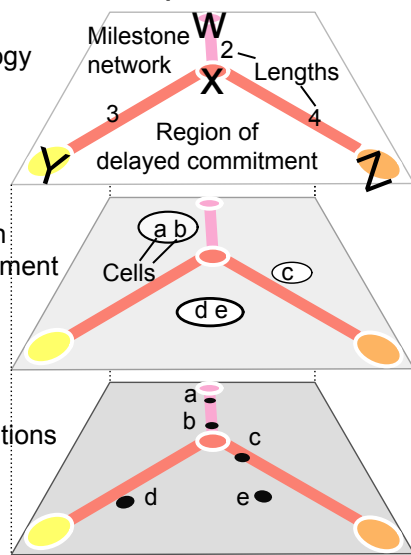# Common probabilistic trajectory model

Topology

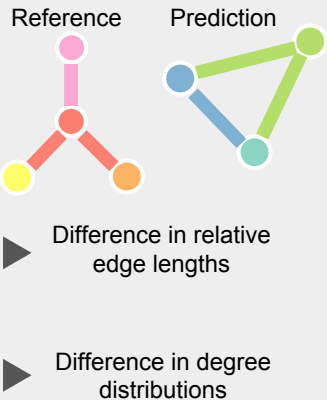Multi-layered

Branch assignment
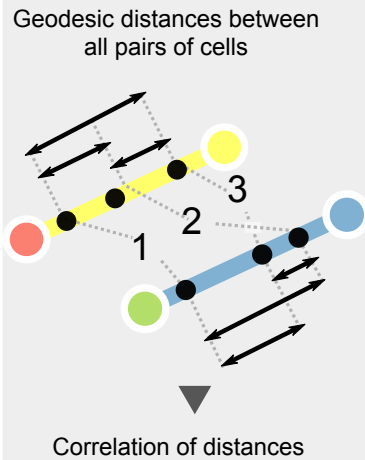
Cell positions

Topology: *HIM*

Reference   Prediction

▶ 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
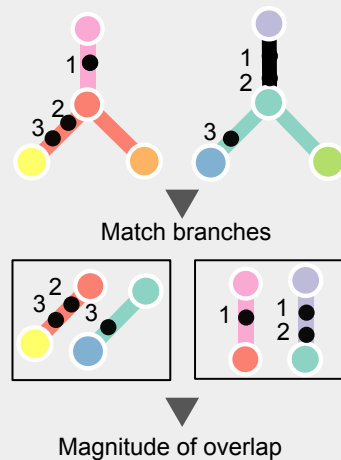
Milestone percentages

region	to	is_begin
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
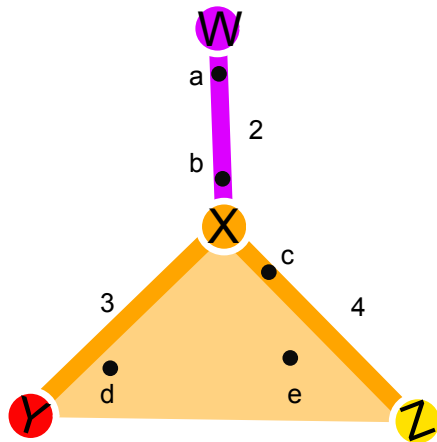
Milestone network

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

Region of delayed commitment

region	to	is_begin
XYZ	X	TRUE
XYZ	Y	FALSE
XYZ	Z	FALSE

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 × (0.7 − 0.2) + 4 × (0.5 − 0.2) = 1.8
d(d,e) = 3 × (0.7 − 0.2) + 4 × (0.5 − 0.1) = 3.1

Geodesic distance