dyno: Inferring, visualizing and interpreting trajectories



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dyno is a toolkit for inferring, visualizing and interpreting trajectories in R

dyno.dynverse.org



Selecting the most optimal method(s)

Choice of method depends on the:

Expectations about the topology

Available computing resources
Relative importance to particular trajectory aspects

Number of cells and features

Drier information (such as stars

Prior information (such as start cells)

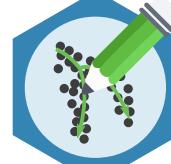
Our app gives recommendations based on these criteria

Install locally in R: devtools::install_github("dynverse/dynguidelines")

Or go to: guidelines.dynverse.org

These recommendations use the results from our **benchmark**:

Poster 1033 benchmark.dynverse.org Published soon!



Inferring trajectories

- > 71 tools for trajectory inference
 - ...and counting
 - ...each with their own interface...
- We developed a common input and output interface for 55 methods
- Each method can be run with one line

infer_trajectory(dataset, "my_favorite_ti_method")

New methods can be included through

Input

Examples:

- Raw counts
- Normalised counts
- RNA velocity (soon!)- Default parameters
- Start cell(s)
- End cell(s)
- Cell groupsTimecourse
- # of end states
- # of branches- Marker genes

Trajectory inference

TI method

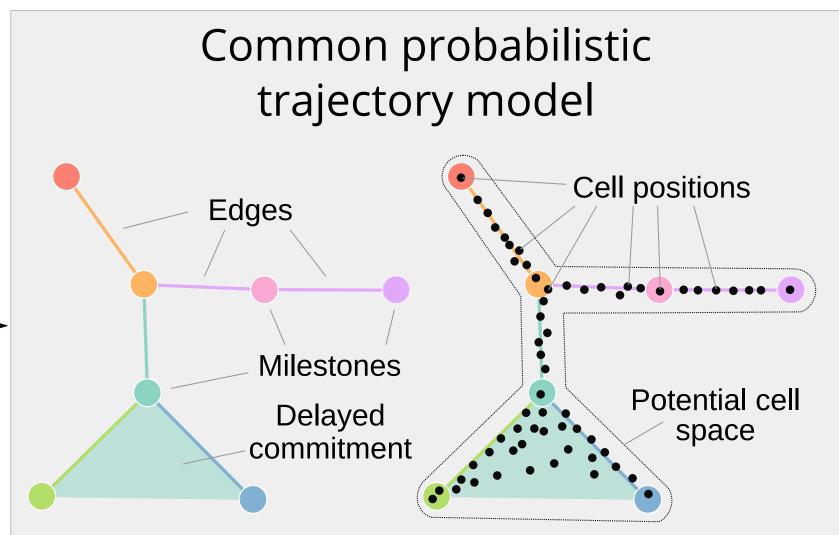
required or

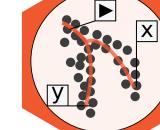
information

optional prior

outputs

subset of





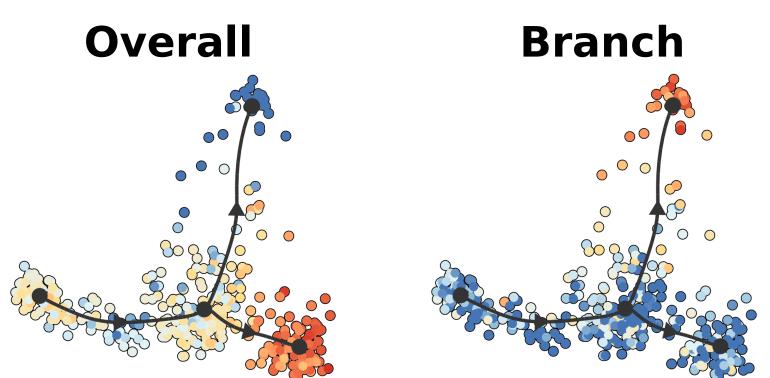
Annotating the trajectory

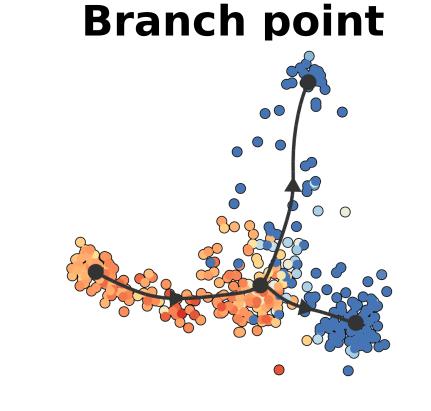
methods.dynverse.org

- Include additional information on top of the trajectory to make it **interpretable**
 - Rooting based on markers (or manually)
- (soon!) Directionality of edges based on RNA velocity
- Labelling milestones based on markers (or manually)
- We welcome additional ideas about common operations

Detecting differential expression

Various **expression patterns** can be detected







Visualizing the trajectory

Visualize a model in **multiple ways**

