dyno: Inferring, Visualizing and Interpreting trajectories

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by dyno is a toolkit for inferring, visualizing and interpreting trajectory inference methods in R

http://dyno.dynverse.org



Selecting the most optimal method(s)

Choice of method depends on the:

Examples:

User Available computing resources

Available computing resources
Relative importance to particular trajectory aspects

Data
Number of cells and features
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: http://guidelines.dynverse.org

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

Poster 1033 http://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")
- Next methods can be included through

http://methods.dynverse.org

Input - Raw counts - Normalised counts - RNA velocity (soon!) - Default parameters - Start cell(s) - End cell(s) - Cell groups Trajectory inference Input Trajectory inference

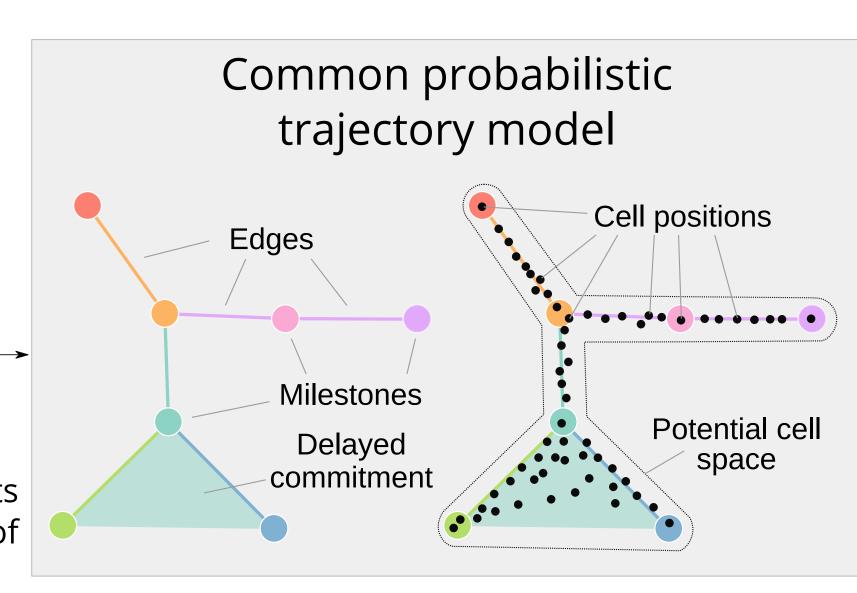
- Timecourse

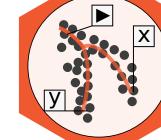
- # of end states

- # of branches

- Marker genes

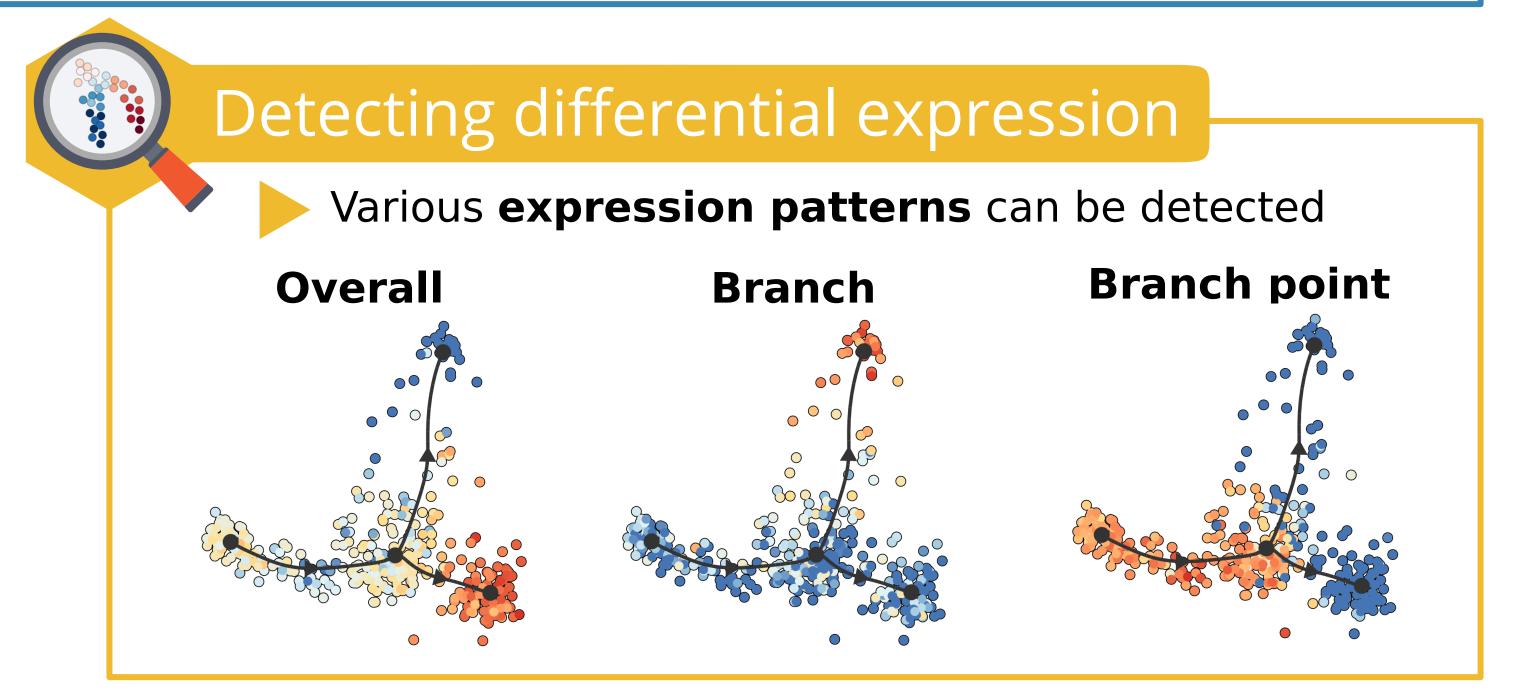
required or optional prior outputs information subset of





Annotating the trajectory

- 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





Visualizing the trajectory

Visualize a trajectory in multiple ways

