

dyno: Inferring, Visualizing and Interpreting trajectories

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► 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:

User Expectations about the topology
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

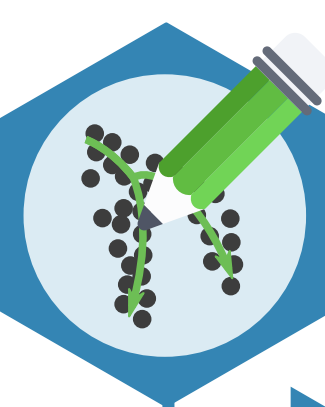
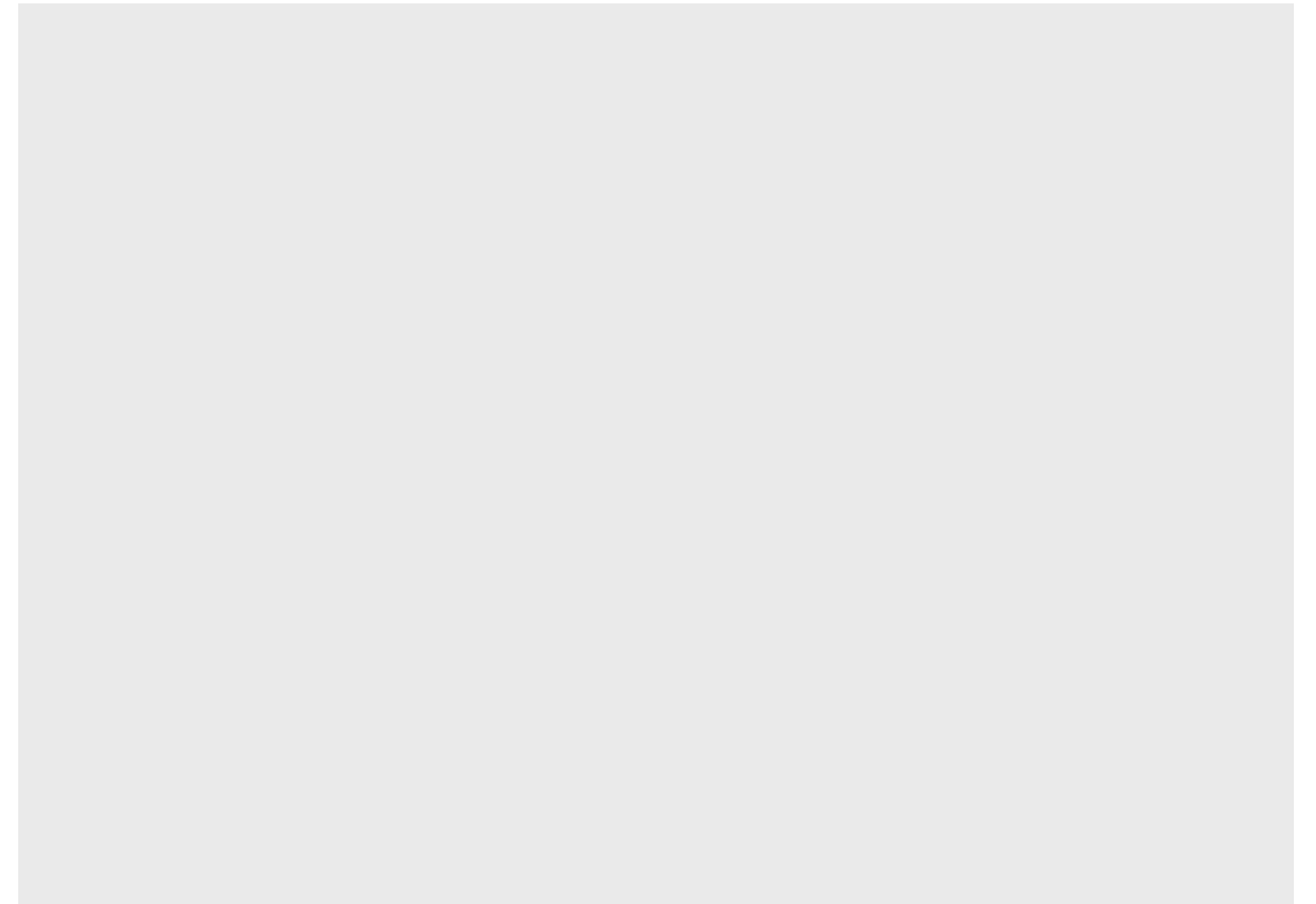
Install locally in R: `devtools::install_github("dynverse/dynguidelines")`

Or go to: <http://guidelines.dynverse.org>

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

Poster **1033** <http://benchmark.dynverse.org> Published soon!

► Examples:



Inferring trajectories

► 71 tools for trajectory inference

...and counting
...each with their own interface...

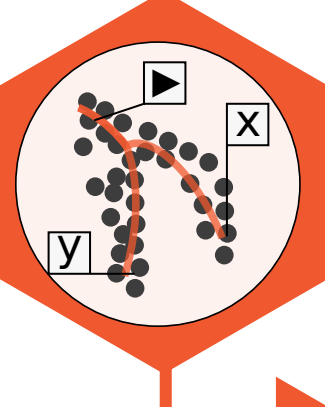
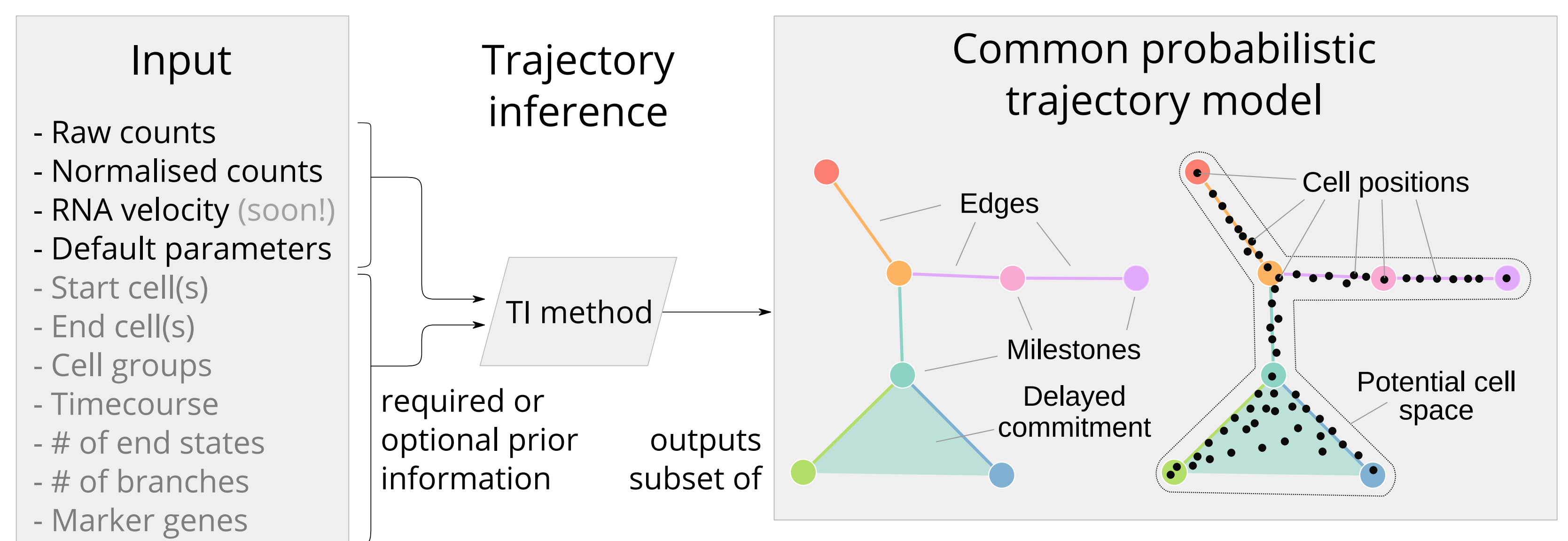
► We developed a **common input and output interface** for **55 methods**

► 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>



Annotating the trajectory

► Include additional information on top of the trajectory to make it **interpretable**

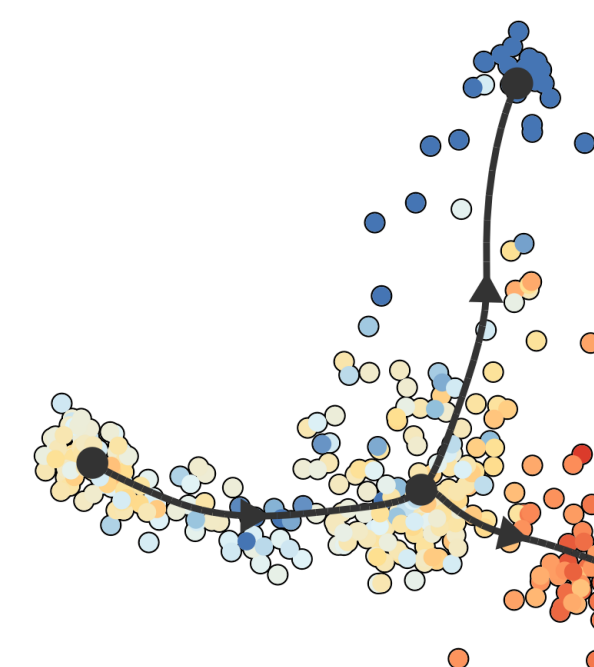
- Rooting based on markers (or manually)
- (soon!) Directionality of edges based on RNA velocity
- Labelling milestones based on markers (or manually)
- We welcome additional ideas about common operations



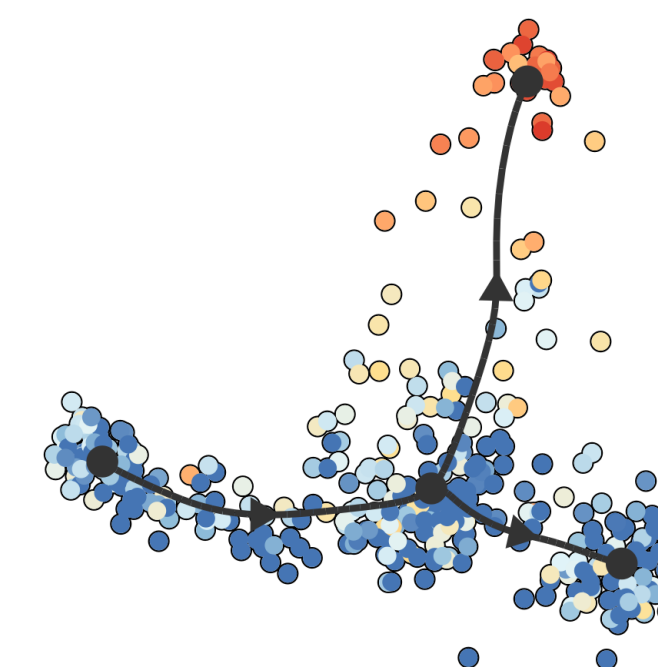
Detecting differential expression

► Various **expression patterns** can be detected

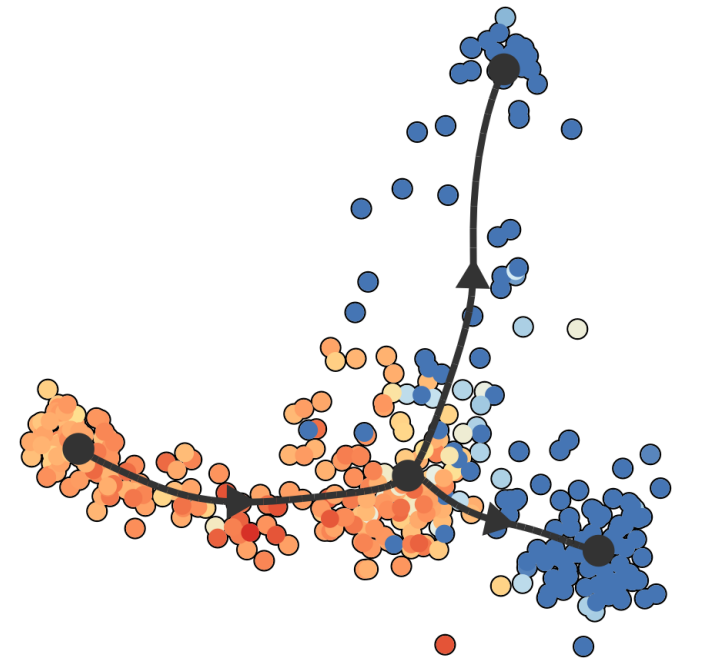
Overall



Branch

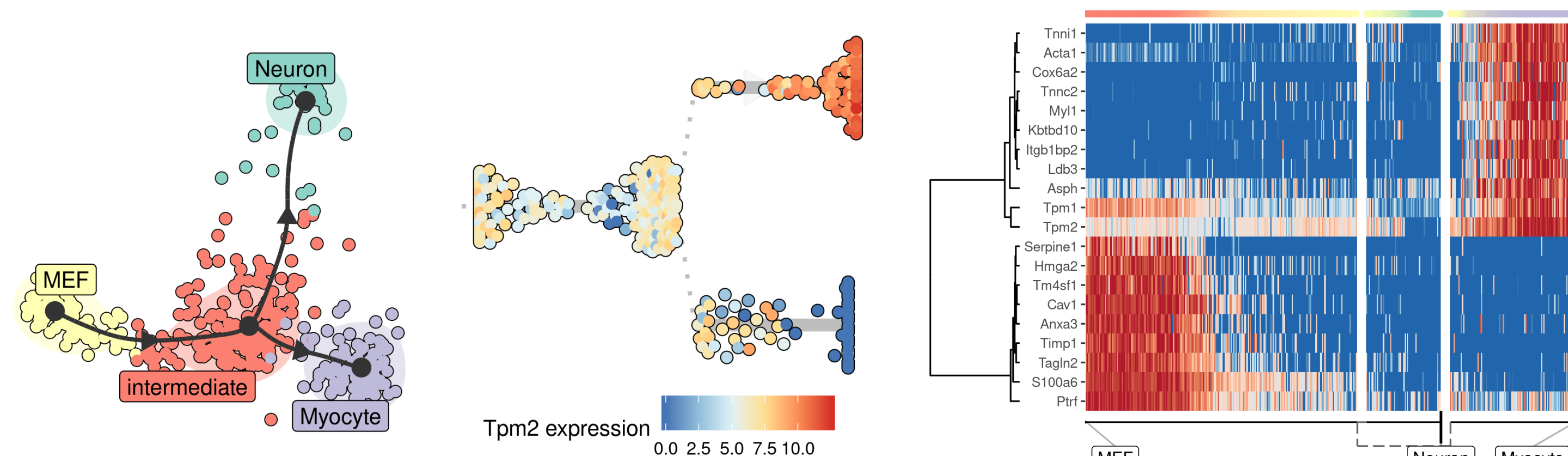


Branch point



Visualizing the trajectory

► Visualize a trajectory in multiple ways



► Compare models on a common embedding

