

# Modelling single-cell dynamics with trajectories and gene regulatory networks

Robrecht Cannoodt

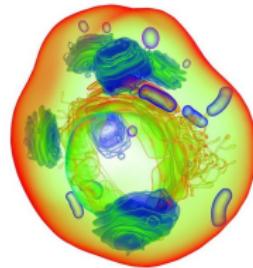


# Single-cell biology

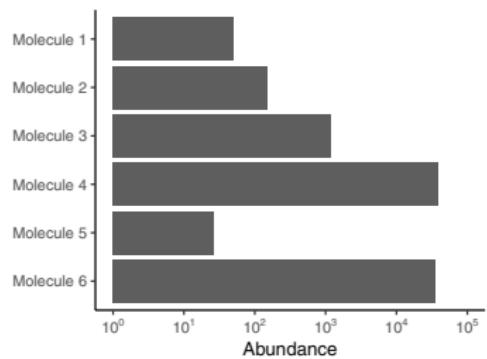
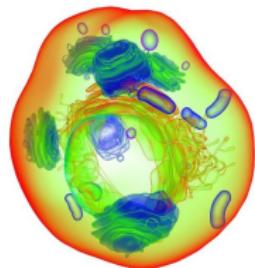
Single-cell biology is to study an organism



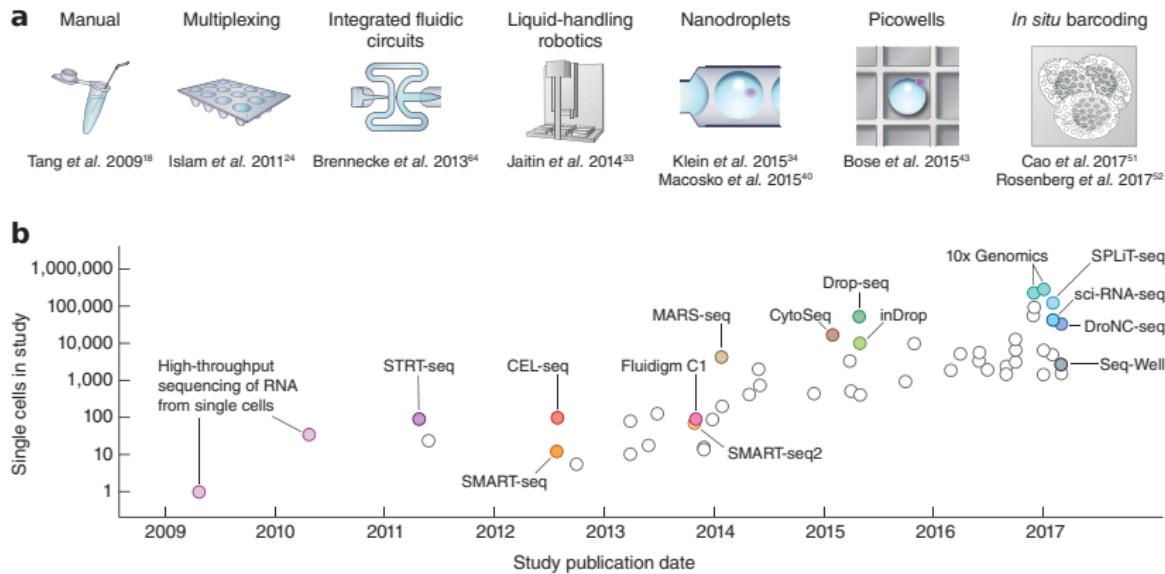
Single-cell biology is to study an organism  
by studying the behaviour of its cells



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by studying the behaviour of its cells

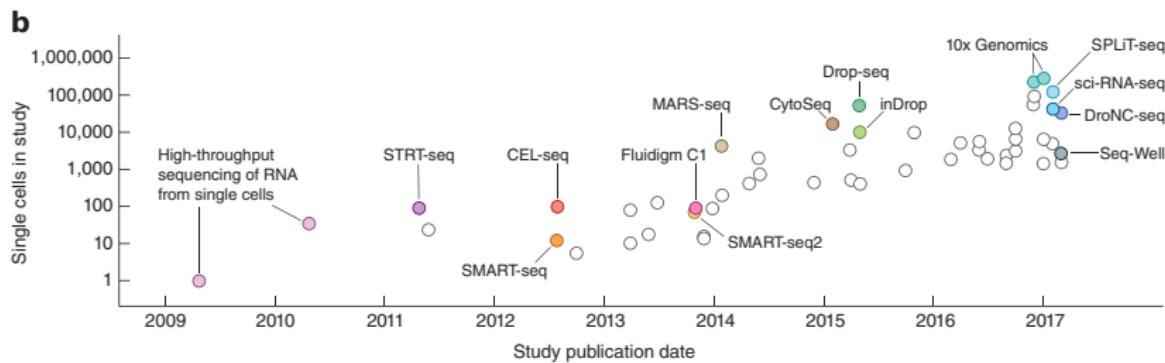
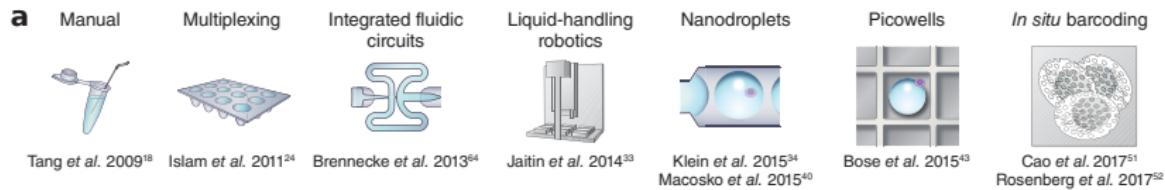


# Technological advances allow high-throughput single-cell biology



Regev et al. 2018

# Technological advances allow high-throughput single-cell biology

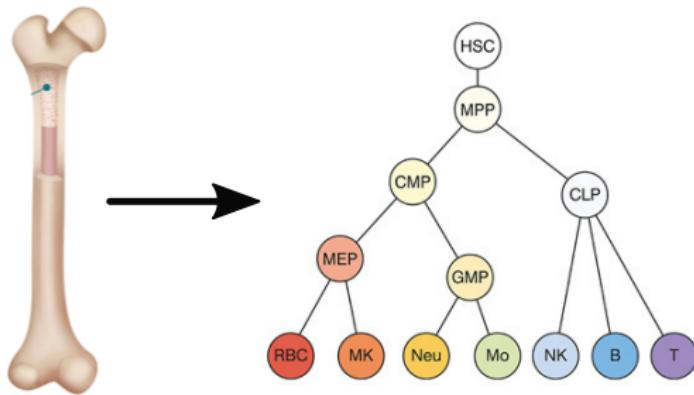


- ↳ Trajectory inference
- ↳ Network inference

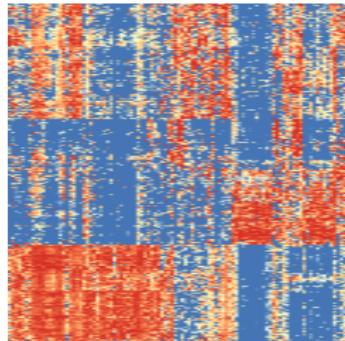
Regev *et al.* 2018

- Single-cell biology
- **Trajectory inference**
- Network inference
- Benchmarking
- Practical implications

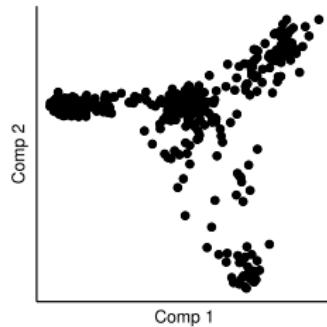
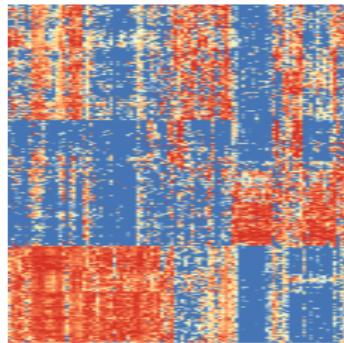
# Cells are highly dynamic entities



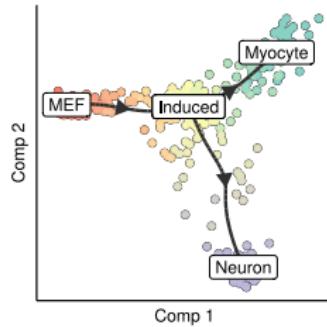
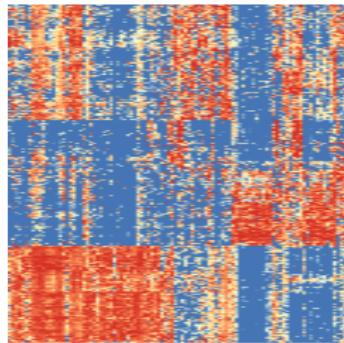
# A typical trajectory inference analysis



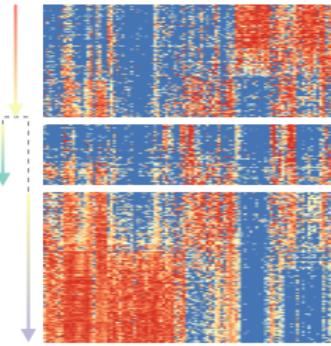
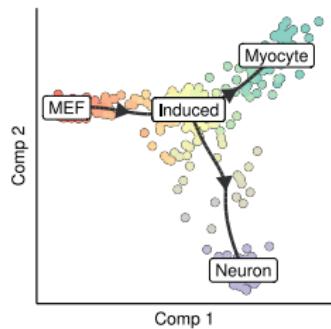
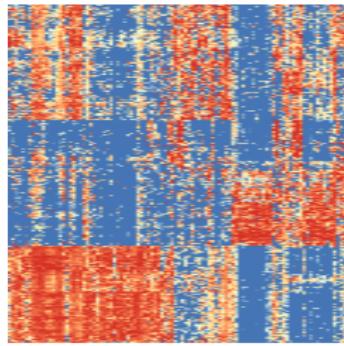
# A typical trajectory inference analysis



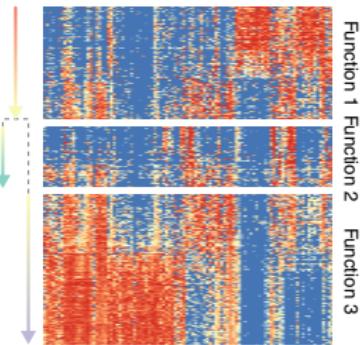
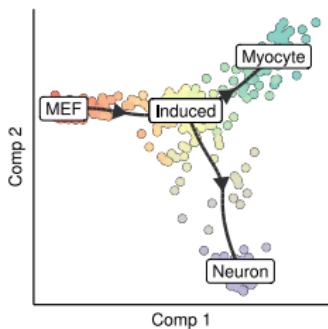
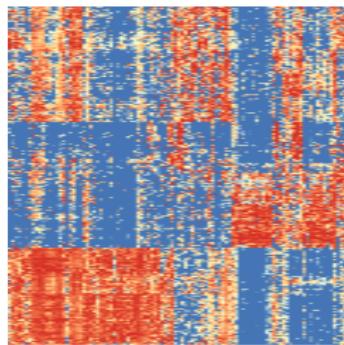
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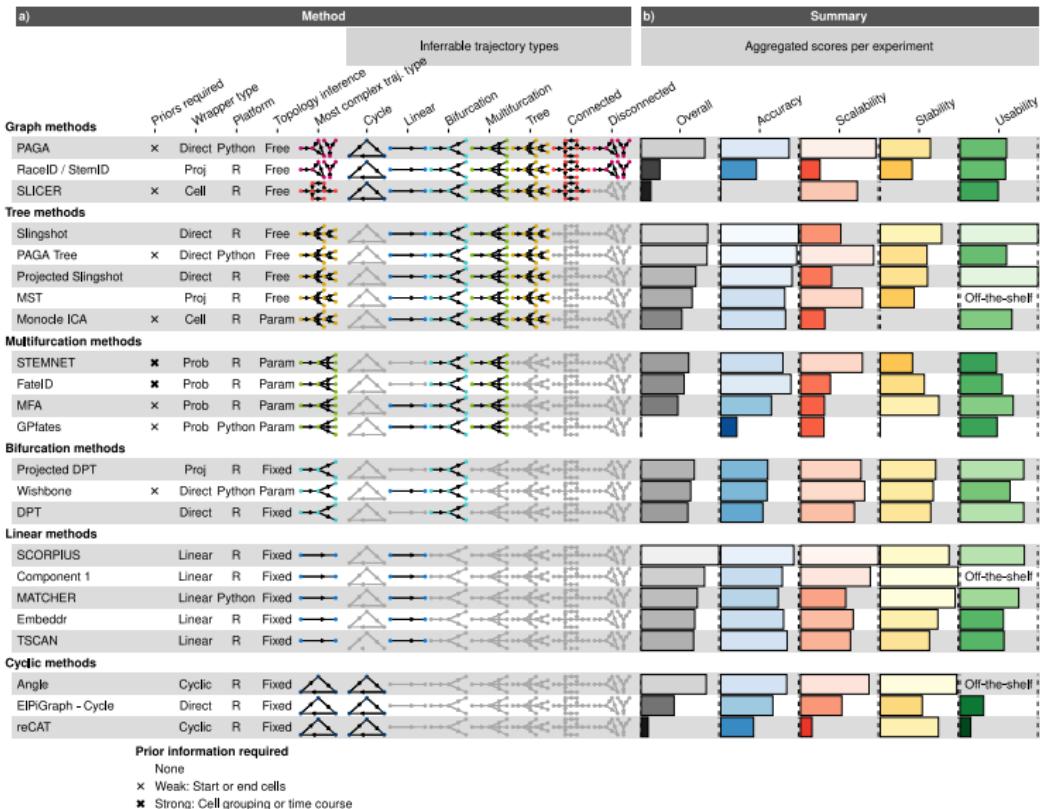
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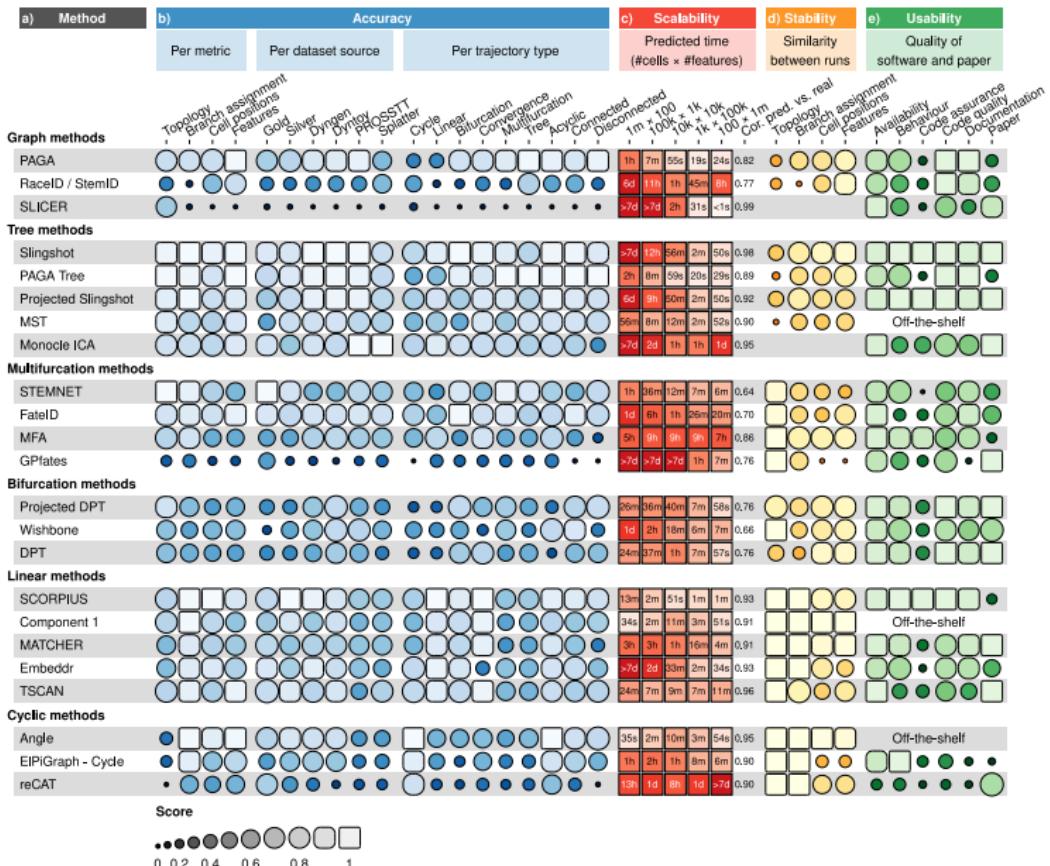
# A typical trajectory inference analysis



# Benchmark of 45 trajectory inference methods



## Benchmark of 45 trajectory inference methods



# Interactive guidelines

dynguidelines

Tutorial Citation

Topology  
Do you expect multiple disconnected trajectories in the data?

Yes I don't know No

Scalability COMPUTED

Number of cells  
1000

Number of features (genes)  
1000

Time limit  
10s 1h

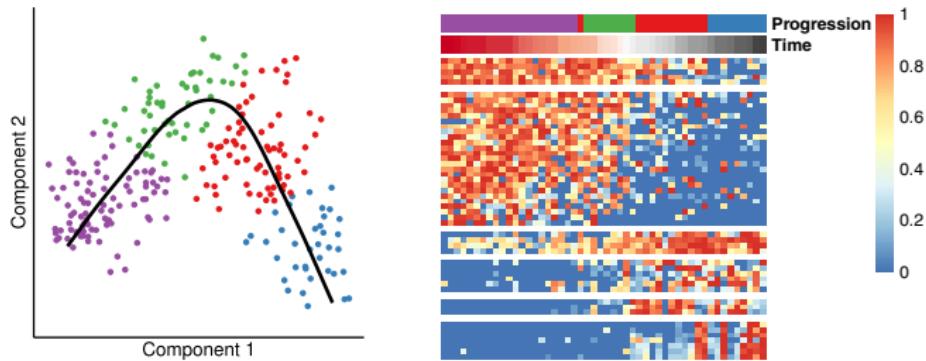
Memory limit  
10MB 10GB

Show code </> Show/hide columns □ Options ⓘ

Benchmark study ↗ Evaluating methods with dynbenchmark ⓘ Part of

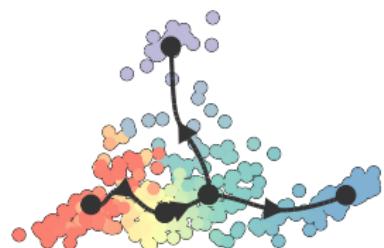
Lenses	Default	Summary (Fig. 2)	Method	Scalability	Stability	Usability	Accuracy	Overall	Everything
Method									
🕒	🕒	Name	Priors				Errors	Overall #	O.T
✓	🕒	Singshot					100	8s	942MB
✓	🕒	SCORPIUS					96	3s	507MB
✓		Angle					92	1s	308MB
✓	🕒	PAGA					59	15s	559MB
	🕒	Embeddr					89	5s	581MB
		MST					69	4s	572MB
	🕒	Waterfall					69	5s	369MB
	🕒	TSCAN					68	5s	476MB
		Component 1					67	1s	516MB
	🕒	SLICE					63	16s	713MB
	🕒	Monocle DDRTree					62	41s	647MB
	🕒	EPIGraph Linear					61	1m	573MB

# SCORPIUS: Linear trajectory inference



# dyno: A toolkit for inferring and interpreting trajectories

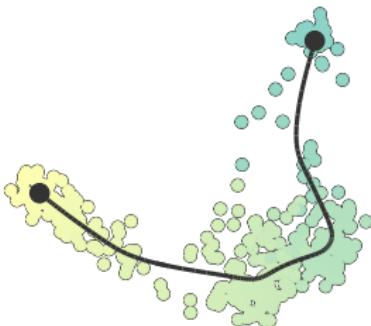
Slingshot



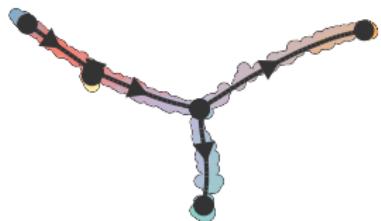
PAGA



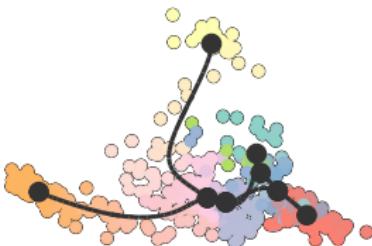
SCORPIUS



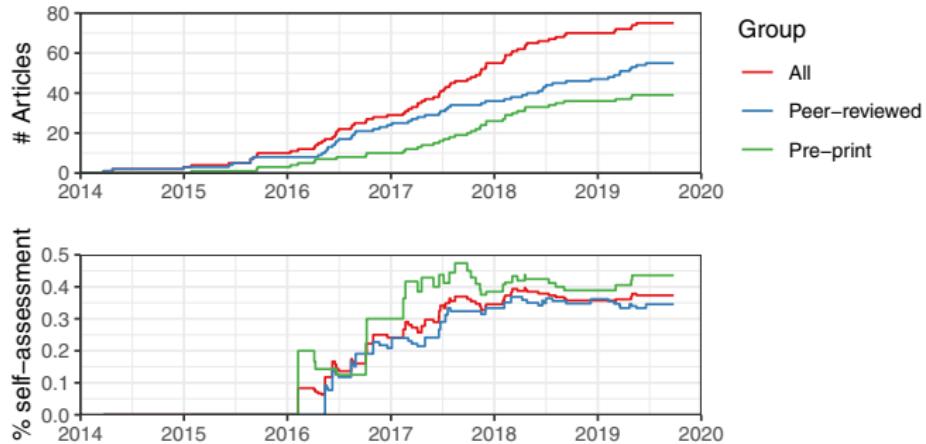
Monocle DDRTree



pCreode



# Perspective: self-assessment in trajectory inference

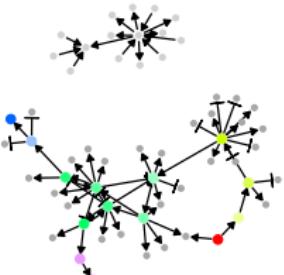


- Single-cell biology
- Trajectory inference
- **Network inference**
- Benchmarking
- Practical implications

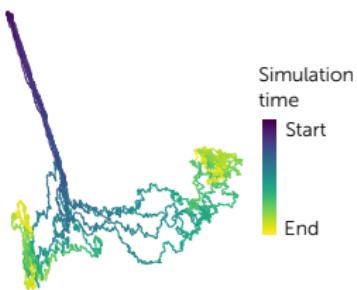
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# dyngen

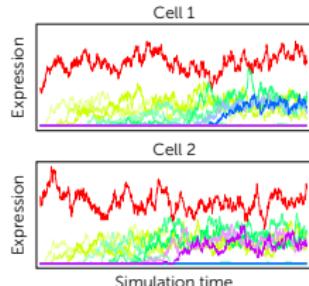
Gene regulatory network



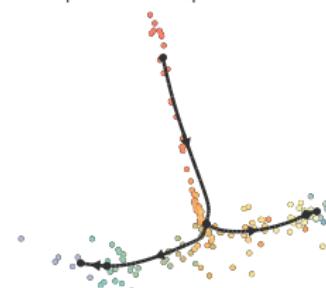
Combine simulations



Simulate expression over time



Sample cells & map to backbone



# Guidelines for benchmarking computational tools

1. Define the purpose and scope of the benchmark.
2. Include all relevant methods.
3. Select (or design) representative dataset.
4. Choose appropriate parameter values and software versions.
5. Evaluate methods according to key quantitative performance metrics.
6. Evaluate secondary measures including computational requirements, user-friendliness, installation procedures, and documentation quality.
7. Interpret results and provide recommendations from both user and method developer perspectives.
8. Publish results in an accessible format
9. Design the benchmark to enable future extensions.
10. Follow reproducible research best practices, by making code and data publicly available.

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