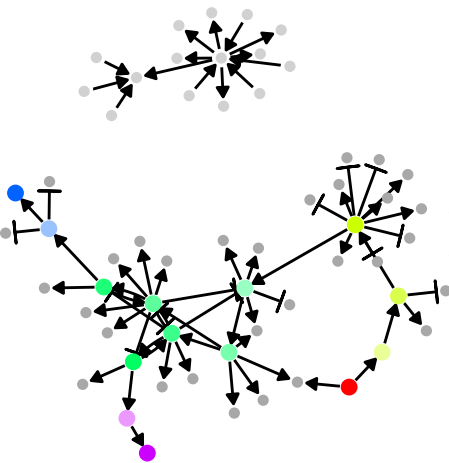
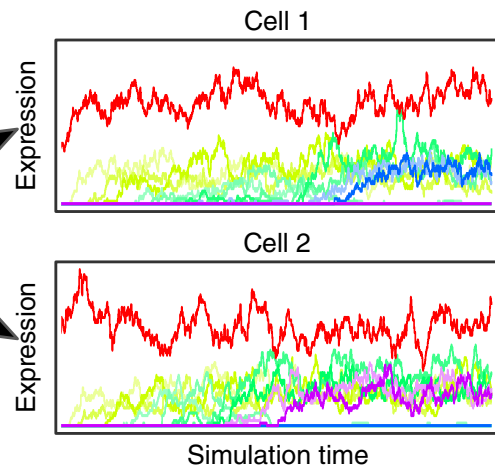
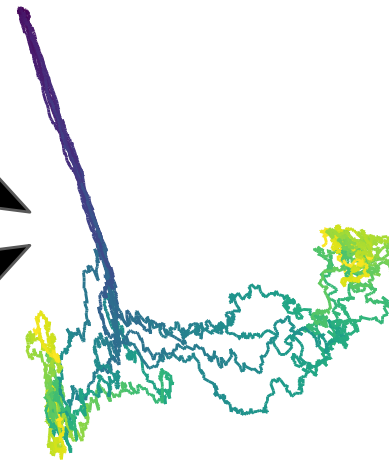


A Gene regulatory network

Simulate expression over time



Combine simulations

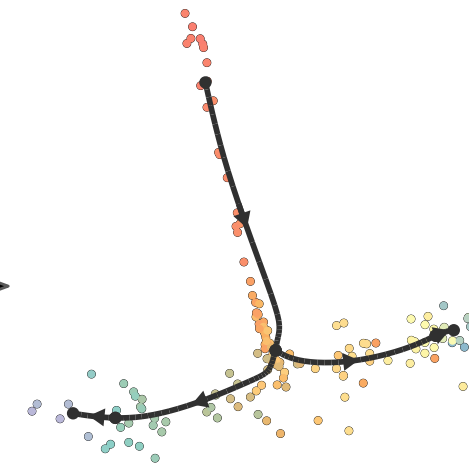


Sample cells & map to backbone

Simulation
time

Start

End

**B**

At any given time point, measure:

- molecule abundance (pre-mRNA, mRNA, protein)
- no. of reactions occurring
(transcription, splicing, translation, degradation)
- which regulatory interactions are active

Simulate experimental conditions:

- snapshot experiment
- time series experiment
- batch effect
- perturbation experiment

Evaluate computational tools:

- dimensionality reduction
- batch effect correction
- trajectory inference / alignment
- (differential) network inference