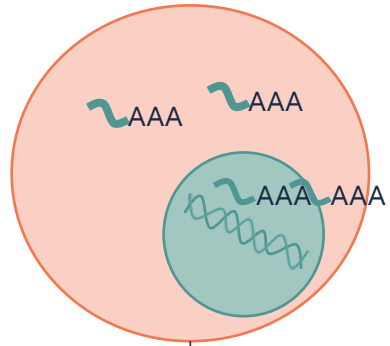


Benchmark on existing trajectory inference methods

For single cell RNA-Seq data

BIOSYL

Single-cell RNA-Seq data:



100-10 000 of cells

Sequencing

Pre-processing

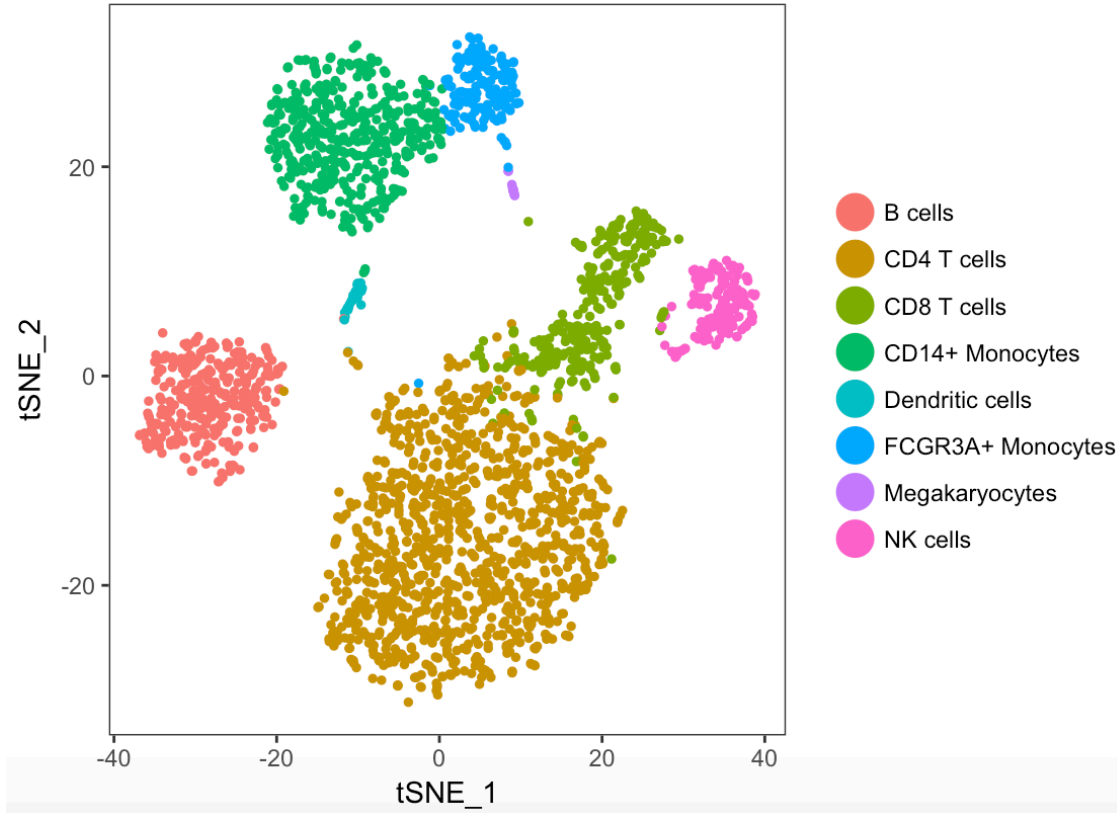


	AAACATACAACCAC	AAACATTGAGCTAC	AAACATTGATCAGC	AAACCGTGCTTCCG	AAACGCACTGGTAC	AAACGCTGACCAGT	AAACGCTGGTTCTT	AAACGCTGTAGCCA	AAACGCTGTTTCTG
AL627309.1	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
AP006222.2	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
RP11-206L10.2	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
RP11-206L10.9	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
LINC00115	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
NOC2L	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
KLHL17	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
PLEKHN1	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
RP11-5407.17	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
HES4	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
RP11-5407.11	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
ISG15	0.000000	0.000000	1.429744	3.558310	1.726902	0.000000	0.000000	0.000000	3.339271
AGRN	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
C1orf159	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
TNFRSF18	0.000000	1.625141	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
TNFRSF4	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.179642	0.000000
SDF4	0.000000	0.000000	1.429744	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
B3GALT6	0.000000	0.000000	0.000000	0.000000	0.000000	1.722356	0.000000	0.000000	0.000000
FAM132A	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
UBE2J2	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.179642	0.000000
ACAP3	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
PUSL1	0.000000	0.000000	0.000000	0.000000	0.000000	1.722356	0.000000	0.000000	0.000000
CPSF3L	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
GLTPD1	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
DVL1	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
MXRA8	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
AURKAIP1	0.000000	1.111715	0.000000	1.566387	0.000000	0.000000	1.690977	0.000000	0.000000
CCNL2	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
RP4-758J18.2	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
MRPL20	1.635873	0.000000	1.429744	0.000000	0.000000	0.000000	1.690977	0.000000	0.000000

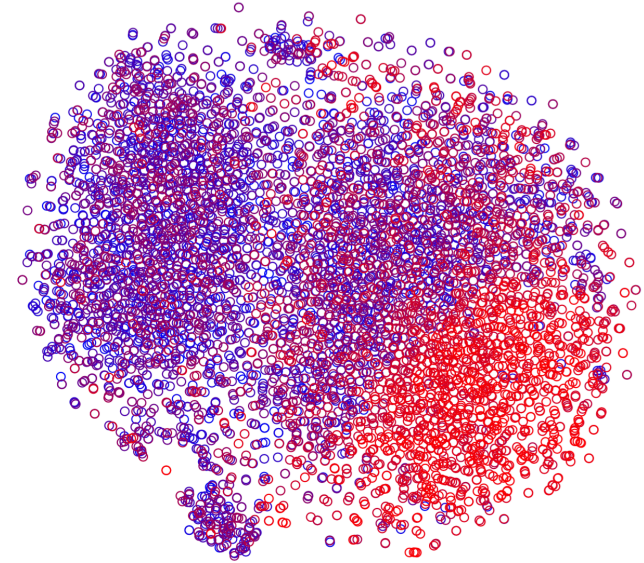
Thousands of genes

SCIENCE MEETS LIFE

Visualisation:

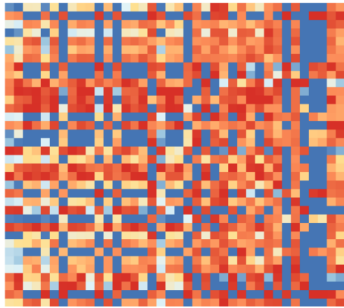


Alveolar macrophages:

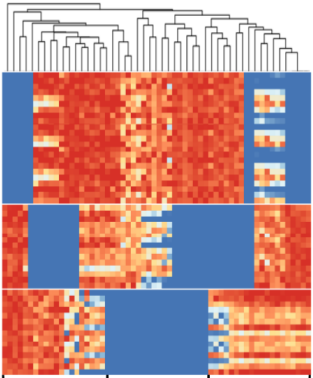
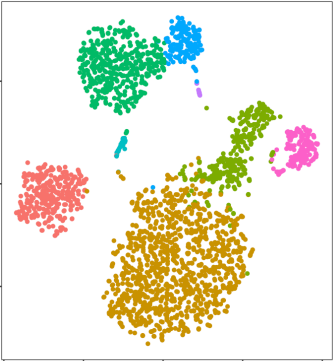


Hard to define populations

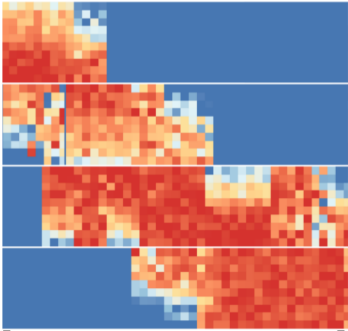
Expression data



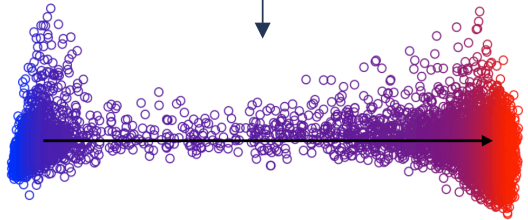
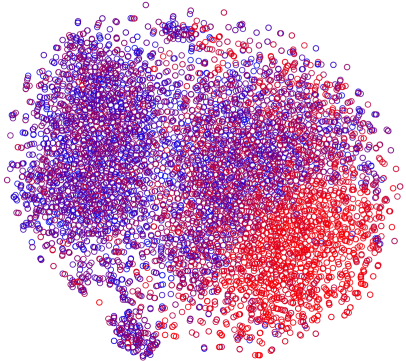
Clustering



Trajectory inference



Trajectory

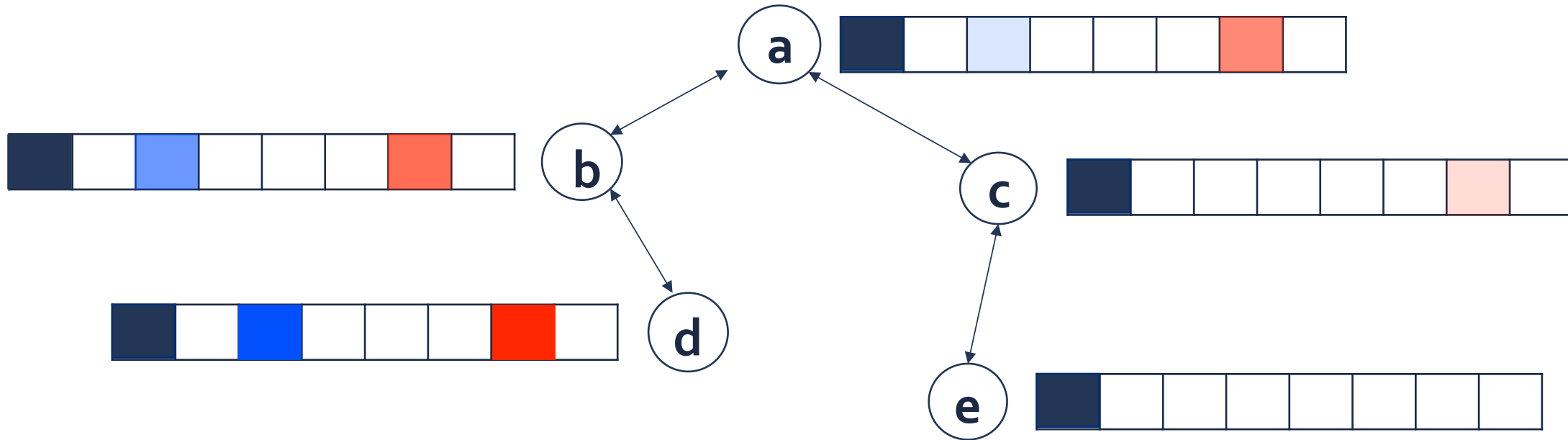


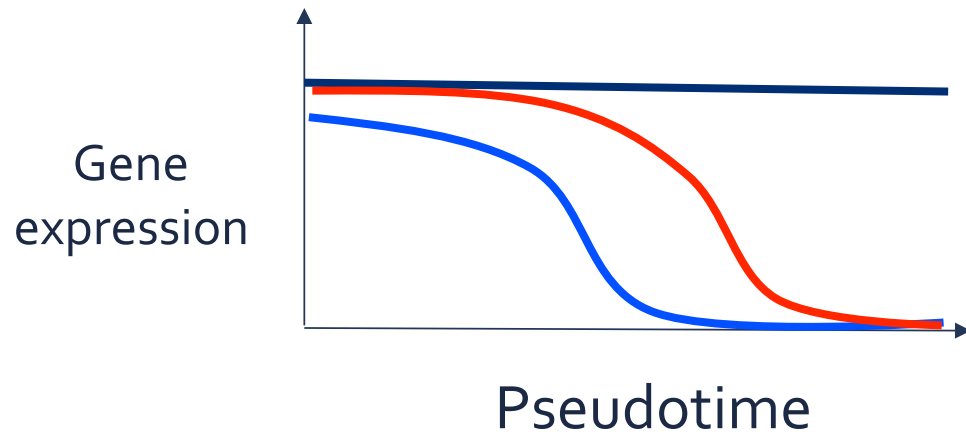
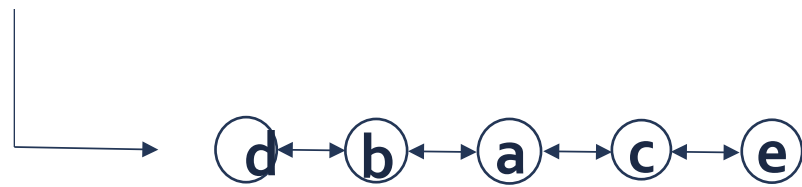
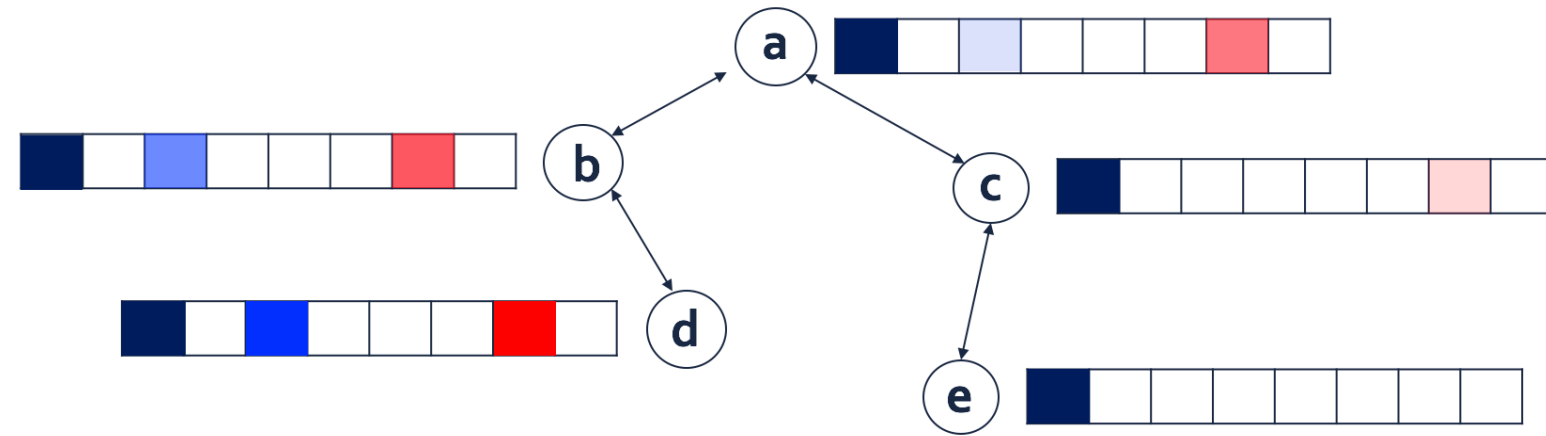
Living cells

Dying cells

SCIENCE MEETS LIFE

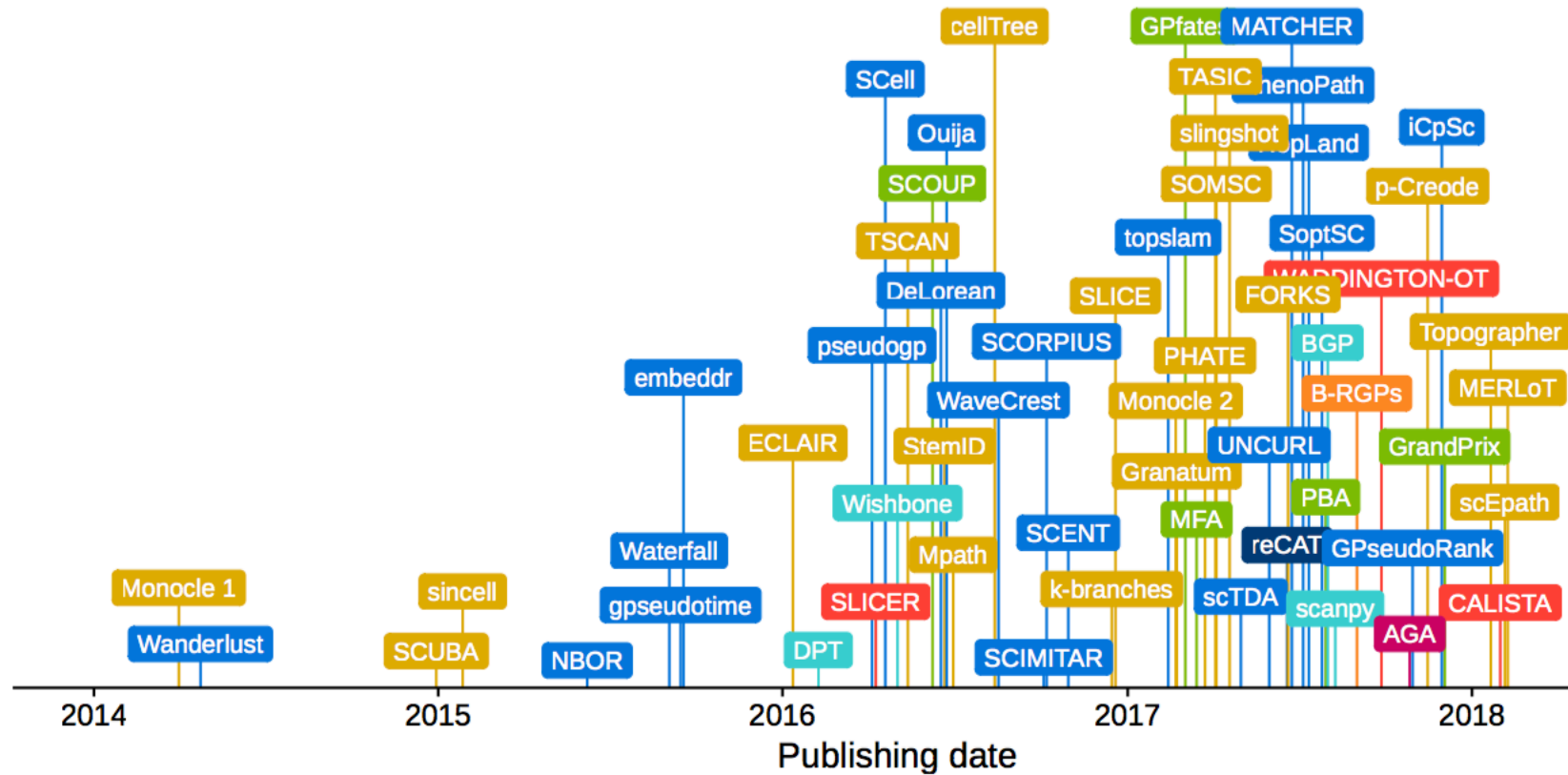
How does it work ?



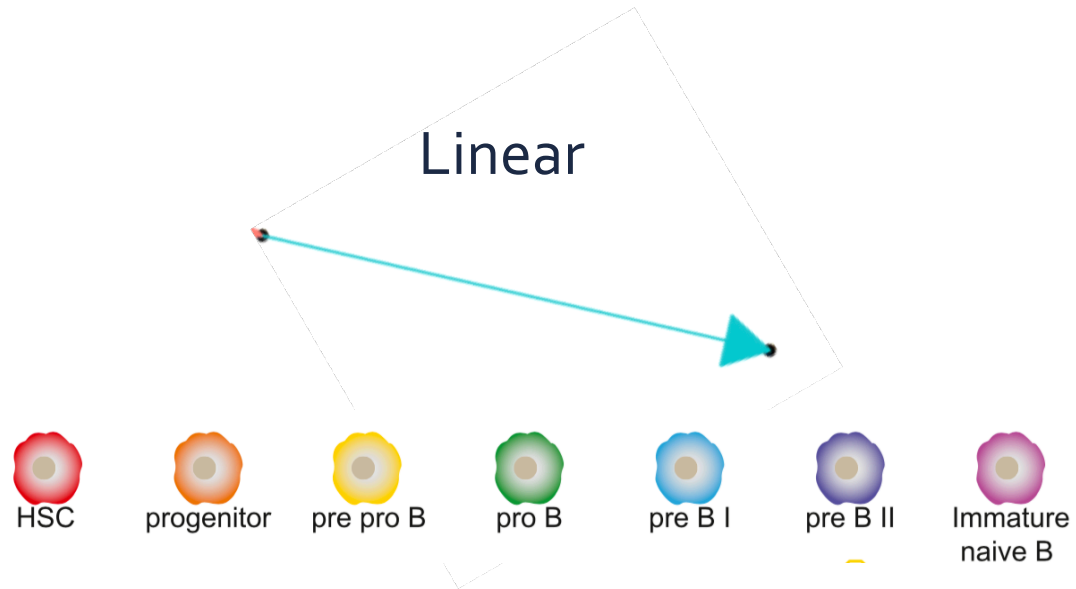


Trajectory inference

Trajectory inference: powerful, popular



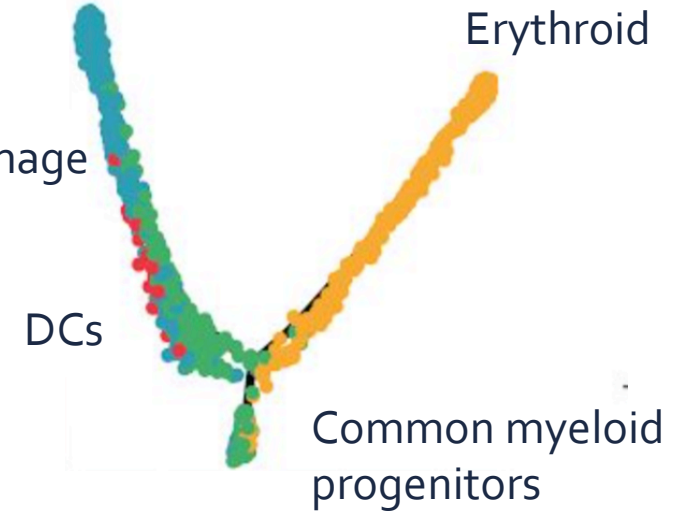
Topology



Wanderlust – Bendall & al, 2014

Bifurcation

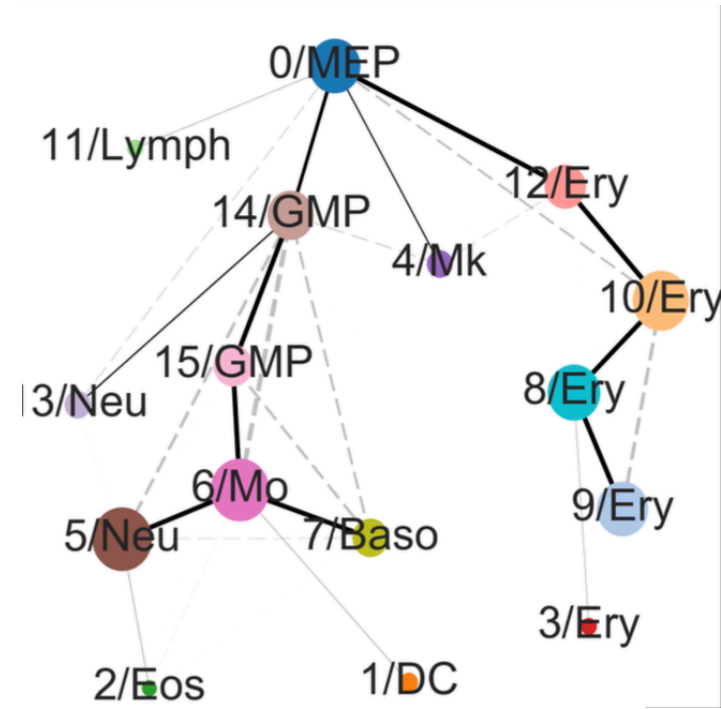
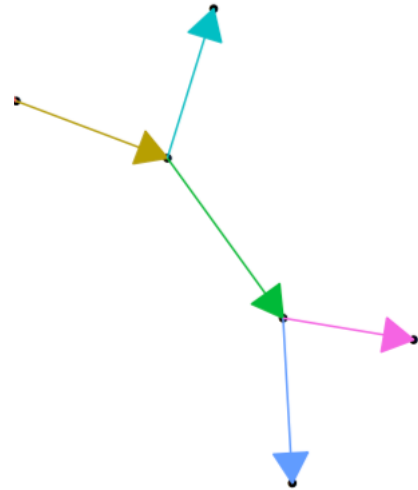
Granulocyte-macrophage progenitors



Monocle 2 – Qiu & al, 2017

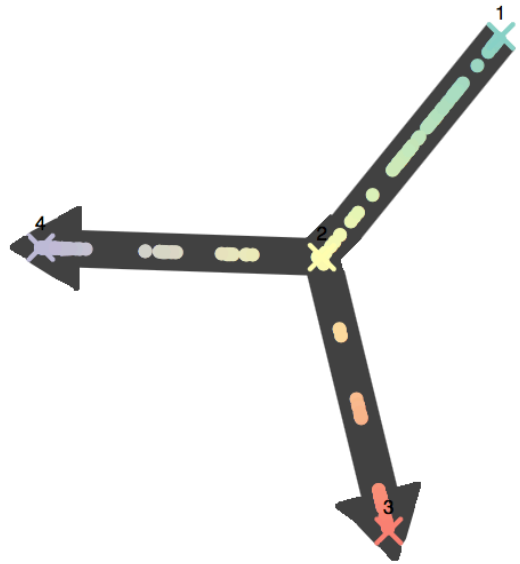
Topology

More complex



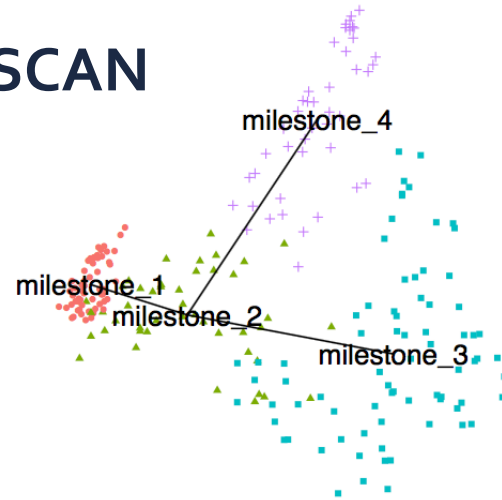
AGA - Wolf & al, Preprint 2017

Different tools, different outputs:



Gold Standard

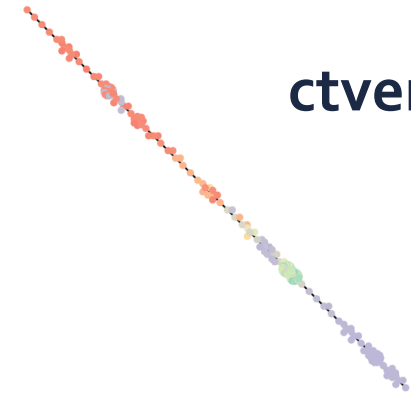
TSCAN



DPT



ctvem



wishbone



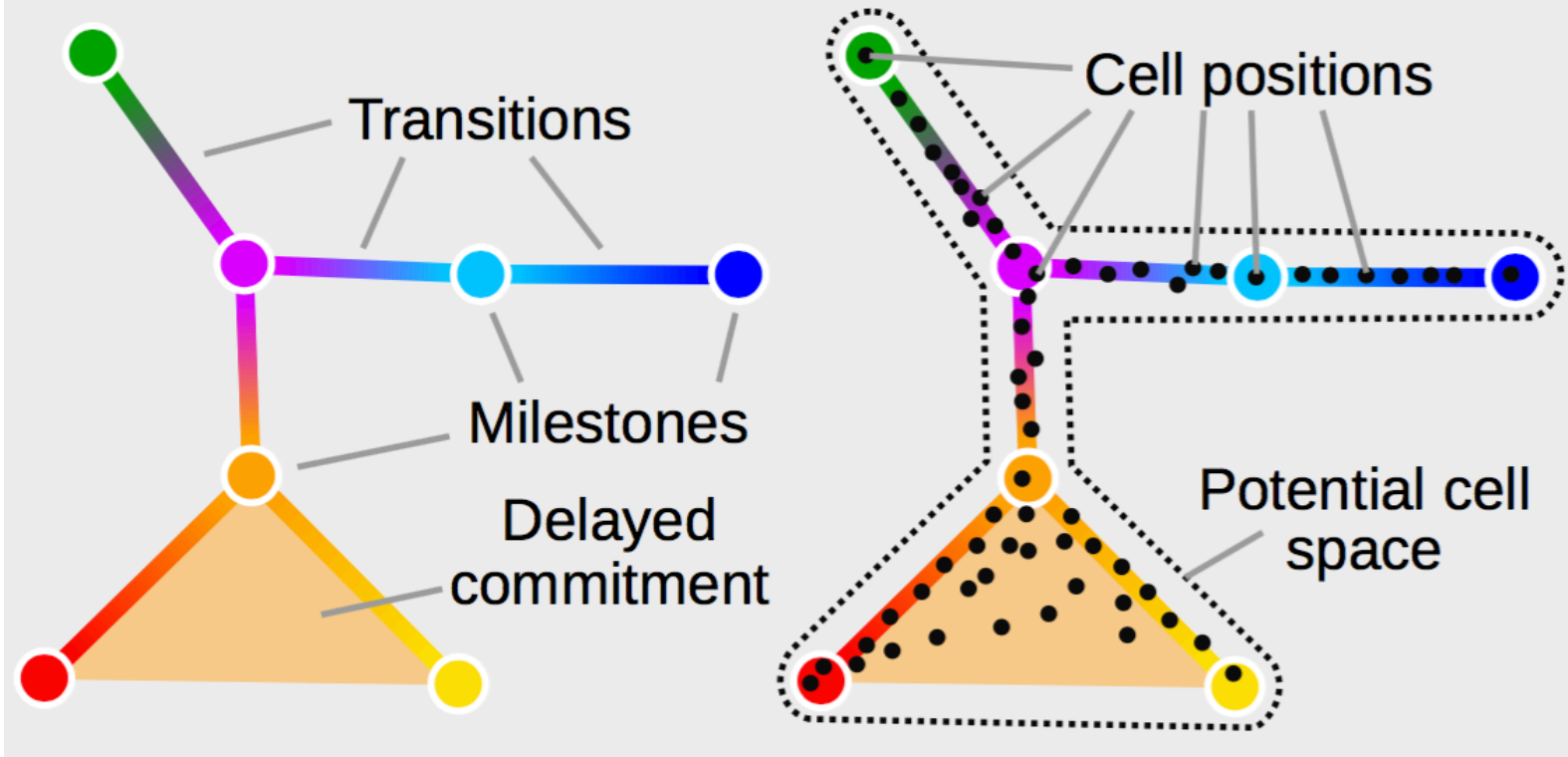
Which method should be used?

Which one returns the right trajectory?

How to compare them?

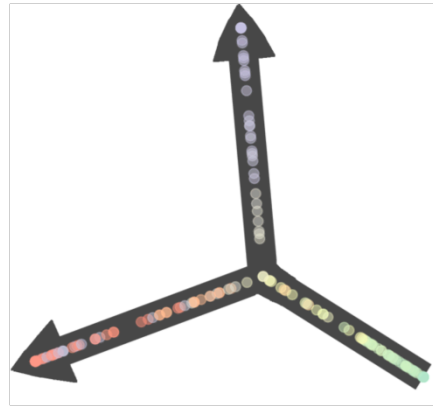
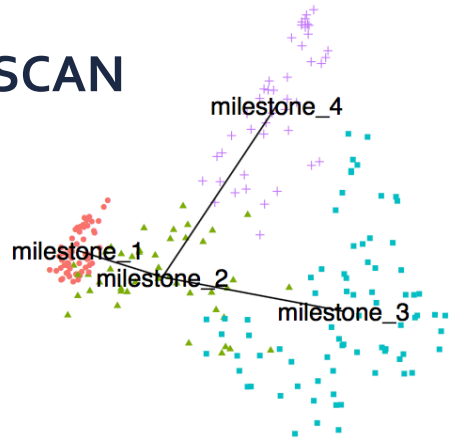
→ **Benchmark of trajectory inference methods**

Common trajectory data structure

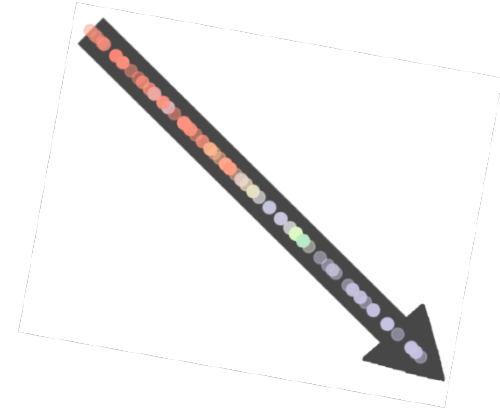
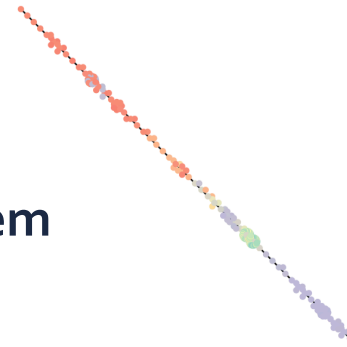


Common structure for all tools:

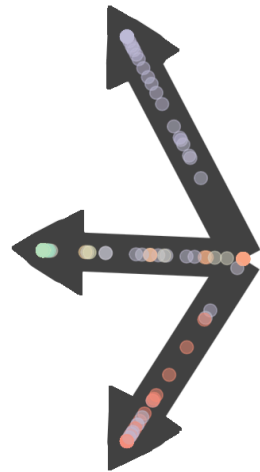
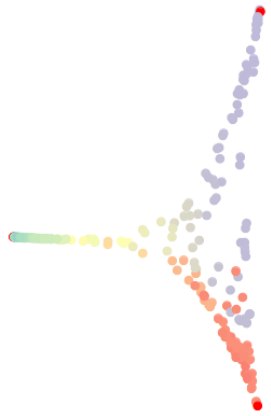
TSCAN



ctvem



DPT



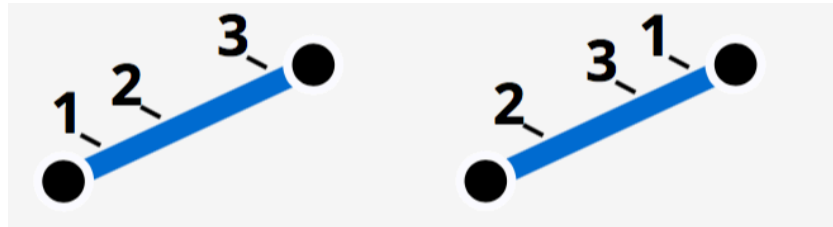
wishbone



Metrics for trajectory comparison:

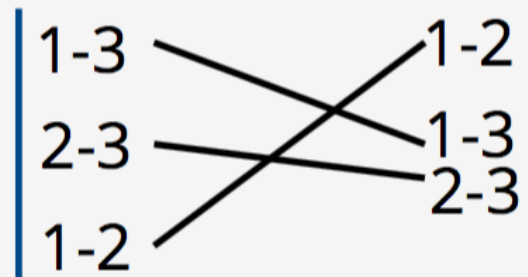
1) Cell ordering :

Gold Standard



Inferred trajectory

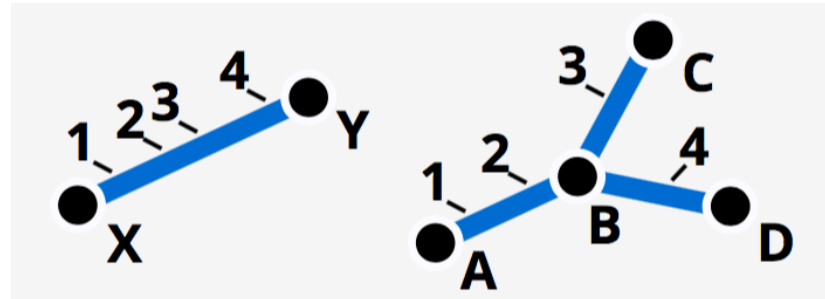
Correlation of distances



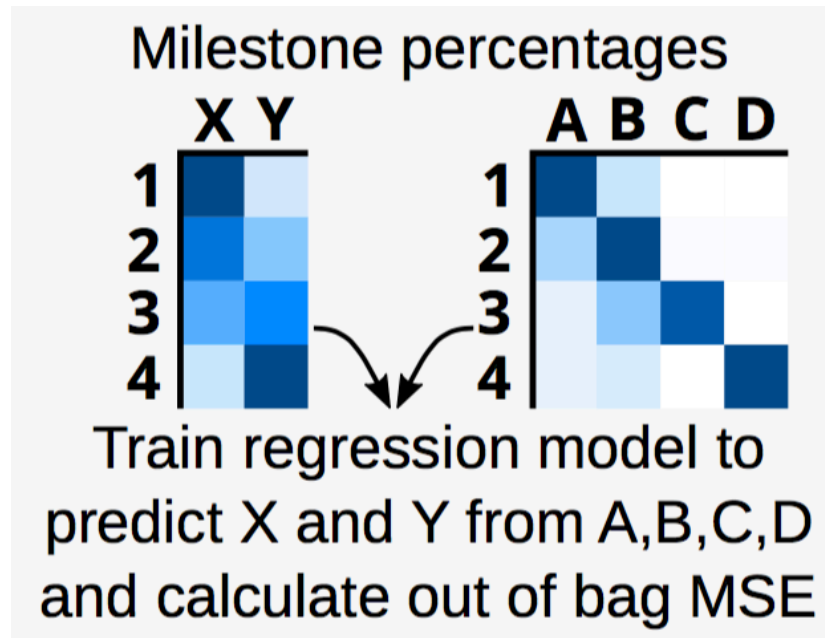
Metrics for trajectory comparison:

2) Neighbourhood:

Gold Standard



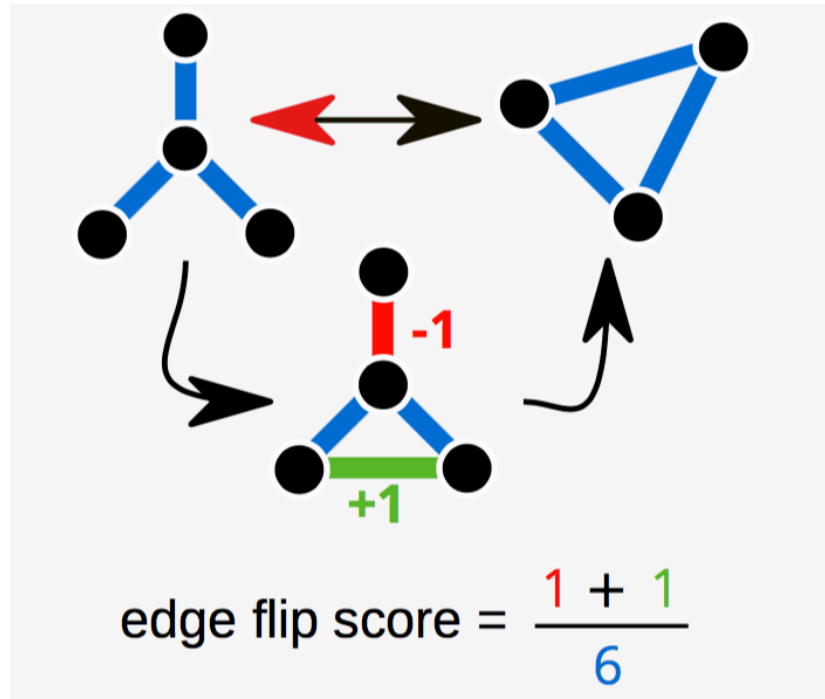
Inferred trajectory



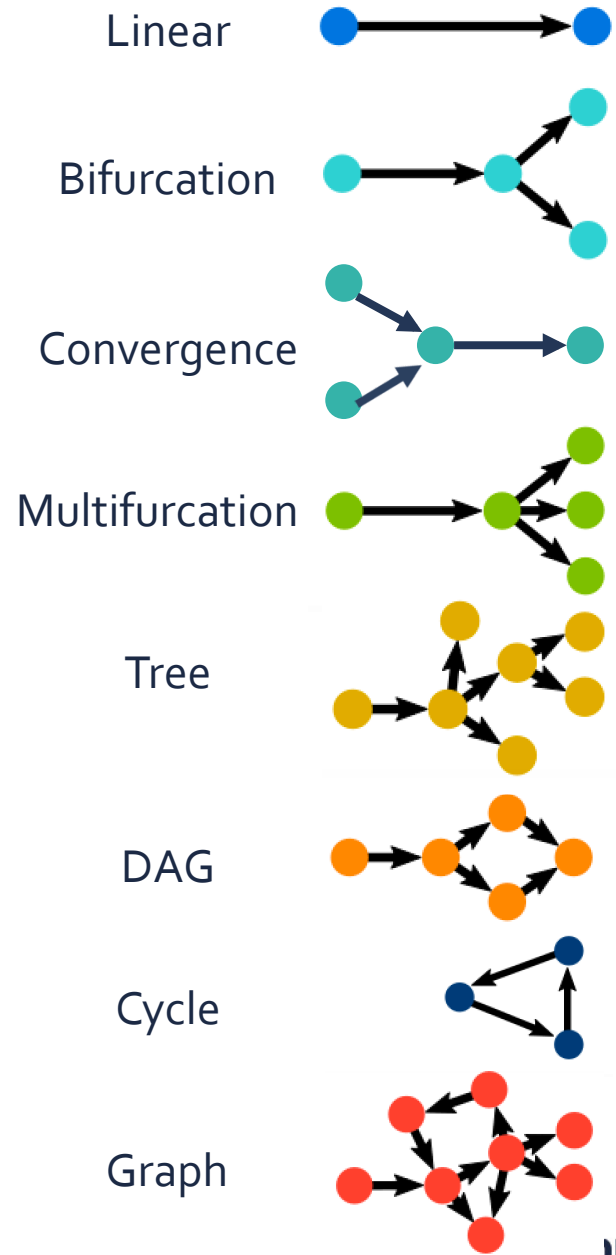
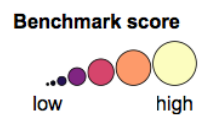
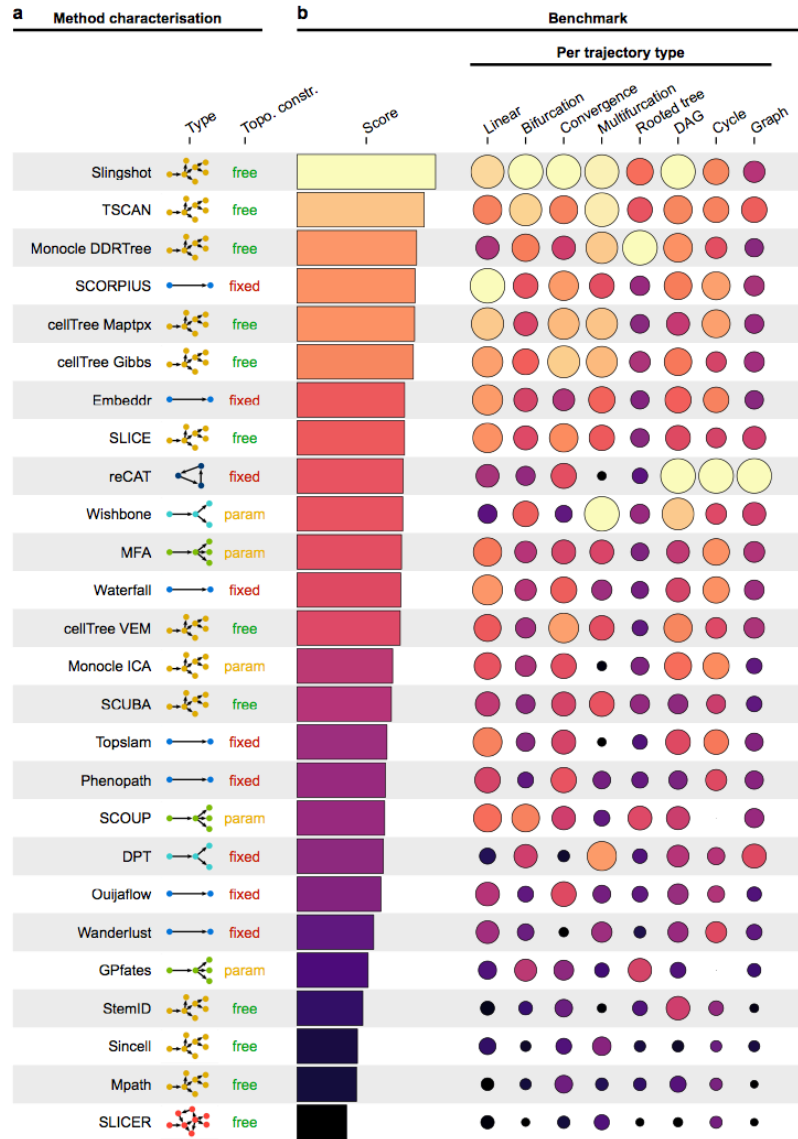
Metrics for trajectory comparison:

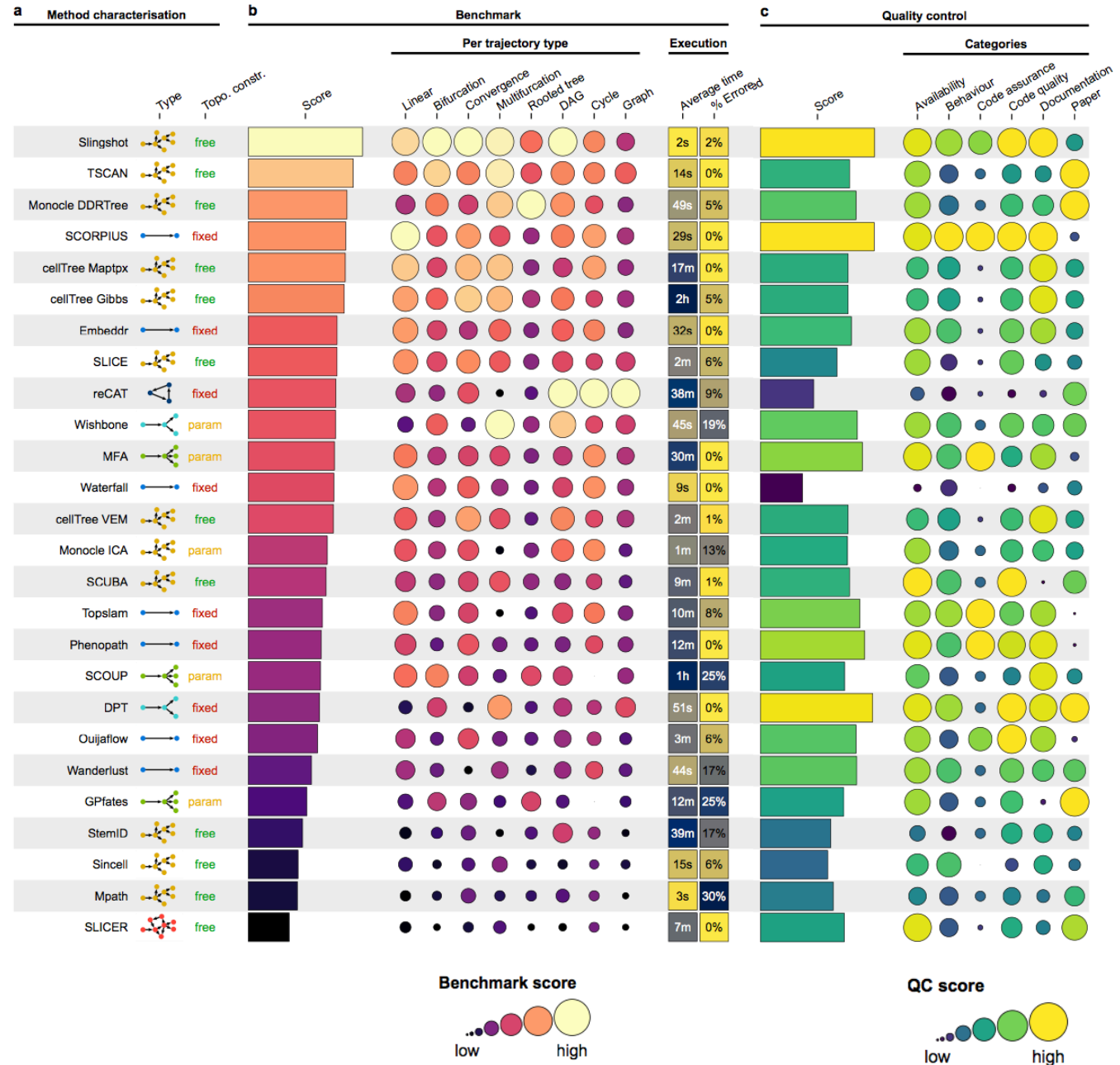
3) Topology:

Gold Standard

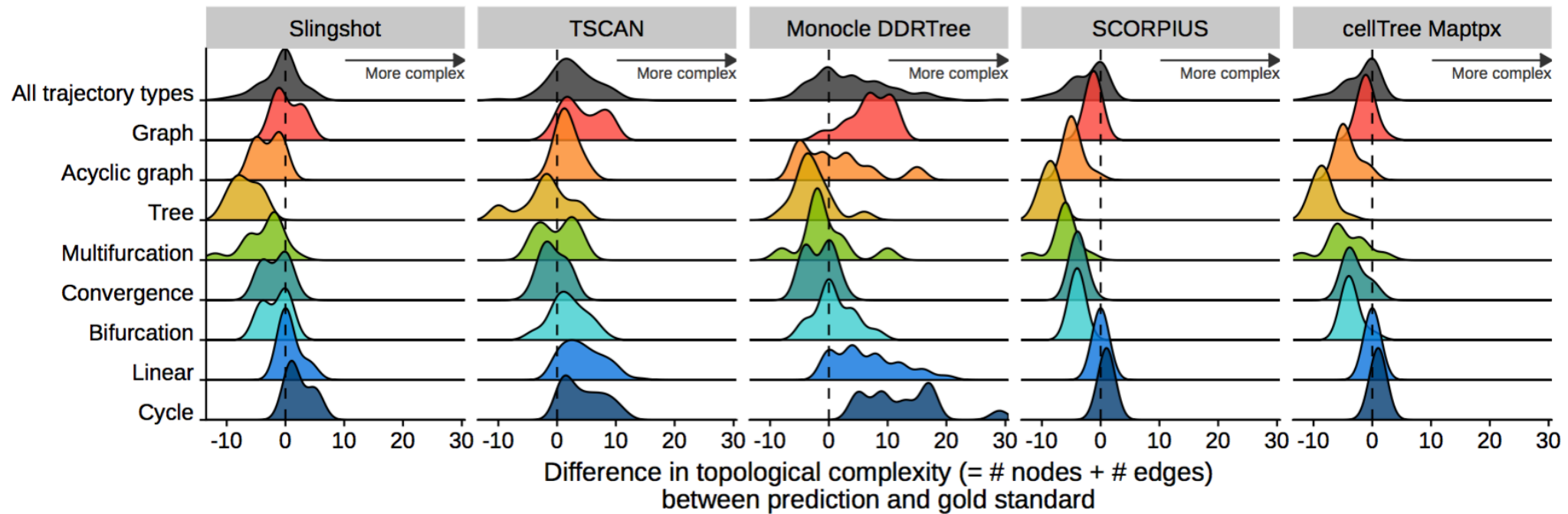


Inferred trajectory

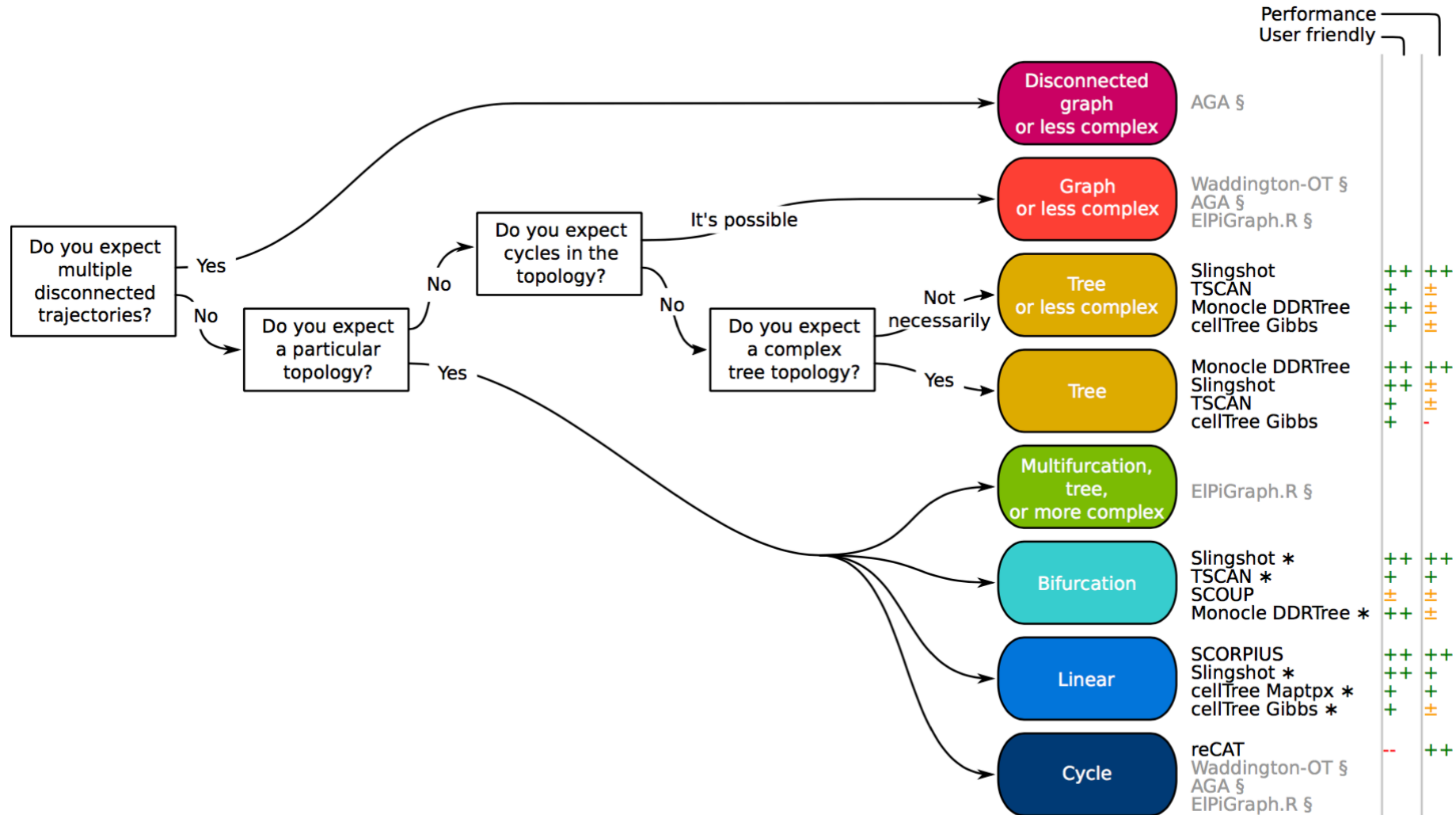




Some methods ↗ or ↘ complexity of trajectory:



Guidelines



* Method may return a different topology than requested
 § Not in the current version of the evaluation

Availability:



New Results

A comparison of single-cell trajectory inference methods: towards more accurate and robust tools

 Wouter Saelens,  Robrecht Cannoodt,  Helena Todorov,  Yvan Saeys

doi: <https://doi.org/10.1101/276907>

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Jacqueline Marvel
Team Marvel



Supplementary content



