

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



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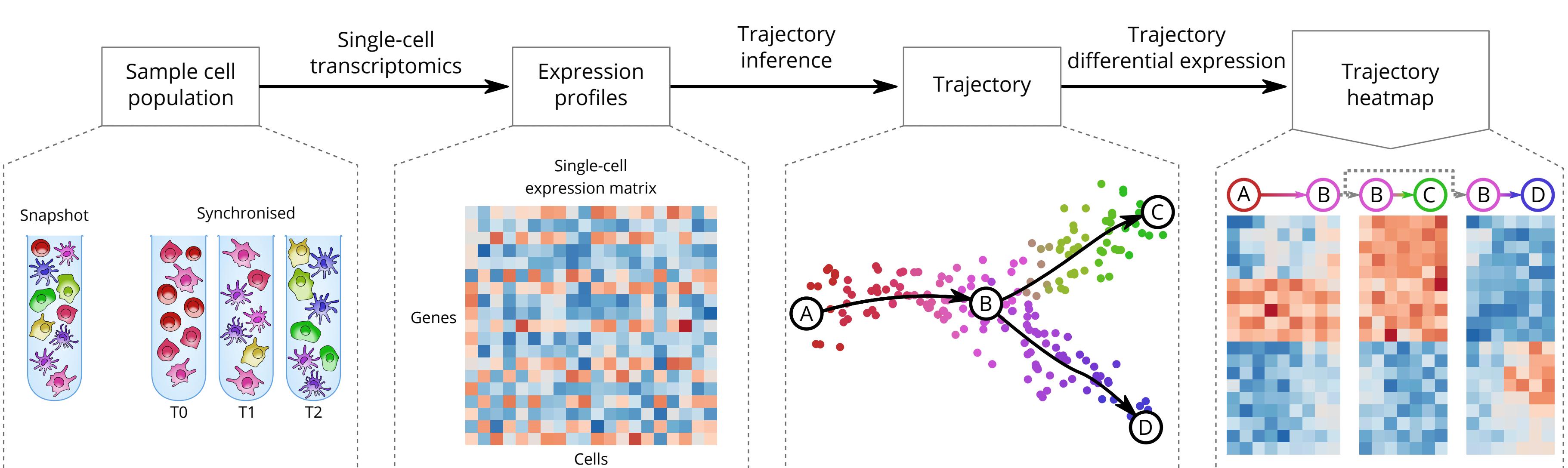
► dynbenchmark is an extensive and extendable **benchmarking** study of **45 trajectory inference** methods.

benchmark.dynverse.org



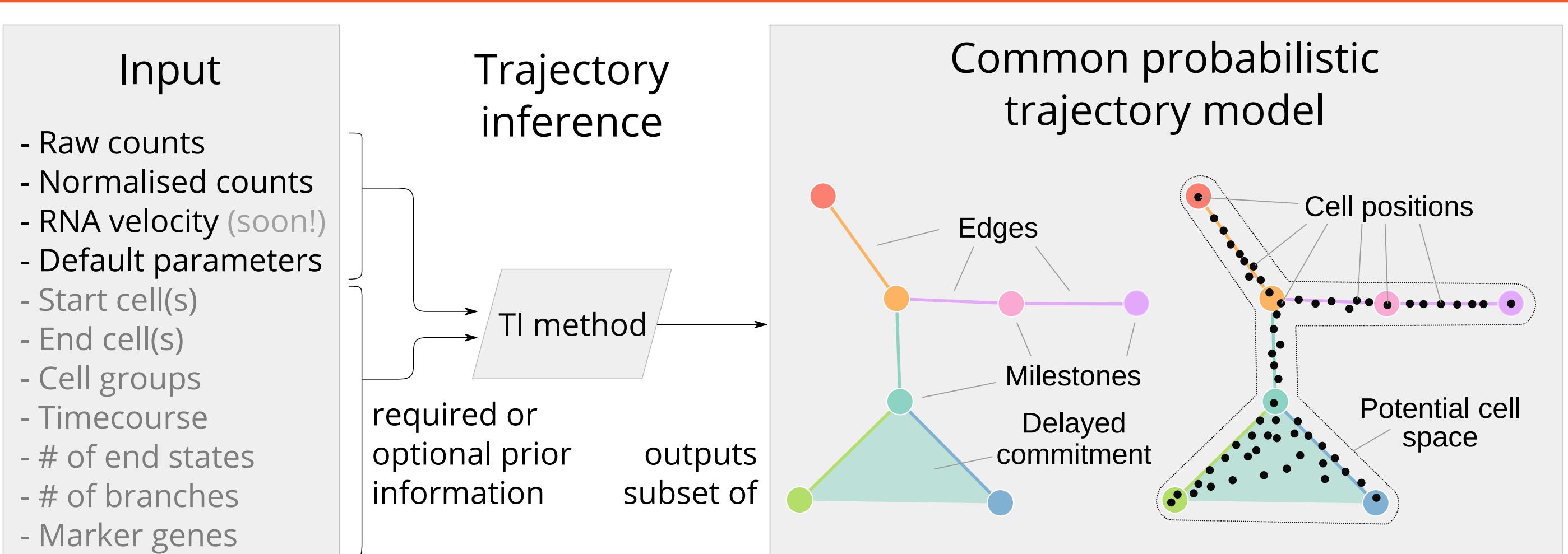
Inferring trajectories to study dynamic processes

- 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.



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 - 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**
(Desktop only, mobile version is in progress)



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



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