

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



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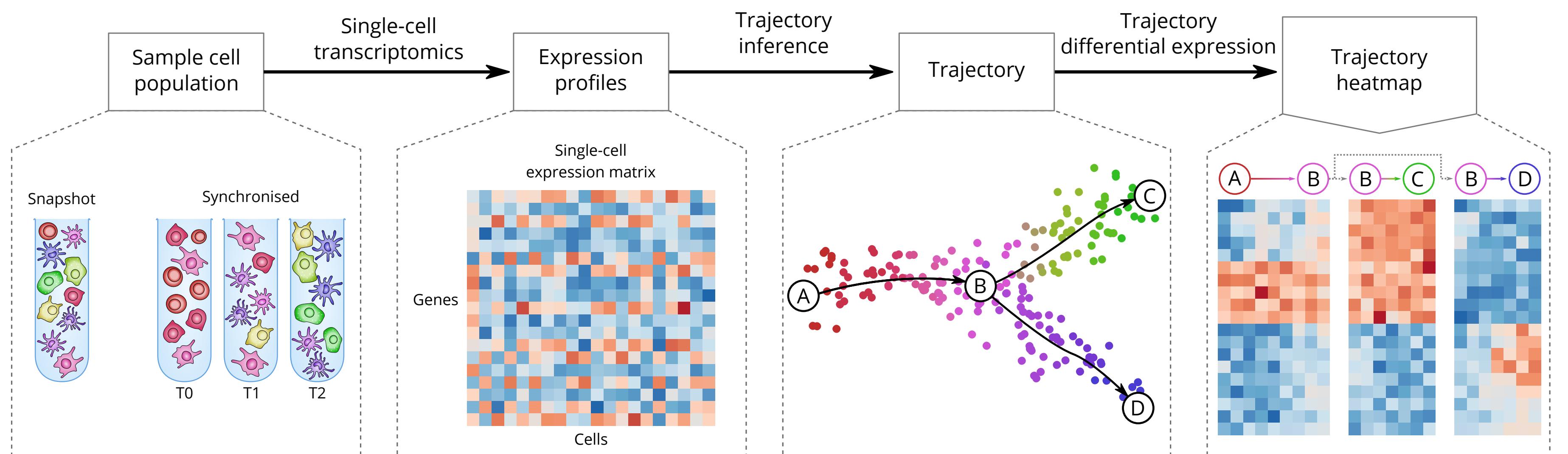
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► dynbenchmark is an extensive and extendable **benchmarking** study of **45 trajectory inference** methods



Inferring trajectories to study dynamic processes

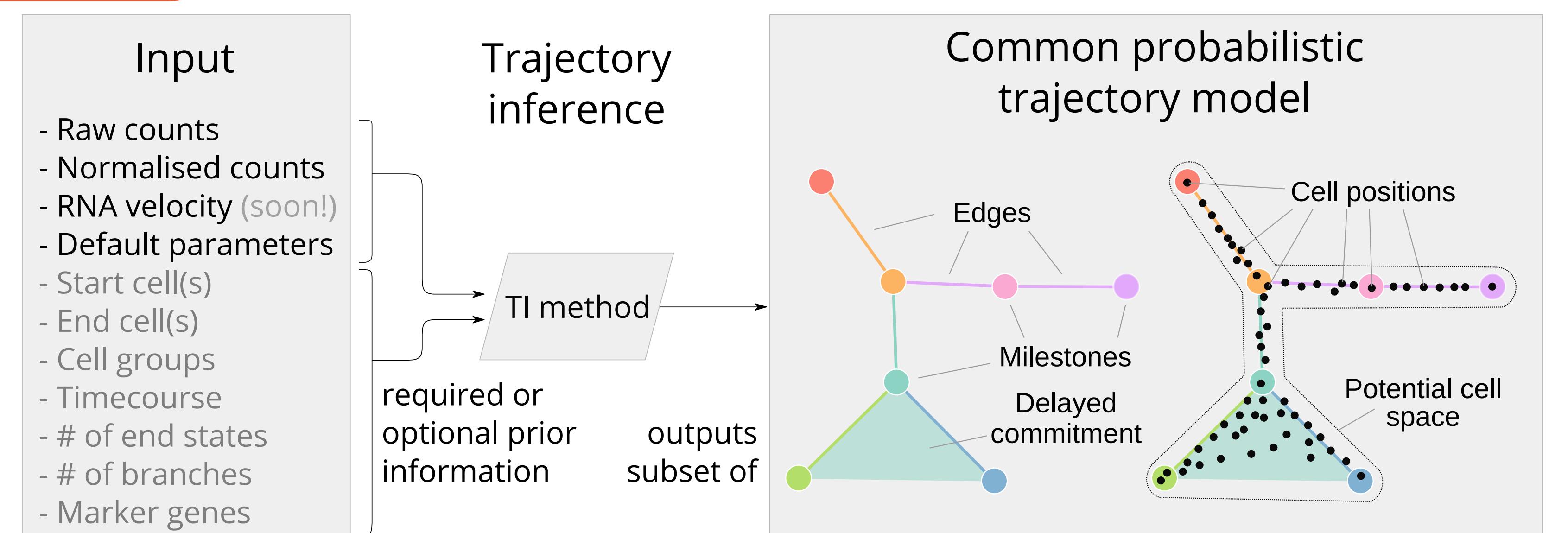
- Trajectory inference (TI) methods aid in **studying dynamic processes** by **ordering** single cells **along a trajectory**.
 - ≥ 71 TI methods have been developed, each with a **unique input/output interface**.
 - Quantitative or qualitative **comparison** of trajectories is thus **very challenging**.





Common interface for trajectory inference

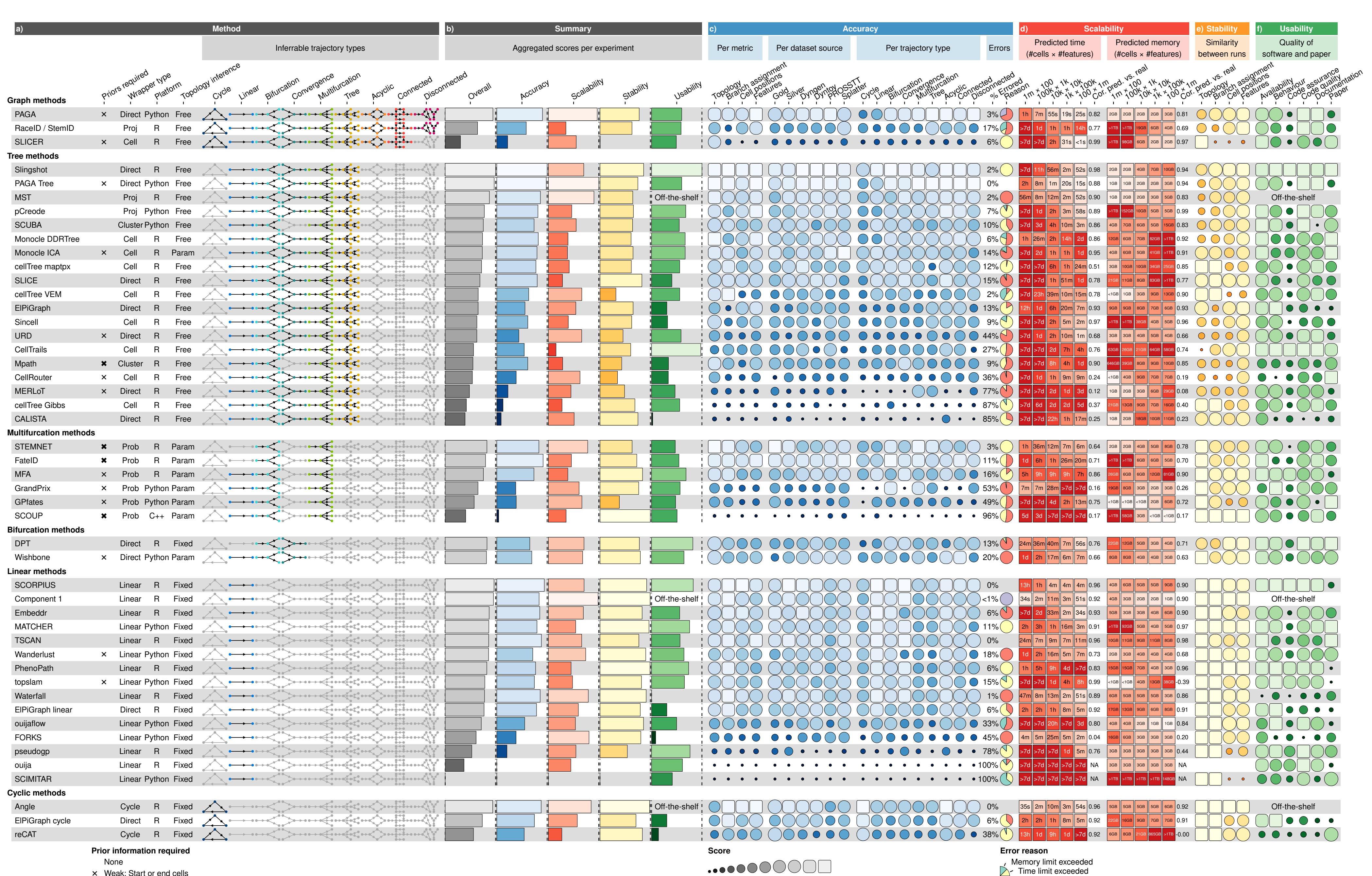
- ▶ In order to quantitatively benchmark TI methods, we developed a **common interface** for TI methods.
 - ▶ This interface is the laid the foundations for **dyno**, a **toolkit for inferring, visualising, and interpreting trajectories**.
 - ▶ Visit **Wouter Saelens** at **poster 3053** for more information.





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



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