

# dynbenchmark: ACCURACY, SCALABILITY, ROBUSTNESS AND USABILITY OF SINGLE-CELL TRAJECTORY INFERENCE METHODS



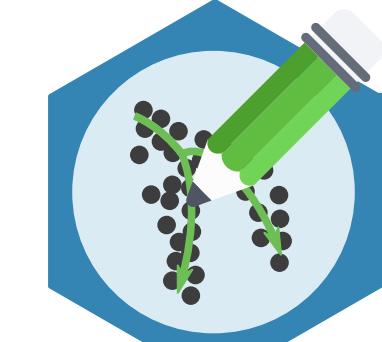
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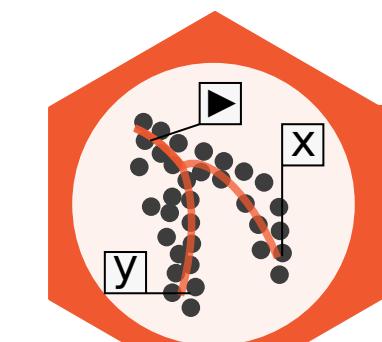
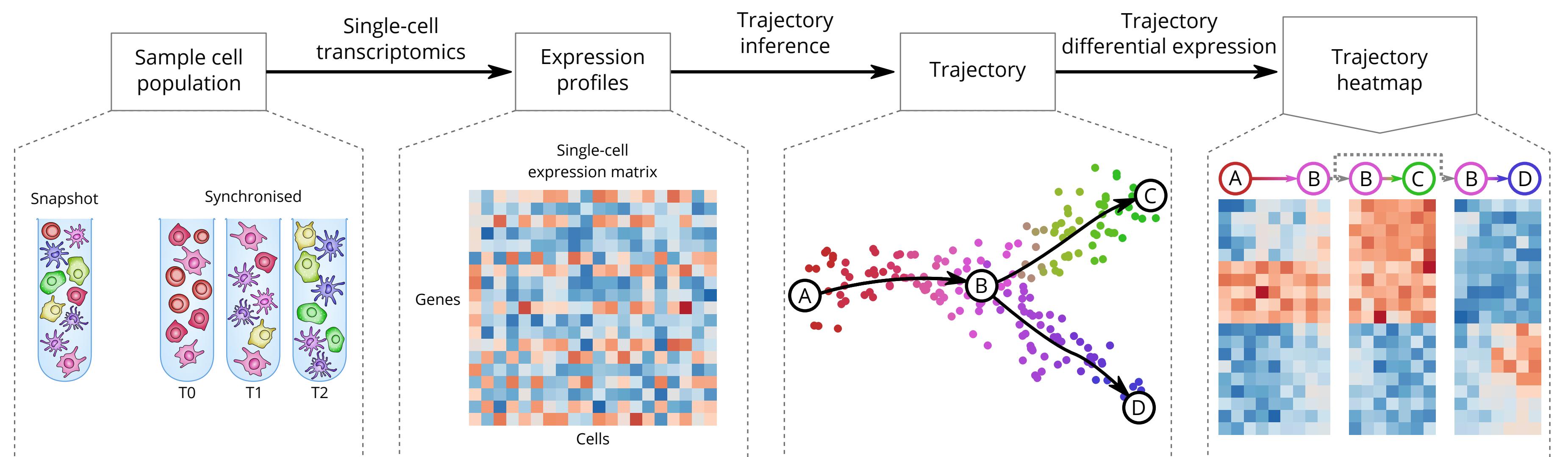
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► dynbenchmark is an extensive and extendable **benchmarking** study of **45 trajectory inference** methods.



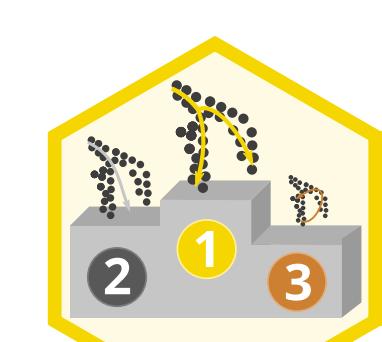
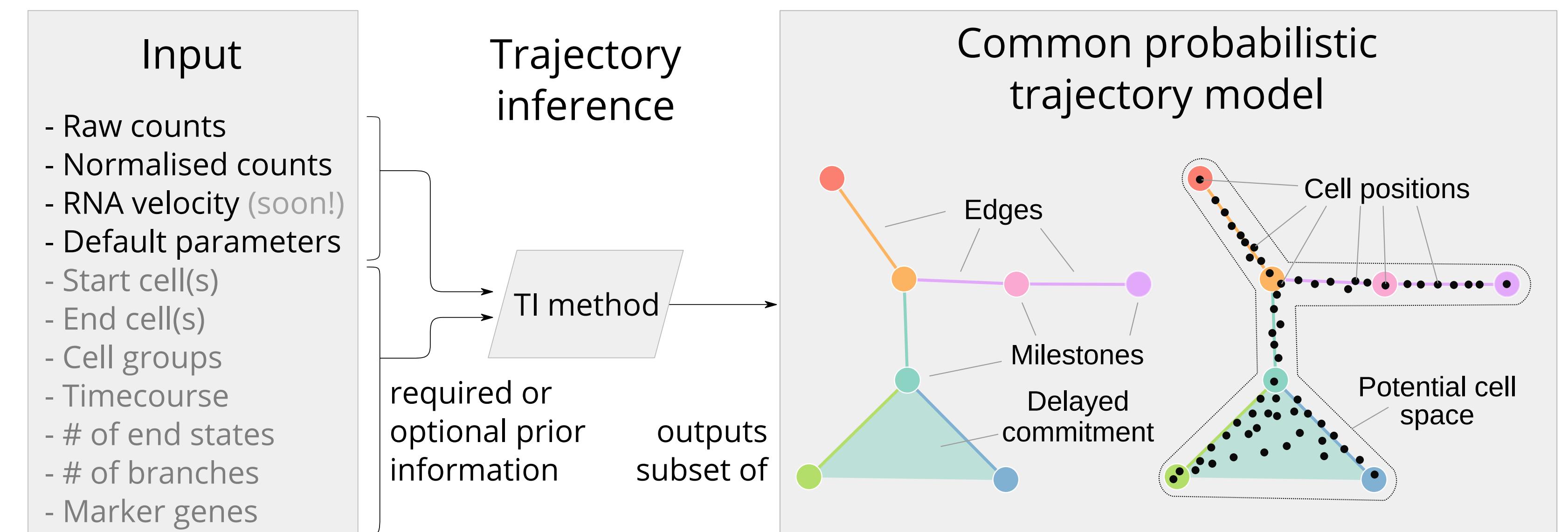
## Inferring trajectories to study dynamic processes

- Trajectory inference (TI) methods aid in **studying dynamic processes** by **ordering** single cells **along a trajectory**.
- ≥ 71 TI methods have been developed, each with a **unique input/output interface**.
- Quantitative or qualitative **comparison** of trajectories is thus **very challenging**.



## Common interface for trajectory inference

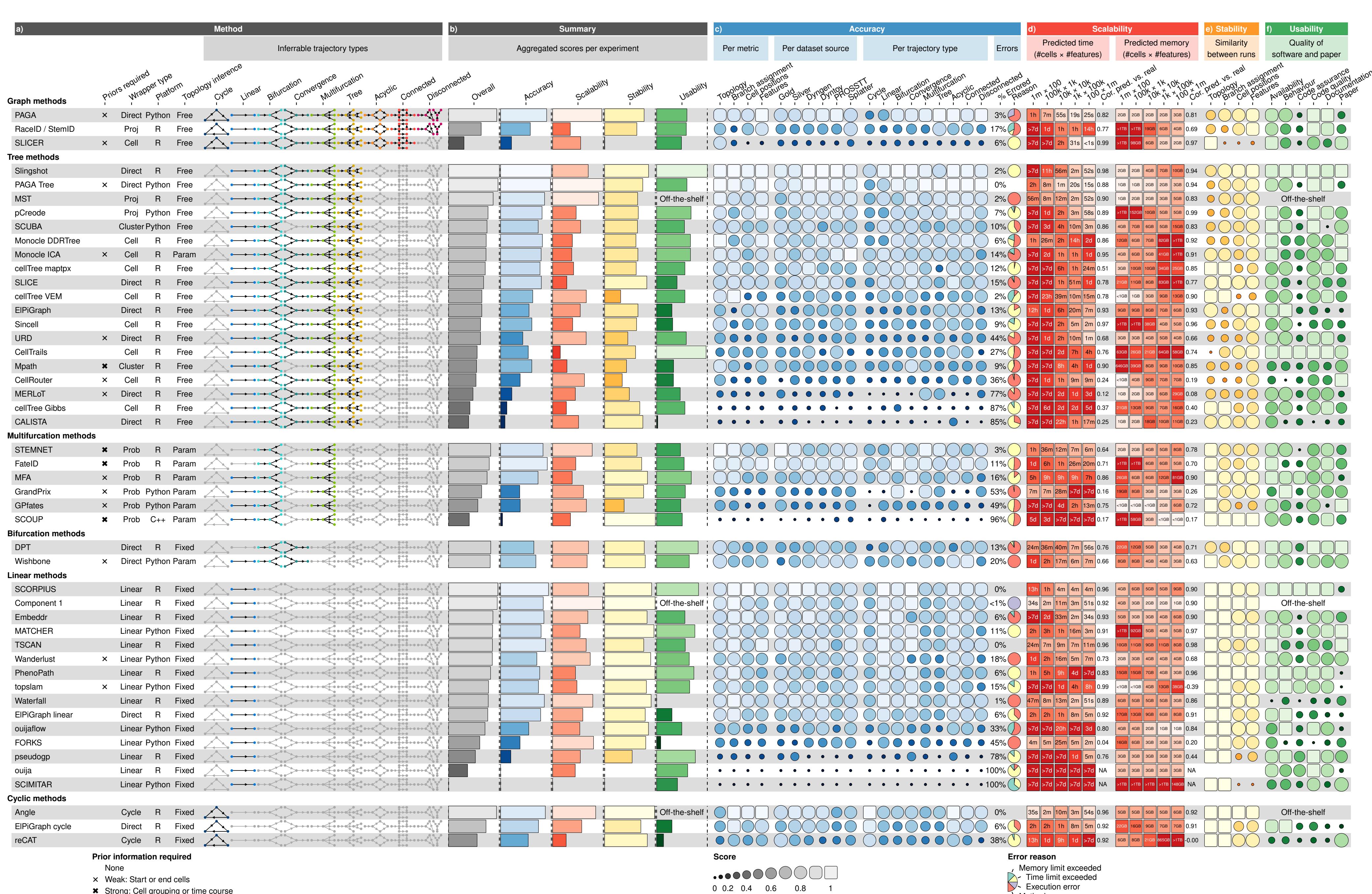
- In order to quantitatively benchmark TI methods, we developed a **common interface** for TI methods.
- This interface is the laid the foundations for **dyno**, a **toolkit for inferring, visualising, and interpreting trajectories**.
- Visit **Wouter Saelens** at **poster 3053** for more information.



## Extensive and extendable benchmark

- We evaluated 45 methods in terms of **cellular ordering**, **topology**, **scalability**, and **usability**.
- Our benchmark highlights that **complementarity of current methods**. The choice of method should currently still depend on dataset characteristics.
- To assist users in selecting the most relevant method(s), we developed an **interactive guideline app**, available at [guidelines.dynverse.org](http://guidelines.dynverse.org).

(Responsiveness under development)



Saelens W.\*, Cannoodt R.\*, Todorov H., Saeys Y. A comparison of single-cell trajectory inference methods. Accepted, Nature Biotechnology, Jan 2019.