3053

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:

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)

Examples:

Our app gives **recommendations** based on these criteria

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

Or go to: `guidelines.dynverse.org`

Recommendations are based on the results from our **benchmark**:

Robrecht Cannoodt @ **Poster 1033** and `benchmark.dynverse.org`

Inferring trajectories

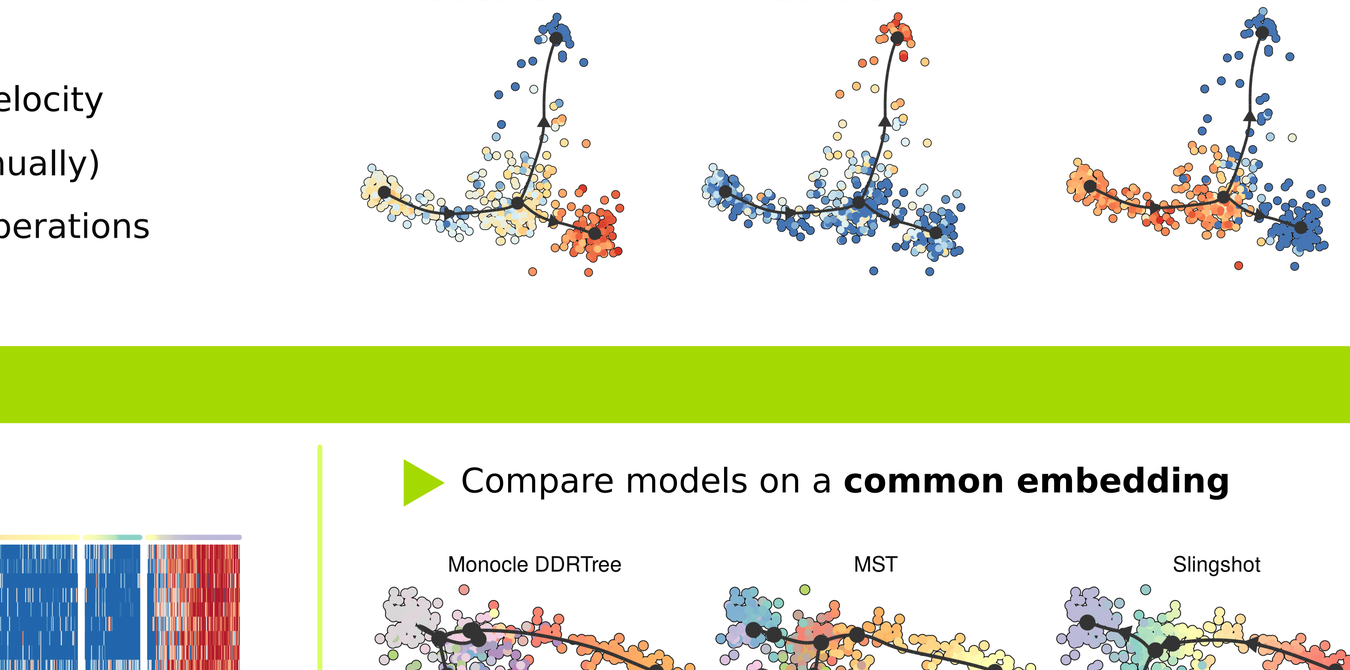
71 tools for trajectory inference
...and counting
...each with their own input/output interface

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 `methods.dynverse.org`



Annotating the trajectory

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

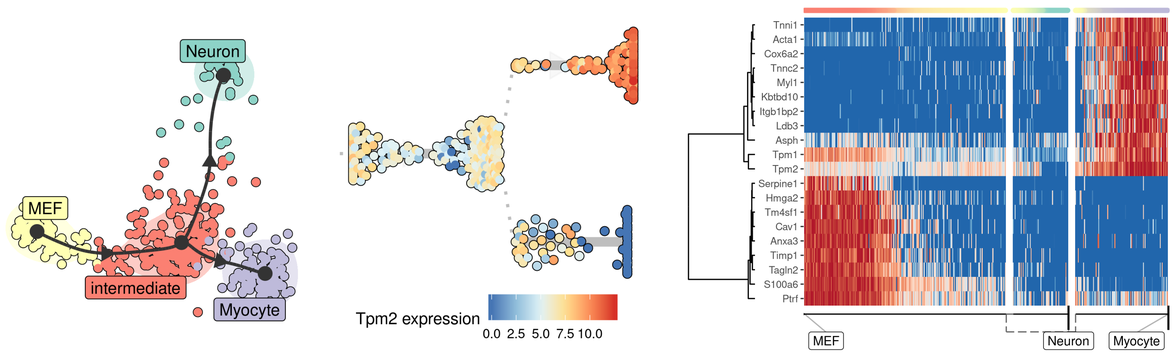
- Rooting based on markers (or manually)
- (soon!) Directionality of edges based on RNA velocity
- Labelling milestones based on markers (or manually)
- We welcome additional ideas about common operations

Detecting differential expression

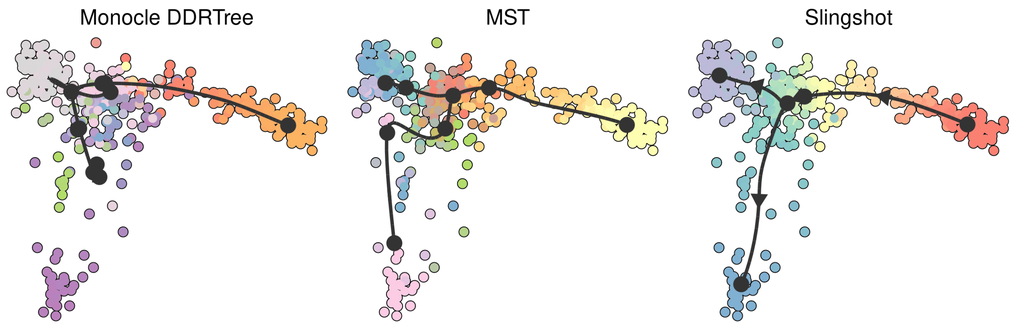
Various **expression patterns** can be detected

Visualizing the trajectory

Visualize a model in **multiple ways**



Compare models on a **common embedding**



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