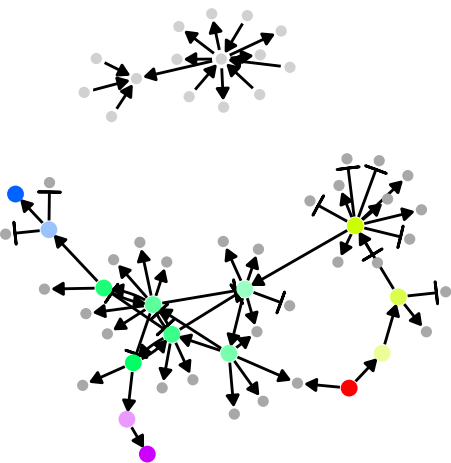
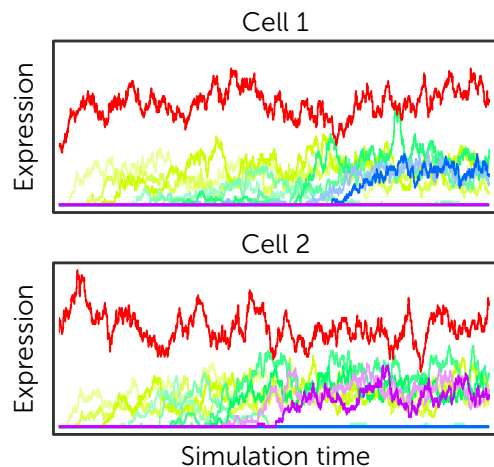


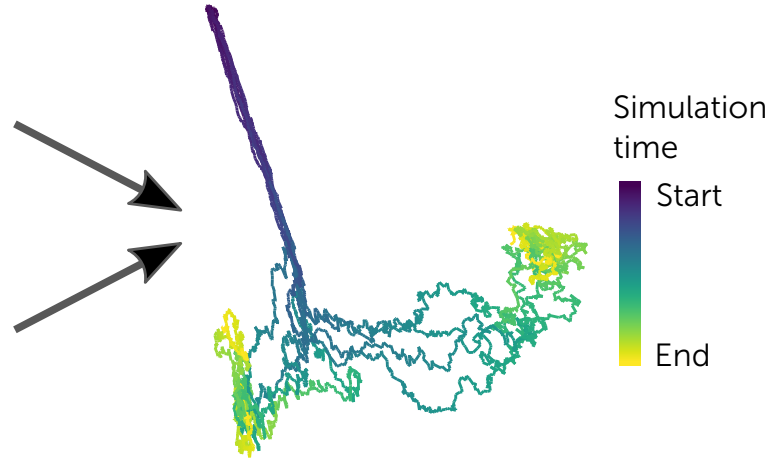
A Gene regulatory network



Expression over time



Visualisation of simulations



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