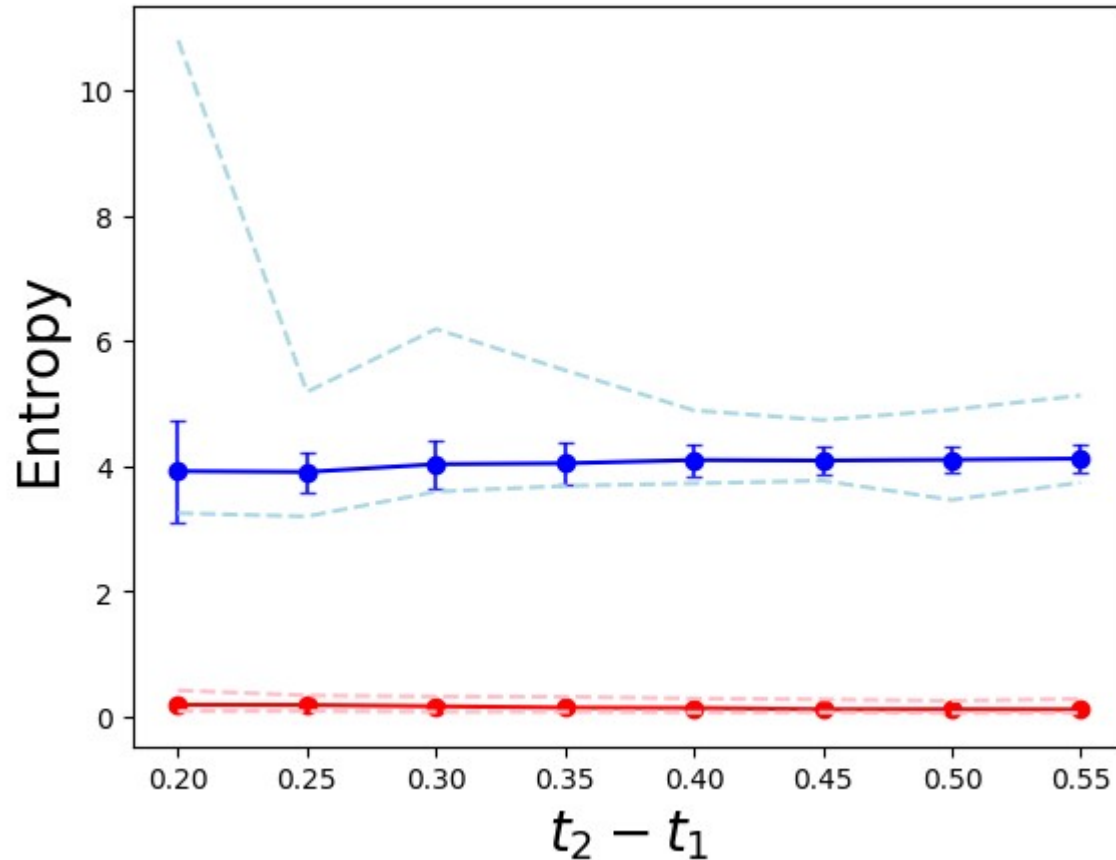


Methods: Schrödinger Problem

$$\arg \min_{Q \in \mathcal{P}(X \times Y)} \{ H(Q | B_{\text{ref}}); Q(t_1) = u, Q(t_2) = v \}$$

$$\text{With } H(Q|R) = \sum_{ij} Q_{ij} \log \left(\frac{Q_{ij}}{R_{ij}} \right)$$

Results: Toggle-switch

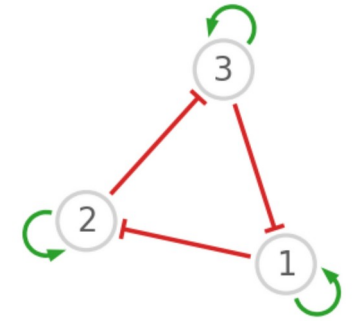
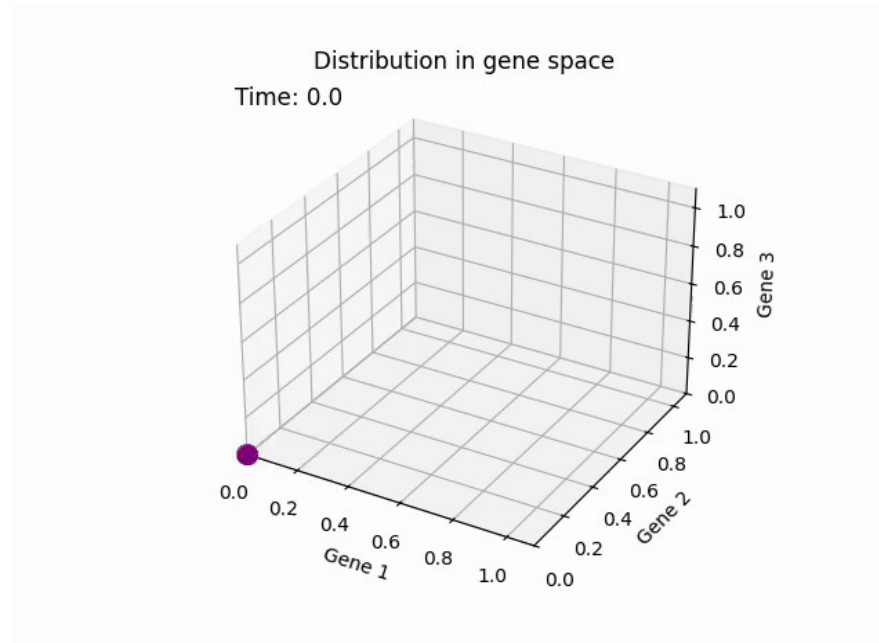


Bursty model vs Diffusion

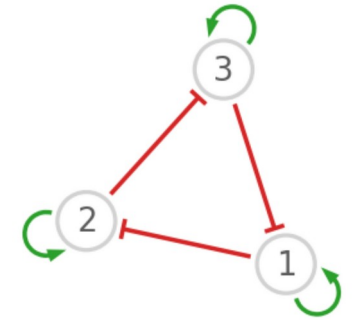
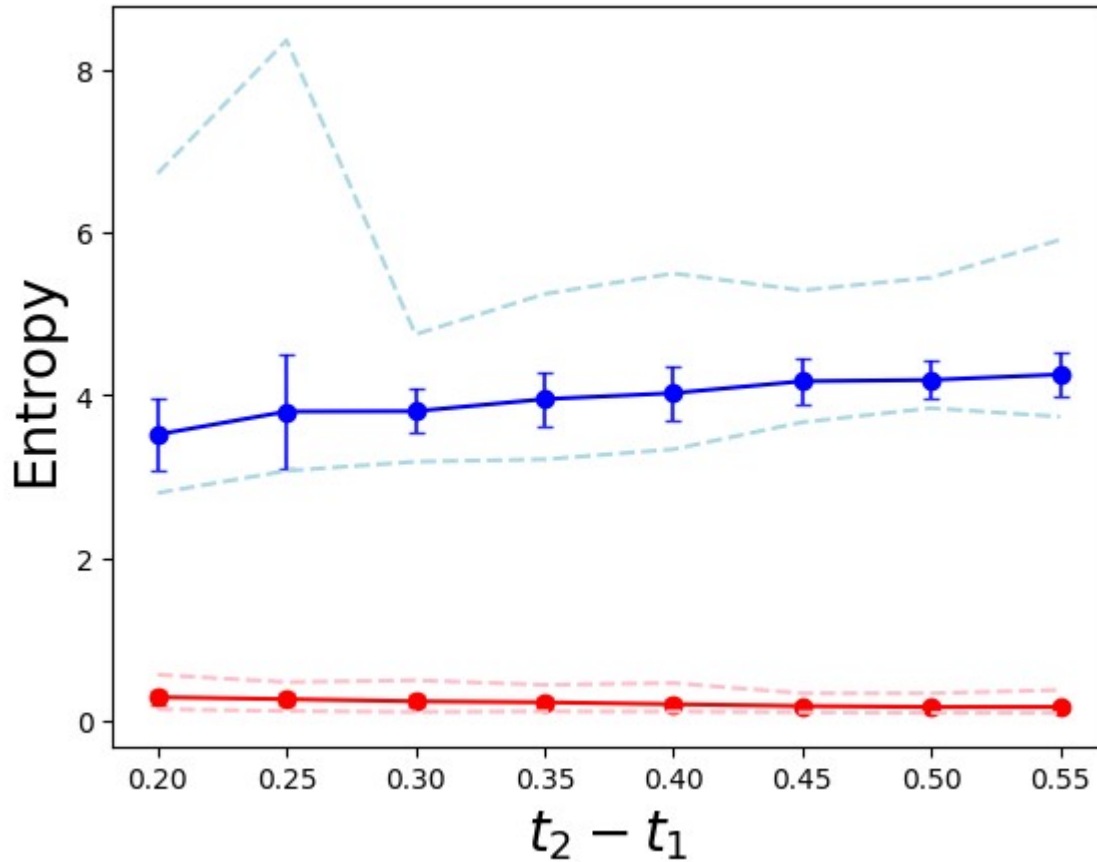
Bursty model vs "ground truth"

The smaller the entropy, the better the Bursty model

Gene Regulatory Network Repressilator



Results: Repressilator



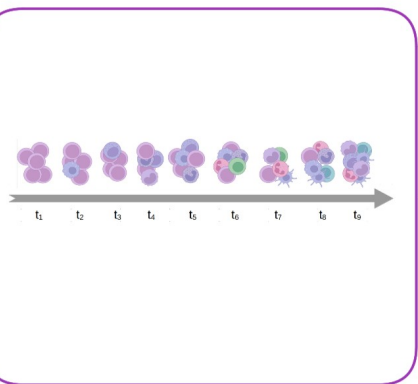
Bursty model vs Diffusion

Bursty model vs “ground truth”

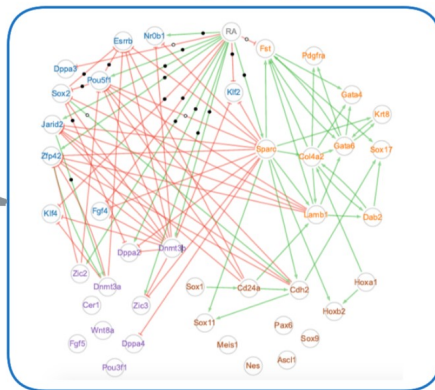
The smaller the entropy, the better the Bursty model

Discussion

Sc RNA seq DATA



Gene Regulatory Network Inference



Bursty Model

$$\begin{cases} \dot{M}(t) = -d_0 M(t), \\ \dot{P}(t) = s_1 M(t) - d_1 P(t). \end{cases}$$
$$k_{on,i}(P_1, \dots, P_G) = \frac{k_{0,i} + k_{1,i} \exp(\beta_i + \sum_{j=1}^G \theta_{ji} P_j)}{1 + \exp(\beta_i + \sum_{j=1}^G \theta_{ji} P_j)}$$

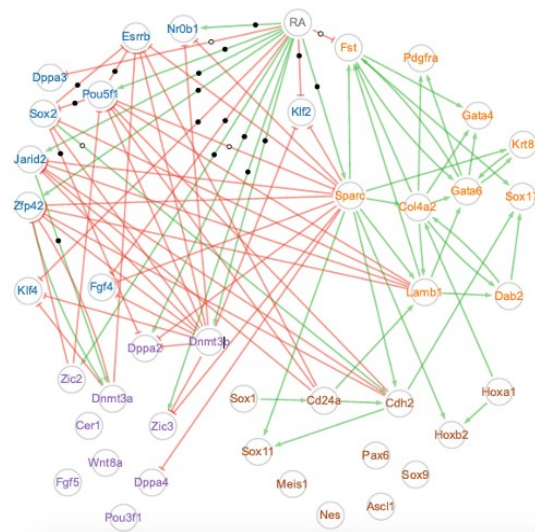
TRAJECTORIES INFERENCE

EVALUATION

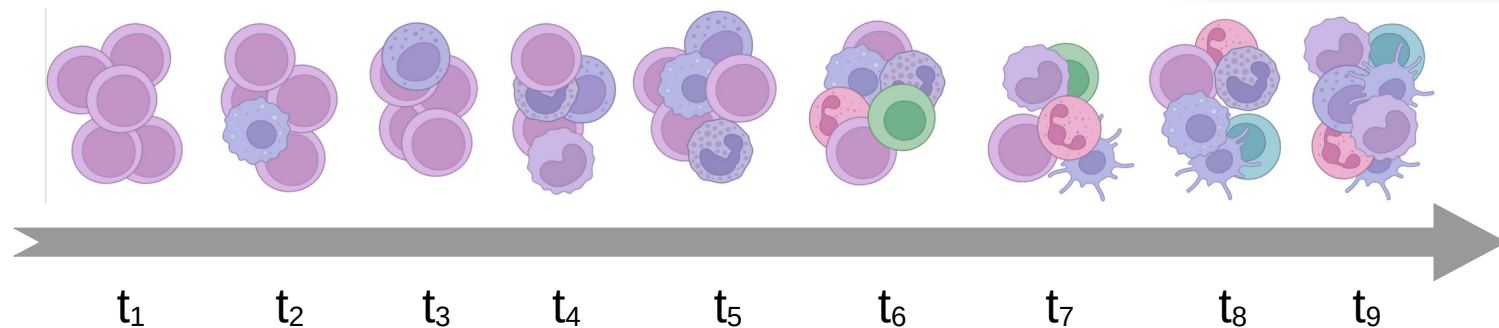
Gene Regulatory Network

scRNA-seq of a retinoic acid-induced differentiation of mouse embryonic stem cells

(Semrau, 2017)

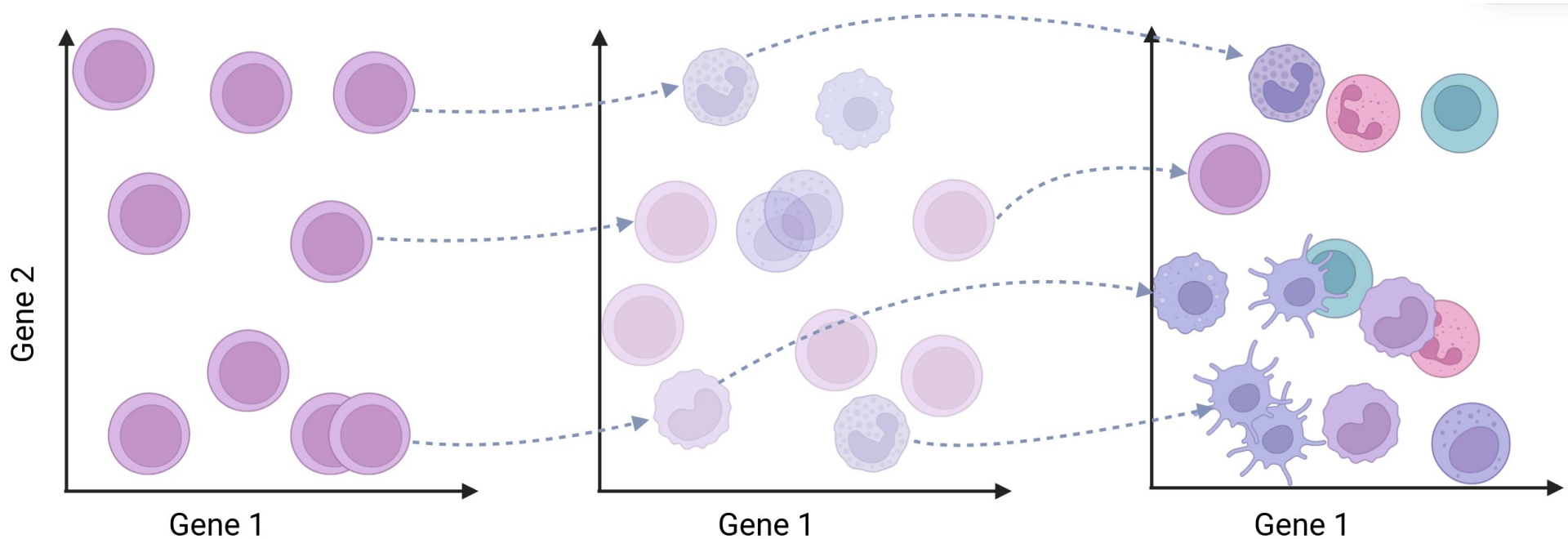


■ Pluripotency
■ Post-implantation epiblast
■ Extraembryonic endoderm
■ Neuroectoderm



(Ventre et al, 2023)

Interpolation



t_1

t_2

t_3

Results: Interpolation

