

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



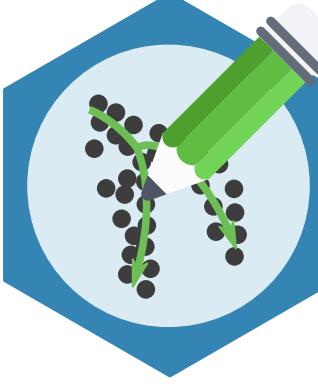
Robrecht Cannoodt*^{1 2 3}, Wouter Saelens*^{1 2}, Helena Todorov^{1 2 4}, Yvan Saeys^{1 2}

* Equal contribution

¹ Data mining and Modelling for Biomedicine, VIB Center for Inflammation Research, Ghent, Belgium. ² Department of Applied Mathematics, Computer Science and Statistics, Ghent University, Ghent, Belgium. ³ Center for Medical Genetics, Ghent University Hospital, Ghent, Belgium.

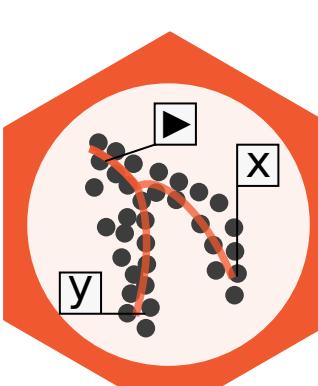
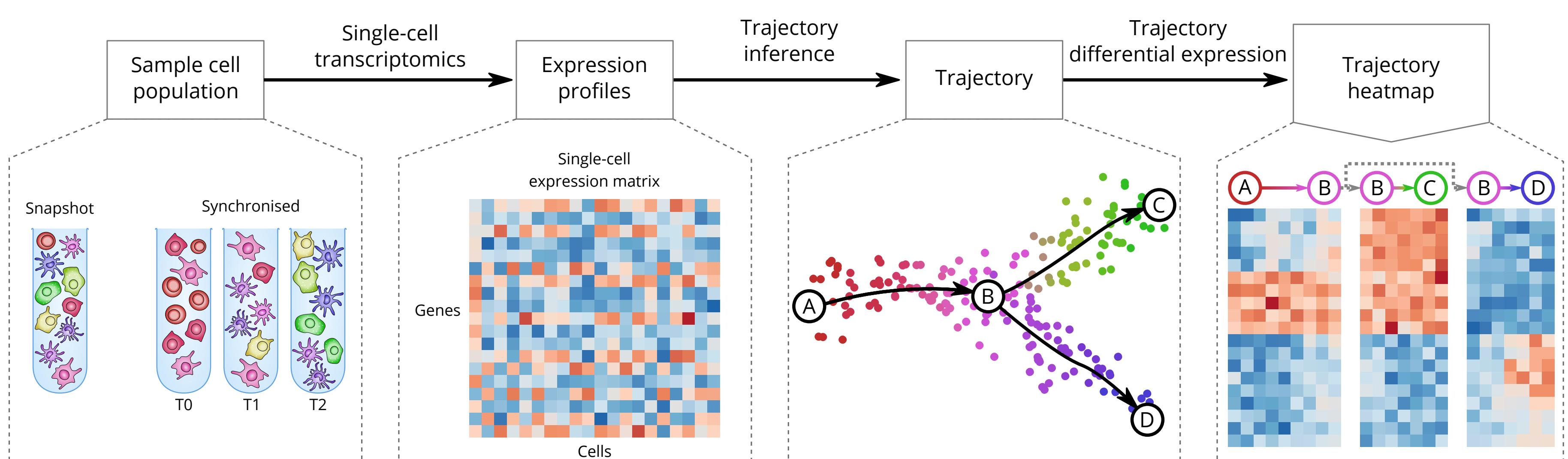
⁴ Centre International de Recherche en Infectiologie, Inserm, U1111, Université Claude Bernard Lyon 1, CNRS, UMR5308, École Normale Supérieure de Lyon, Univ Lyon, F-69007, Lyon, France

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



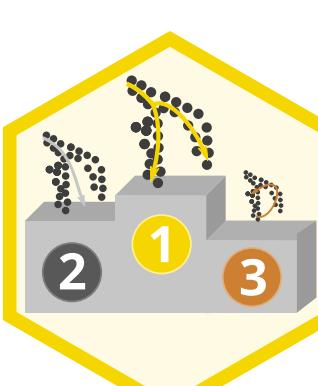
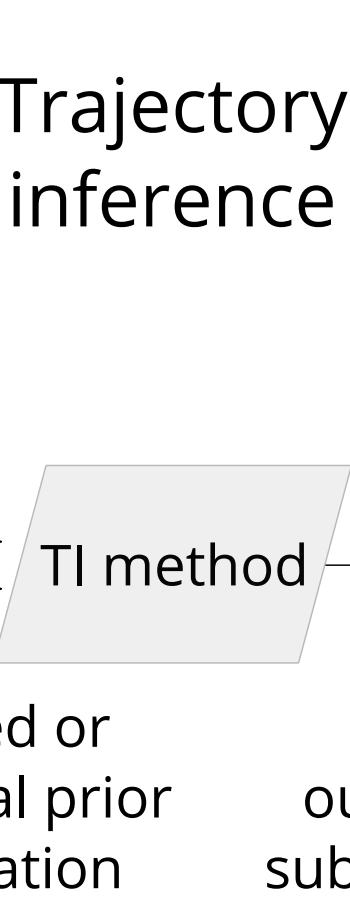
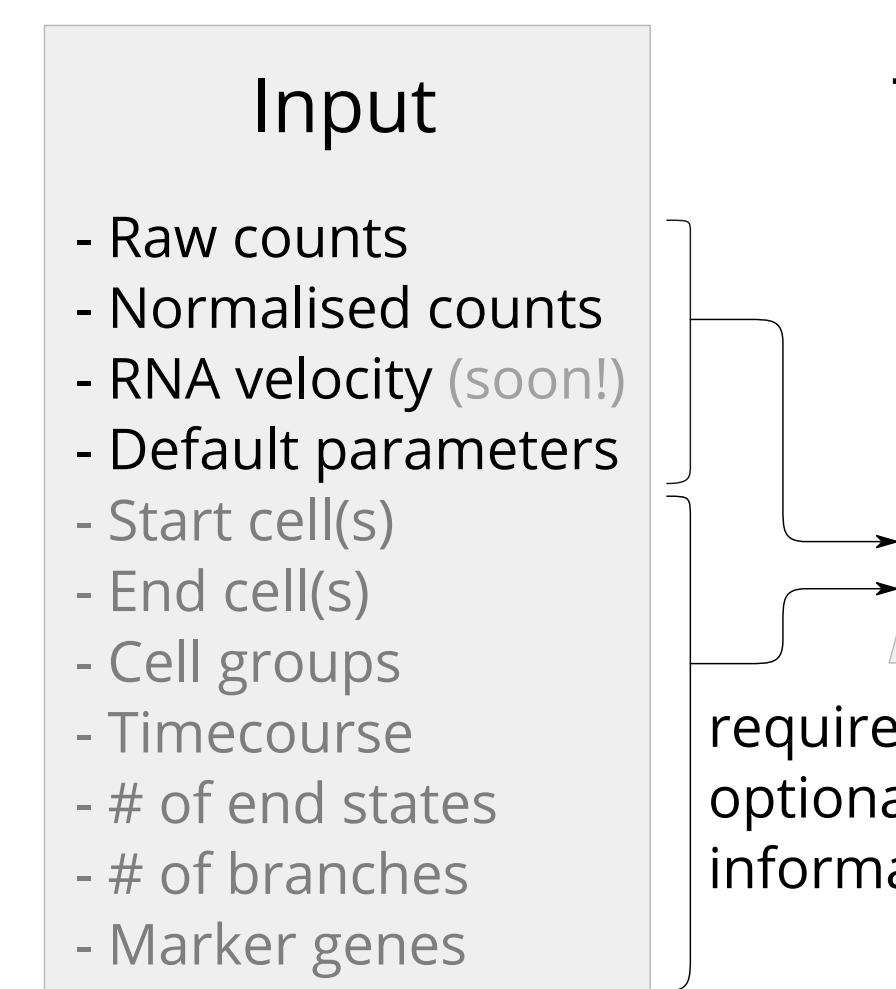
Infering trajectories to study dynamic processes

- 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**.



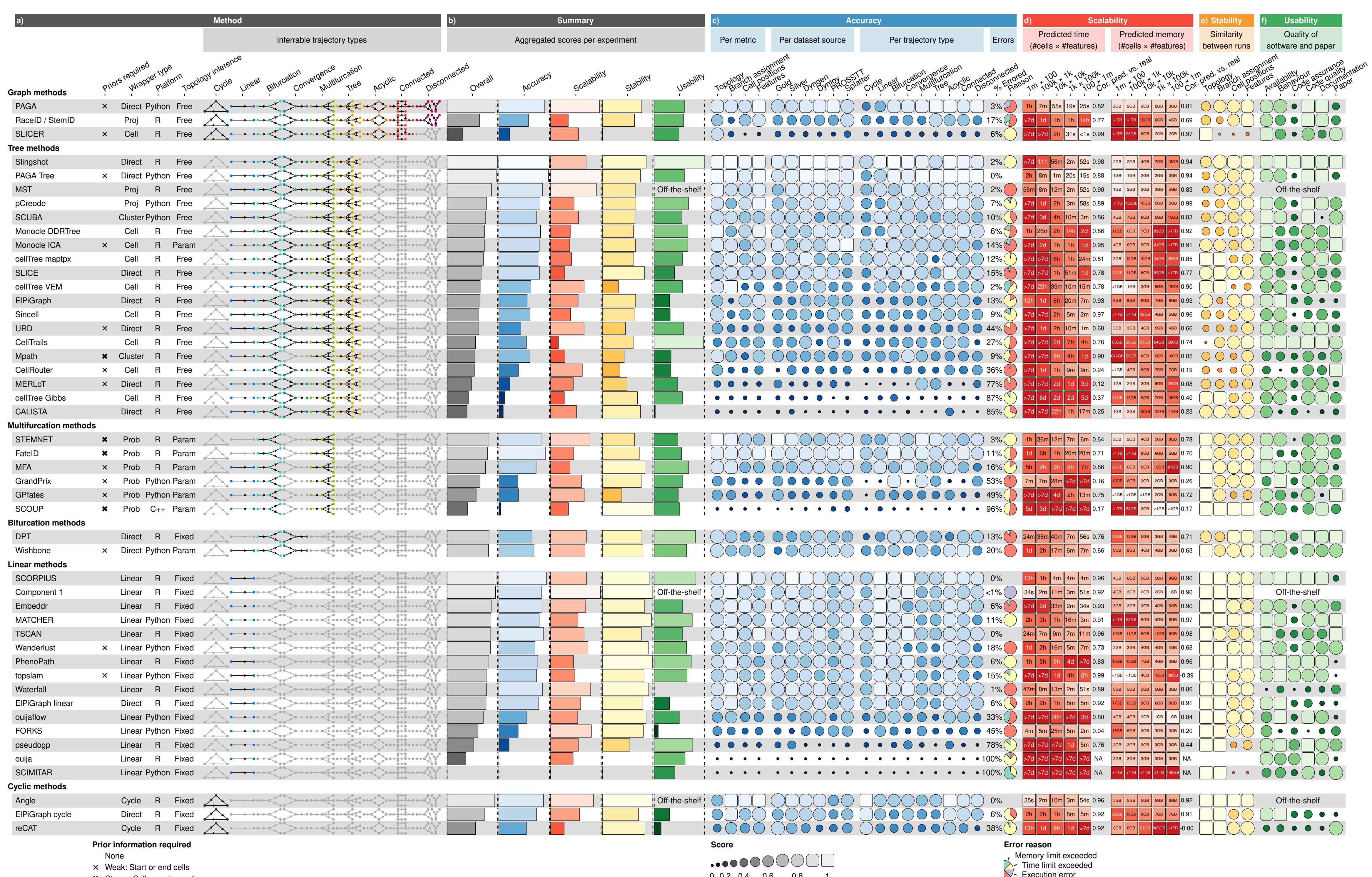
Common interface for trajectory inference

- 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 the **complementarity of current methods**. The choice of method should currently depend on the dataset characteristics.
- We developed an **interactive guidelines** app, available at 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.