

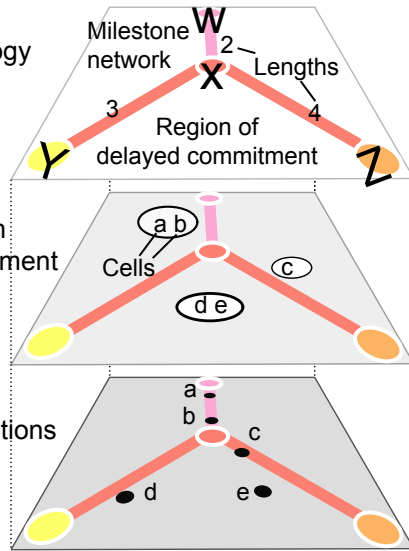
Common probabilistic trajectory model

Multi-layered

Topology

Branch assignment

Cell positions



from to length

W	X	2
X	Y	3
X	Z	4

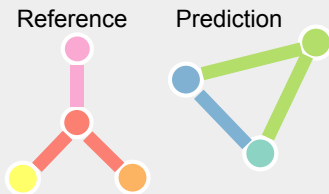
region to is_begin

XYZ	X	TRUE
XYZ	Y	FALSE
XYZ	Z	FALSE

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

Topology: *HIM*

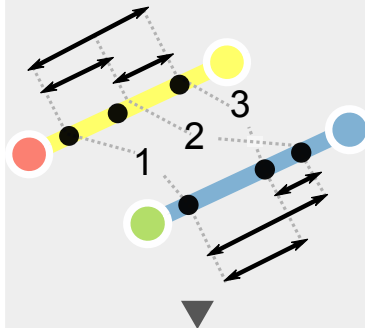


Difference in relative edge lengths

Difference in degree distributions

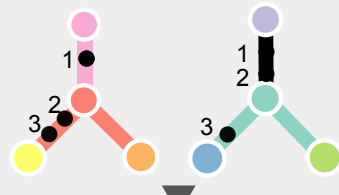
Cell positions: *cor_{dist}*

Geodesic distances between all pairs of cells

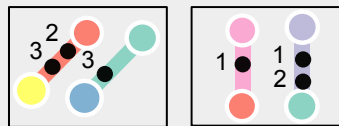


Correlation of distances

Branch assignment: *F1_{branches}*



Match branches



Magnitude of overlap