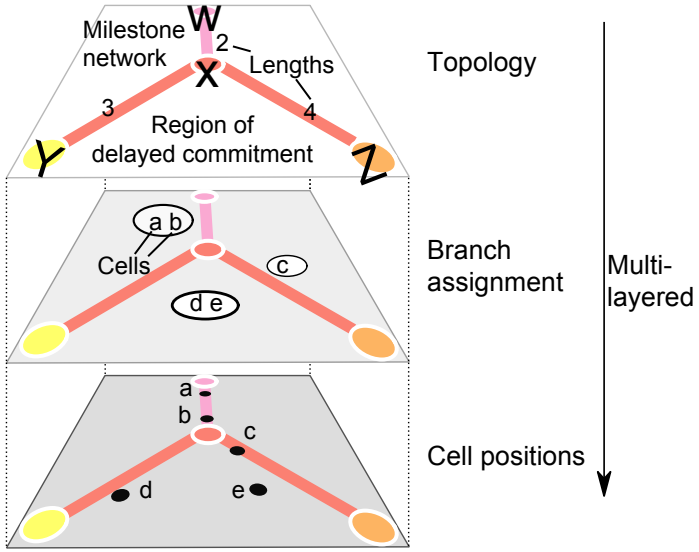
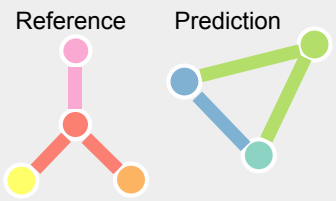
Common probabilistic trajectory model



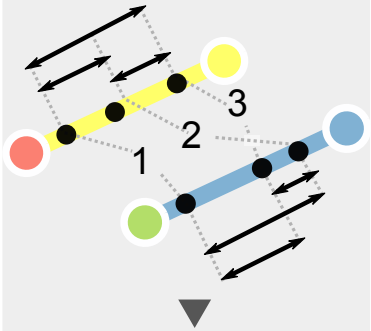
Topology: *HIM*



- Difference in relative edge lengths
- Difference in degree distributions

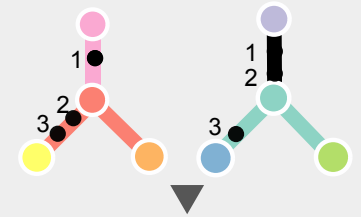
Cell positions: cor_{dist}

Geodesic distances between all pairs of cells

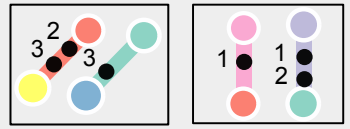


Correlation of distances

Branch assignment: $F1_{branches}$

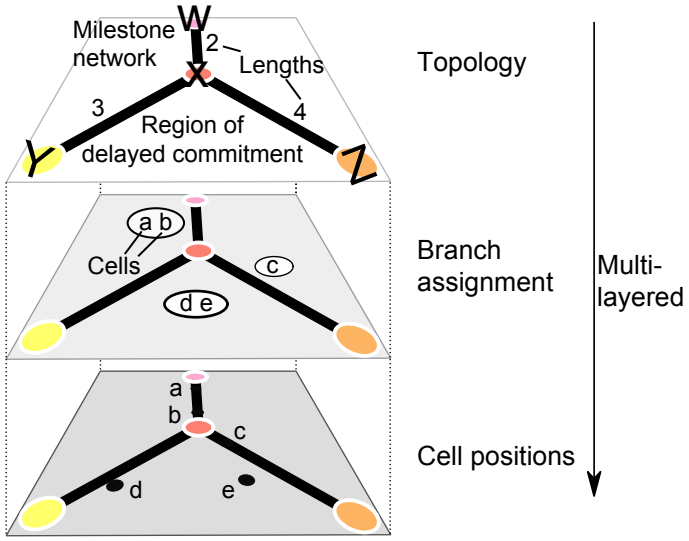


Match branches

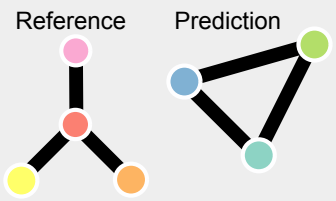


Magnitude of overlap

Common probabilistic trajectory model



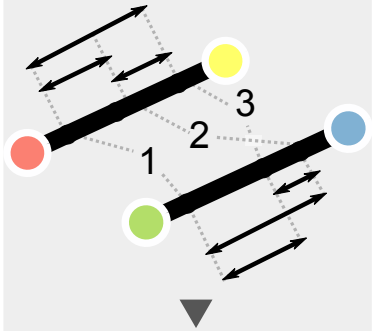
Topology: *HIM*



- Difference in relative edge lengths
- Difference in degree distributions

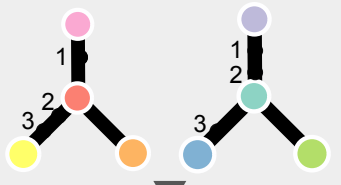
Cell positions: cor_{dist}

Geodesic distances between all pairs of cells

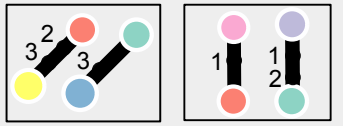


Correlation of distances

Branch assignment: $F1_{branches}$

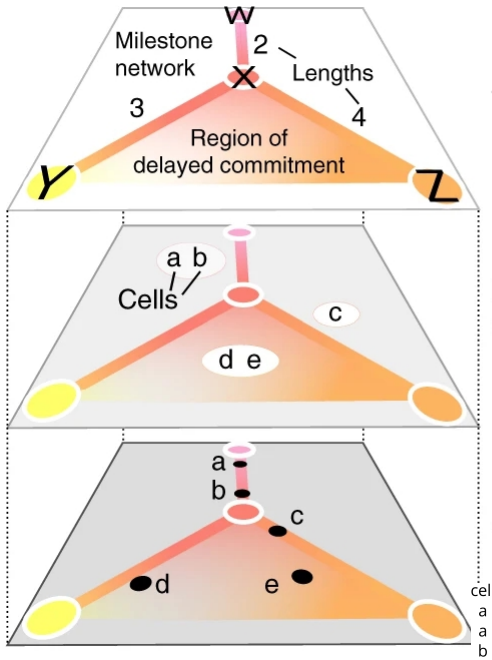


Match branches



Magnitude of overlap

from	to	length
W	X	2
X	Y	3
X	Z	4



Topology

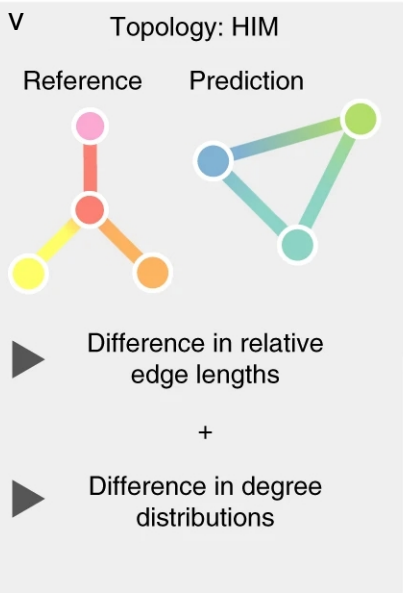
Branch assignment

Cell positions

cell	milestone	percentage
a	W	0.9
a	X	0.1
b	W	0.2
b	X	0.8
c	X	0.8
c	Z	0.2
d	X	0.2
d	Y	0.7
d	Z	0.1
e	X	0.3
e	Y	0.2
e	Z	0.5

Edit distance between two trajectory topologies

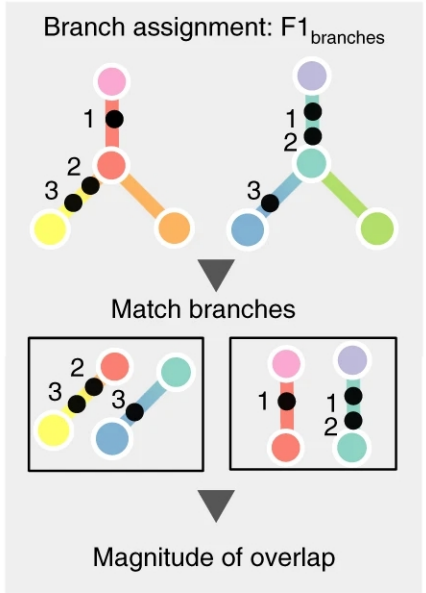
Hamming–Ipsen–Mikhailov

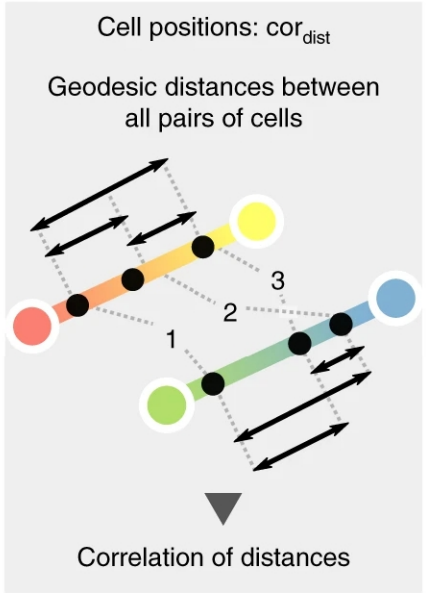


$\text{Jaccard}(c, c') = \frac{|c \cap c'|}{|c \cup c'|}$

$\text{Recovery} = \frac{1}{|C|} \sum_{c \in C} \max_{c' \in C'} \text{Jaccard(c, c')}$

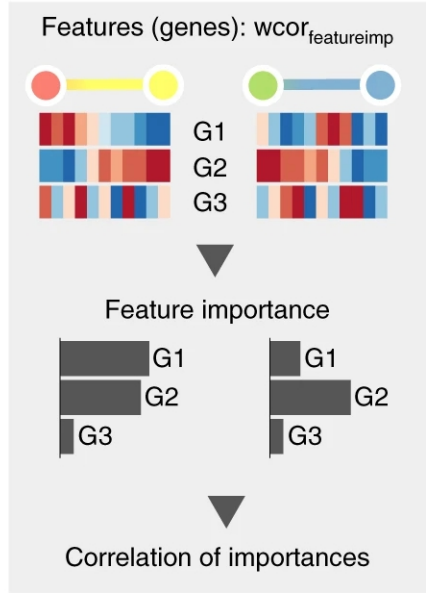
$\text{Relevance} = \frac{1}{|C'|} \sum_{c' \in C'} \max_{c \in C} \text{Jaccard(c, c')}$



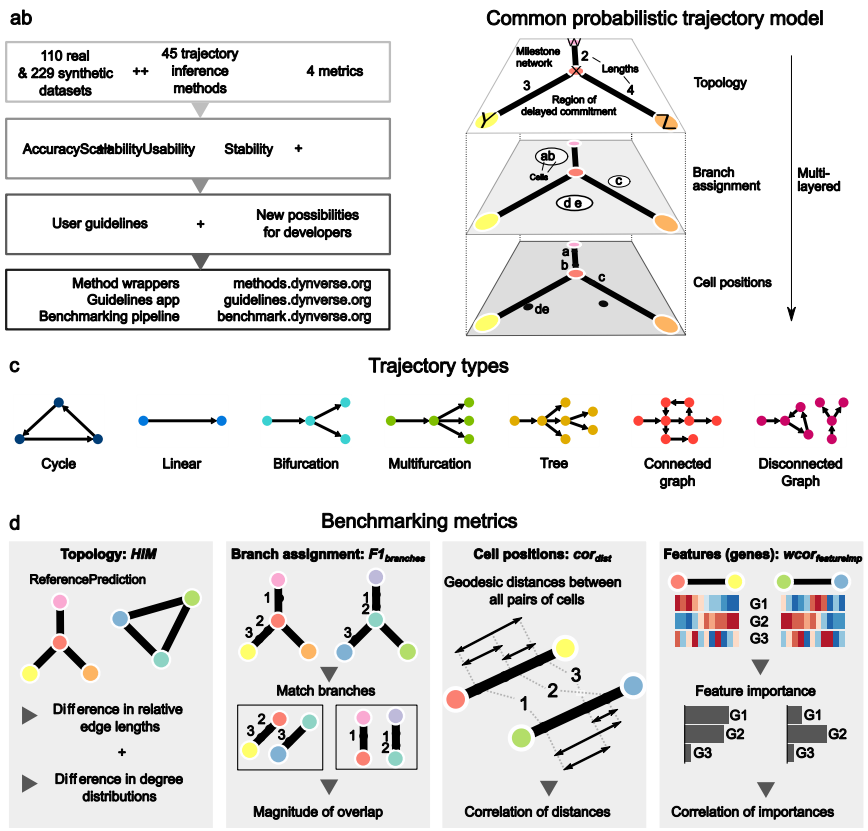


d(a, b) = 2 × (0.9 - 0.2) = 1.4
d(a, c) = 2 × 0.9 + 4 × 0.2 = 2.6
d(b, c) = 2 × 0.2 + 4 × 0.2 = 1.2
d(a, d) = 2 × 0.9 + 3 × 0.7 + 4 × 0.1 = 4.3
d(b, d) = 2 × 0.2 + 3 × 0.7 + 4 × 0.1 = 2.9
d(c, d) = 3 × (0.7 - 0) + 4 × (0.2 - 0.1) = 2.5
d(a, e) = 2 × 0.9 + 3 × 0.2 + 4 × 0.5 = 4.4
d(b, e) = 2 × 0.2 + 3 × 0.2 + 4 × 0.5 = 3.0
d(c, e) = 3 × (0.2 - 0) + 4 × (0.5 - 0.2) = 1.8
d(d, e) = 3 × (0.7 - 0.2) + 4 × (0.5 - 0.1) = 3.1

The accuracy of dynamical differentially expressed genes



3


ab
110 real & 229 synthetic datasets
++
45 trajectory inference methods
4 metrics
Accuracy
Scalability
Usability
Stability
+
User guidelines
+
New possibilities for developers
Method wrappers
Guidelines app
Benchmarking pipeline
methods.dynverse.org
guidelines.dynverse.org
benchmark.dynverse.org
Common probabilistic trajectory model
Milestone network
Lengths
Region of delayed commitment
Topology
Branch assignment
Cell positions
Multi-layered
c
Trajectory types
Cycle
Linear
Bifurcation
Multifurcation
Tree
Connected graph
Disconnected Graph
d
Benchmarking metrics
Topology: HIM
ReferencePrediction
Difference in relative edge lengths
+
Difference in degree distributions
Branch assignment: F1branches
Match branches
Magnitude of overlap
Cell positions: cordist
Geodesic distances between all pairs of cells
Correlation of distances
Features (genes): wcorfeatureimp
G1
G2
G3
Feature importance
Correlation of importances