

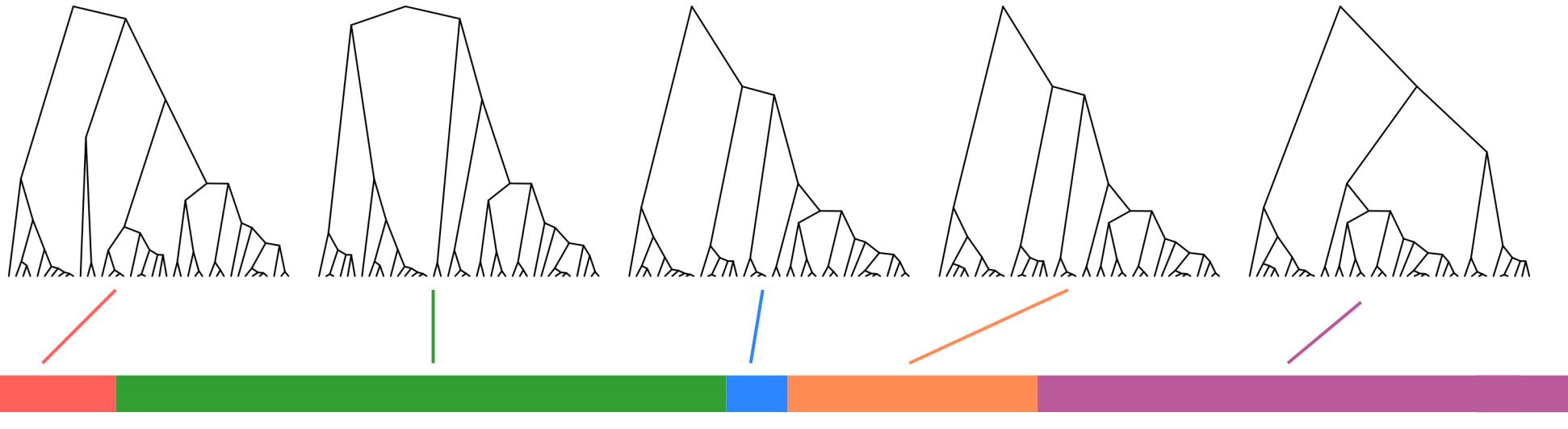
**Twisst:** Topology weighting by iterative sampling of sub-trees

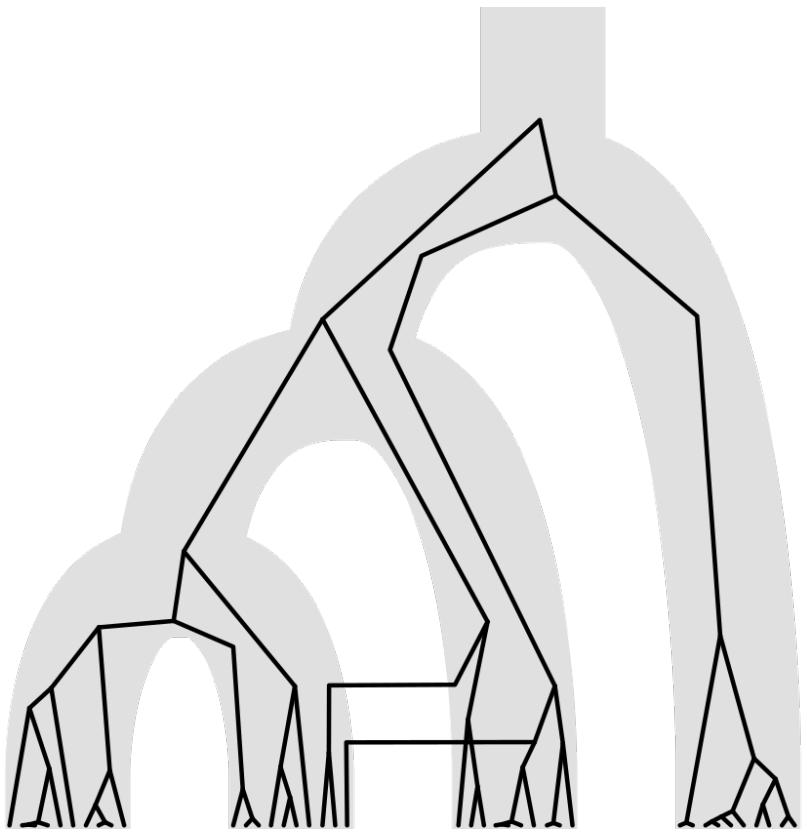
Code: [github.com/simonhmartin/twisst](https://github.com/simonhmartin/twisst)

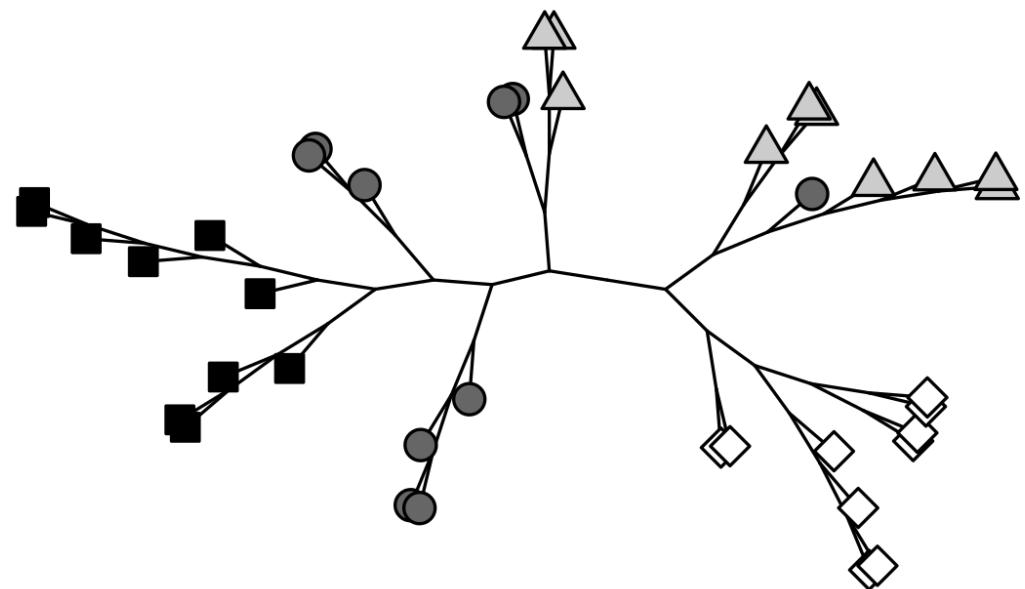
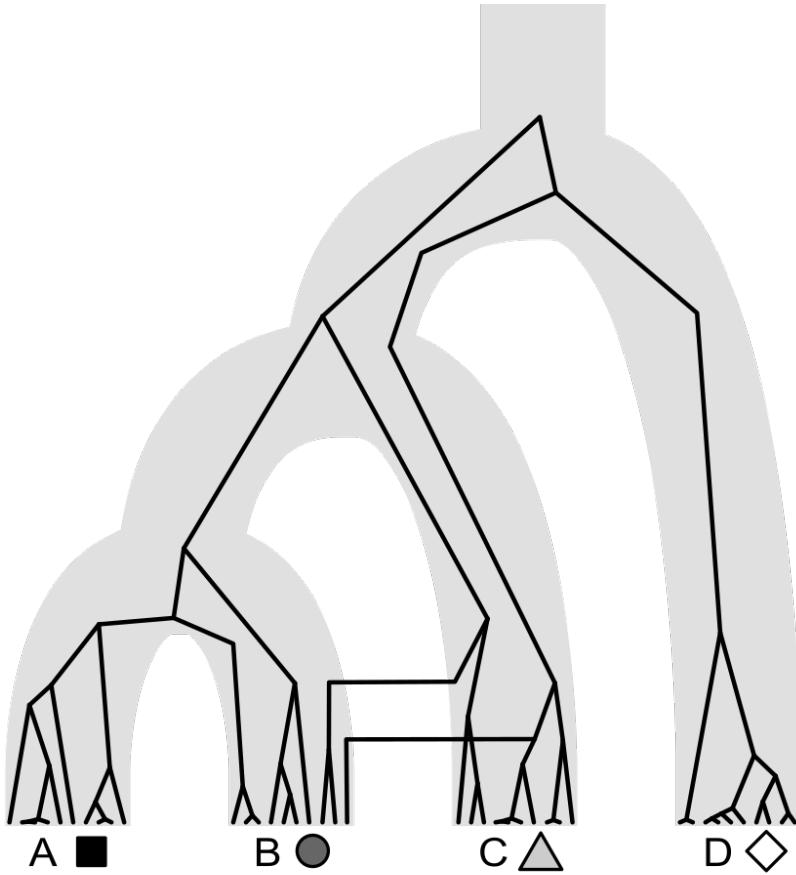
Part 1: Running Twisst on a simulated set of genealogies

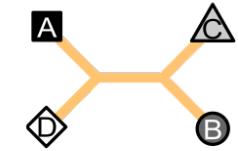
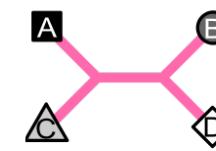
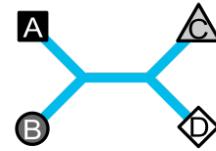
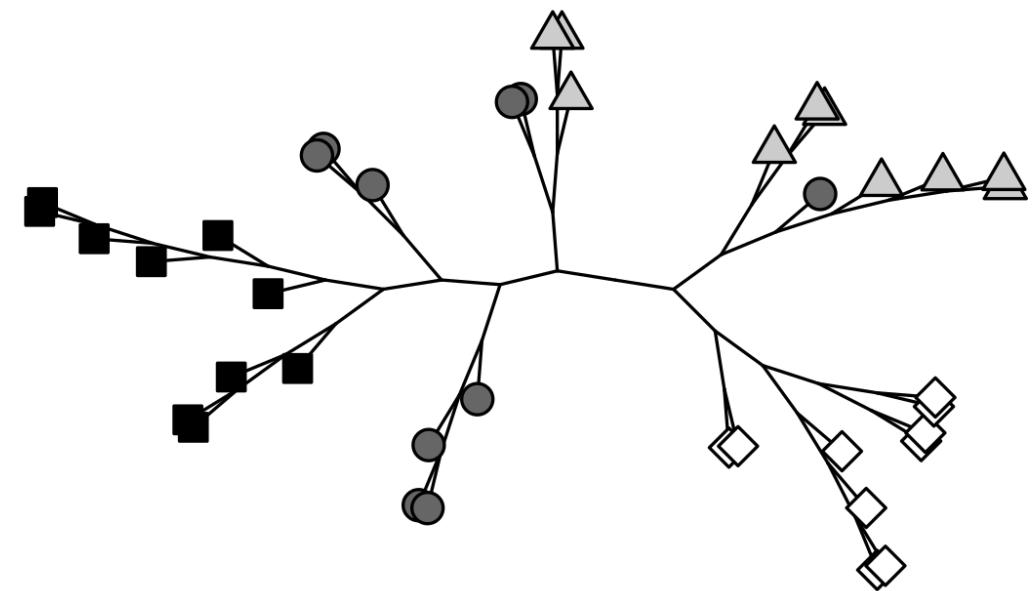
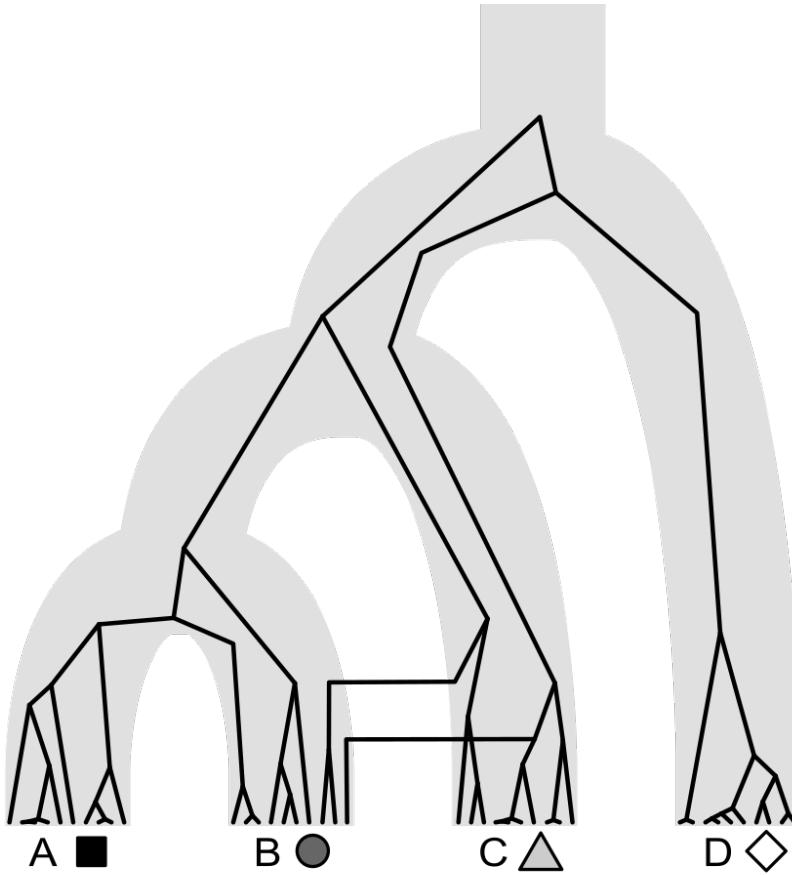
Part 2: Running Twisst on trees inferred from sequence data

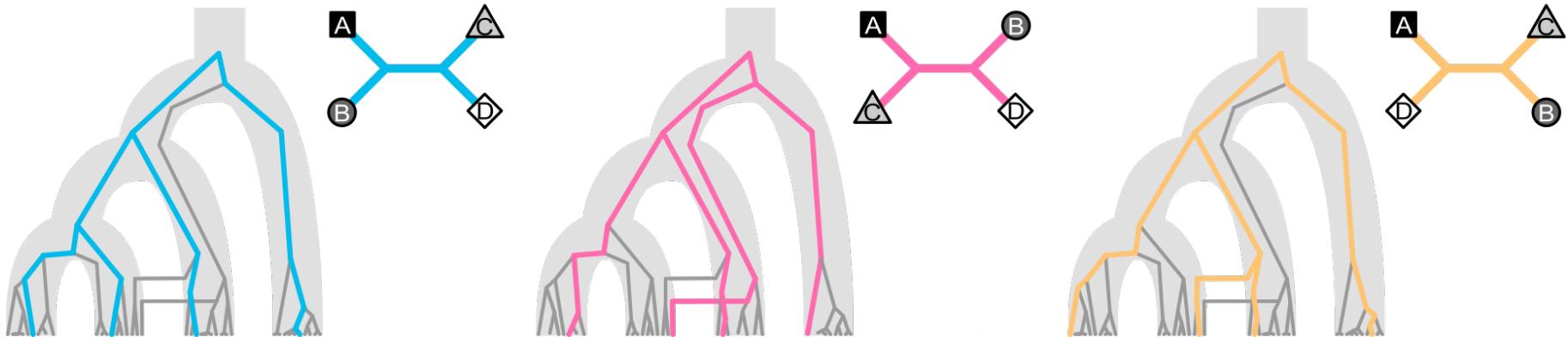
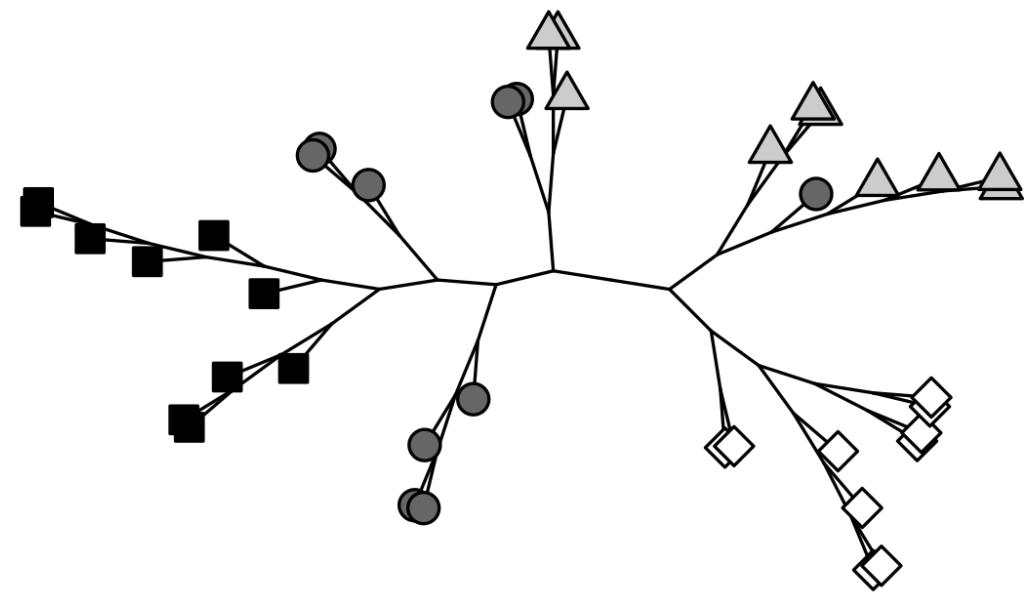
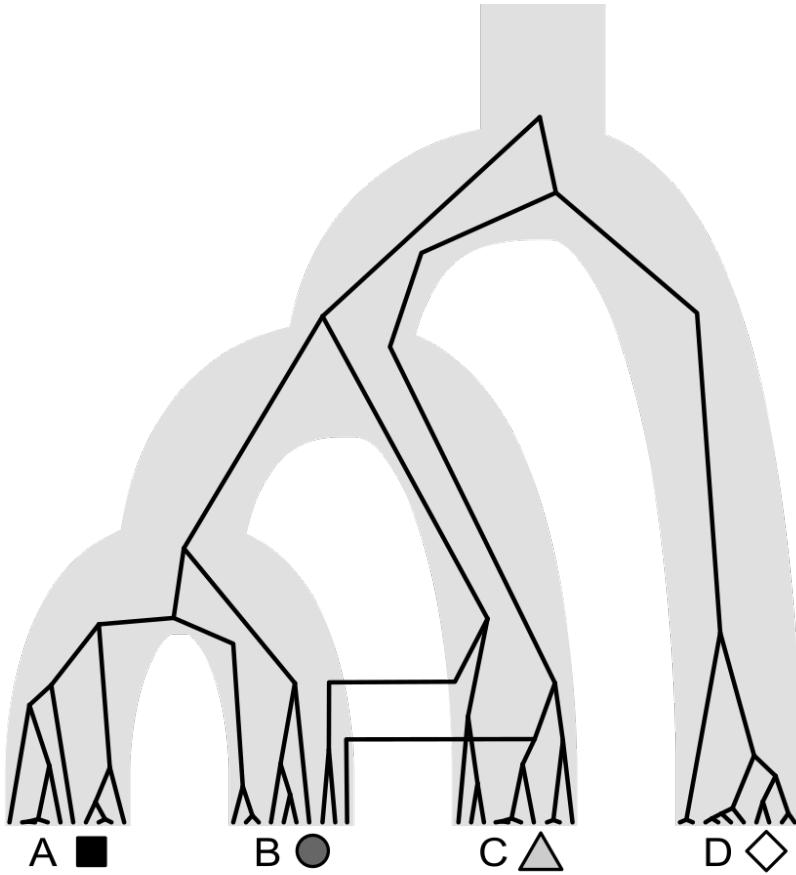
Part 3: Running simulations in msprime to examine the effects on topology weights

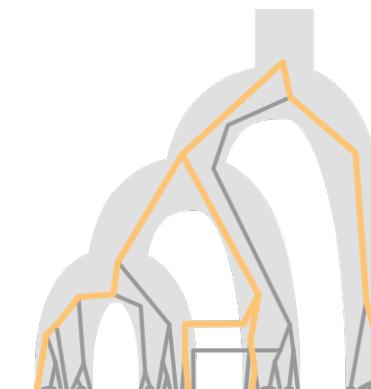
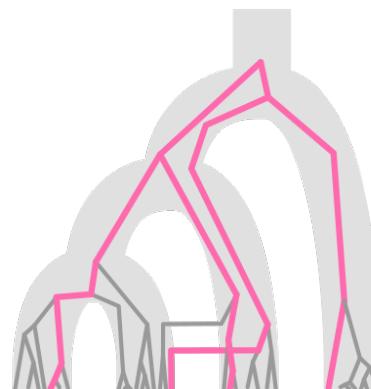
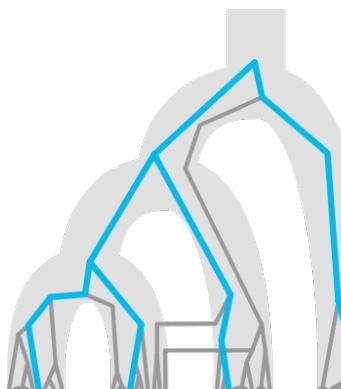
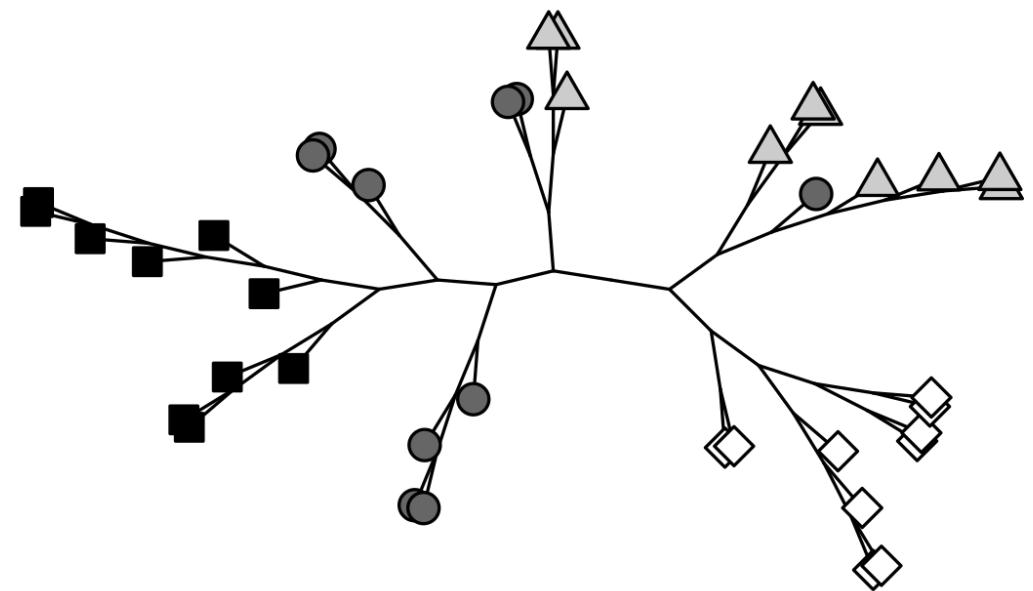
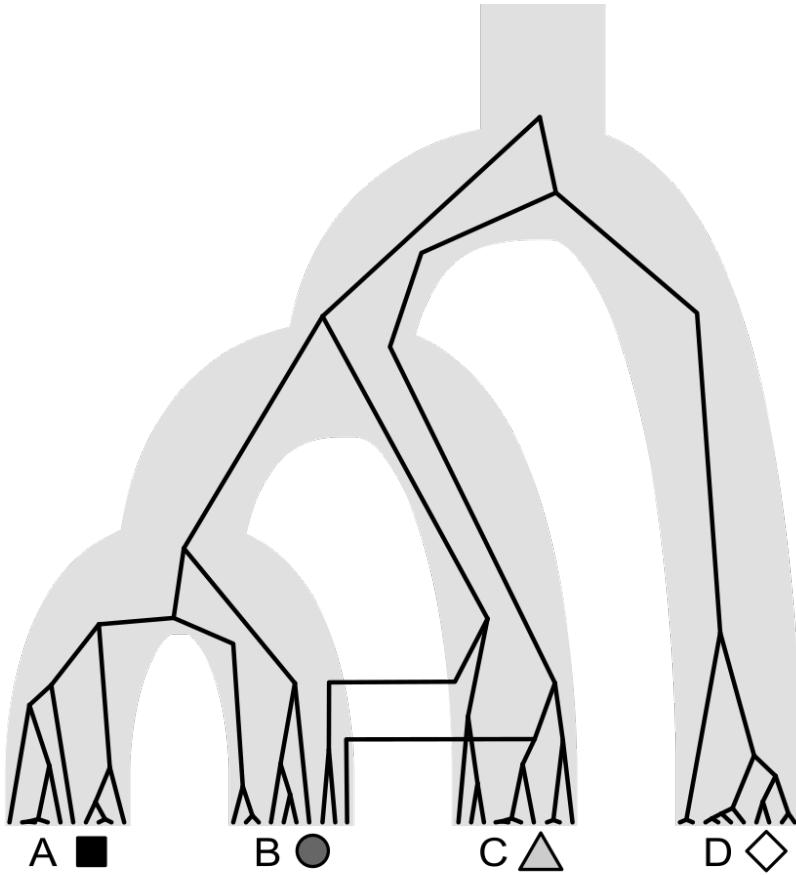


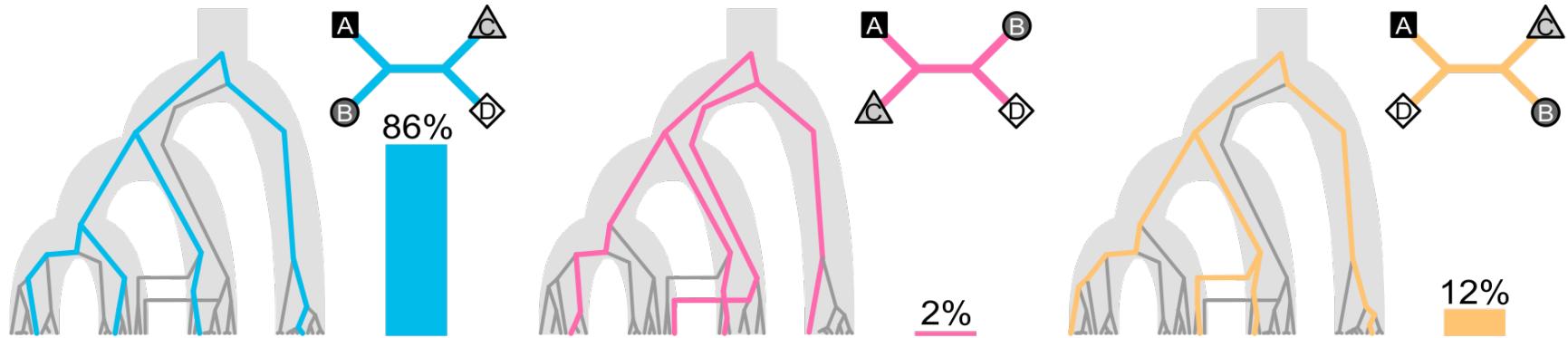






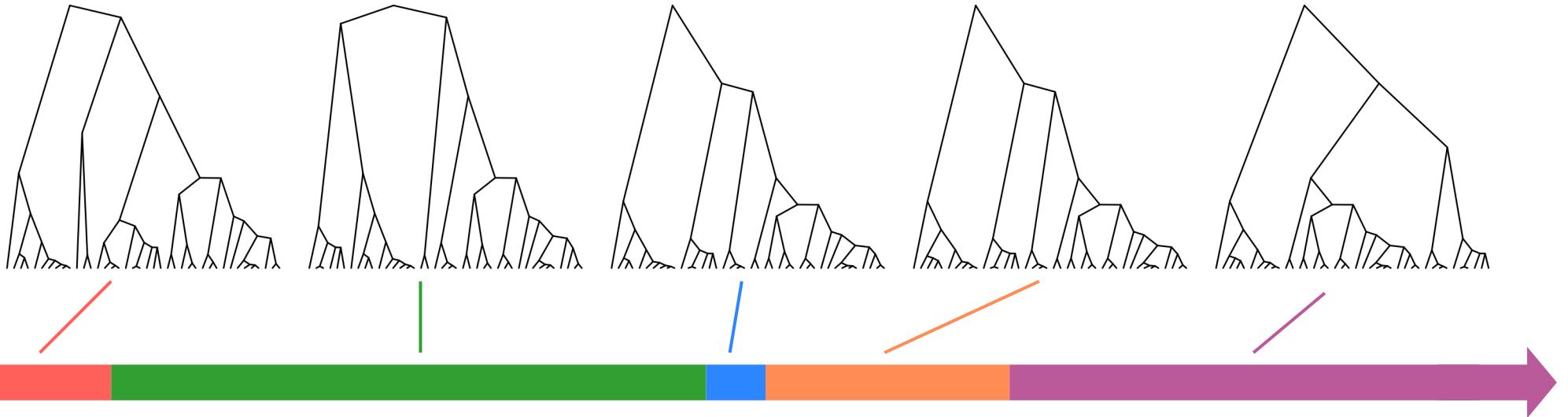






**Twisst:** Topology weighting by iterative sampling of sub-trees

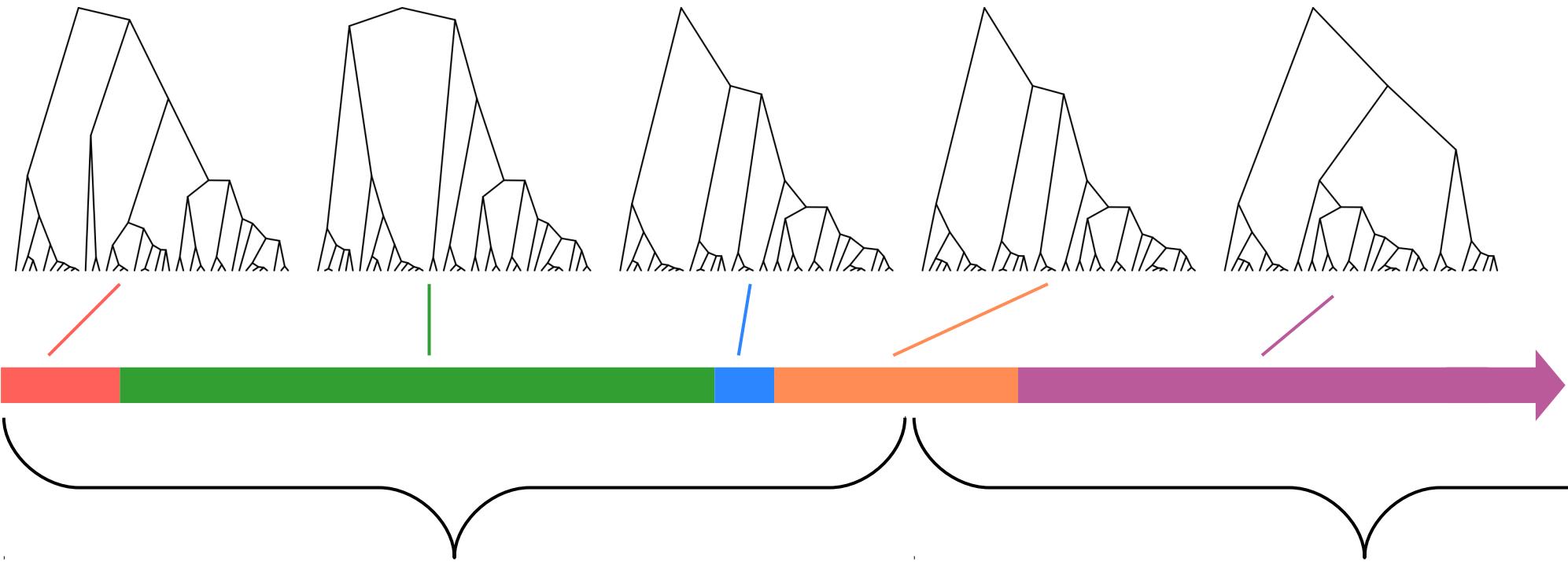
Code: [github.com/simonhmartin/twisst](https://github.com/simonhmartin/twisst)

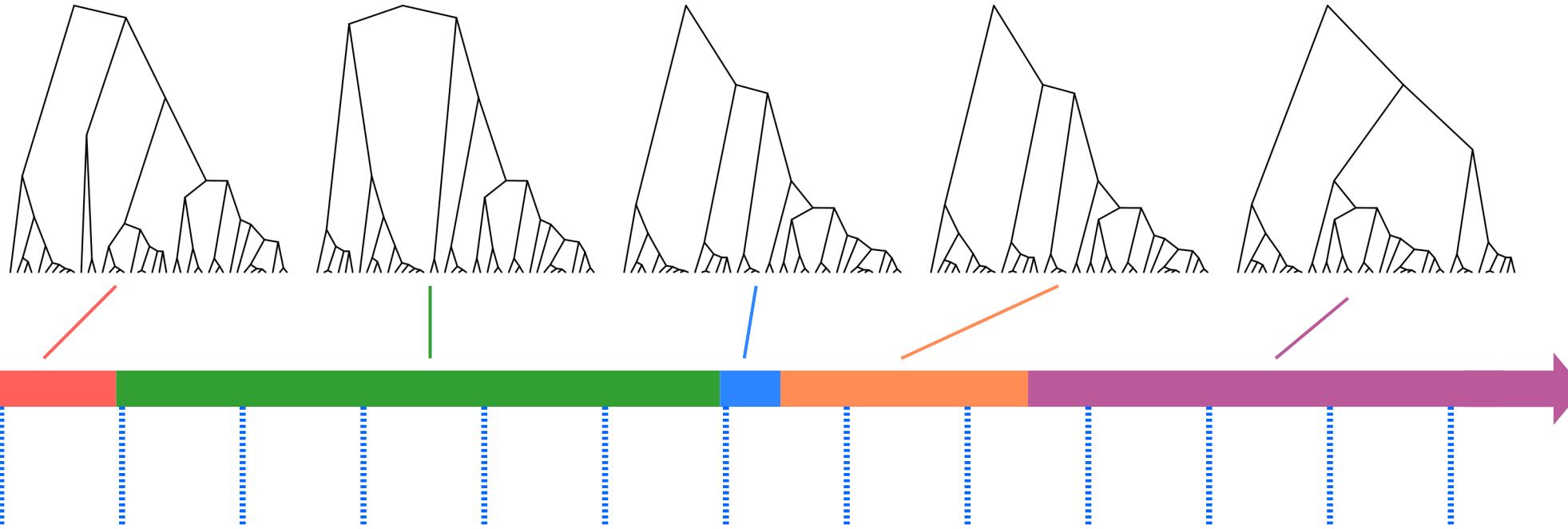


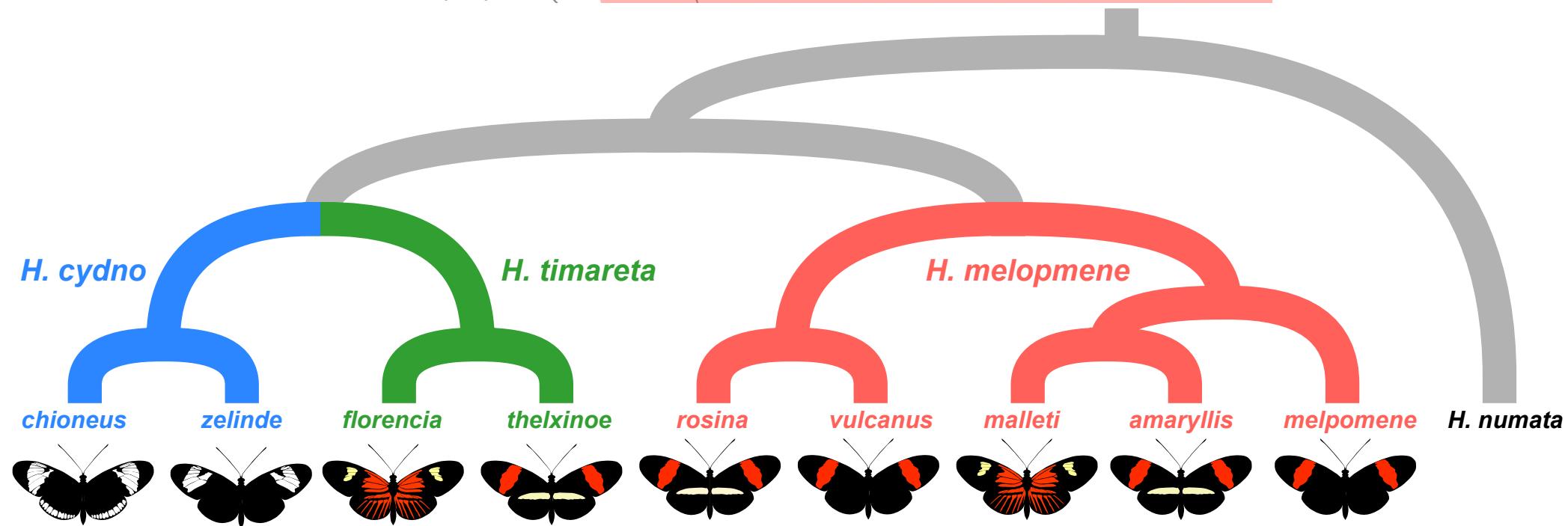
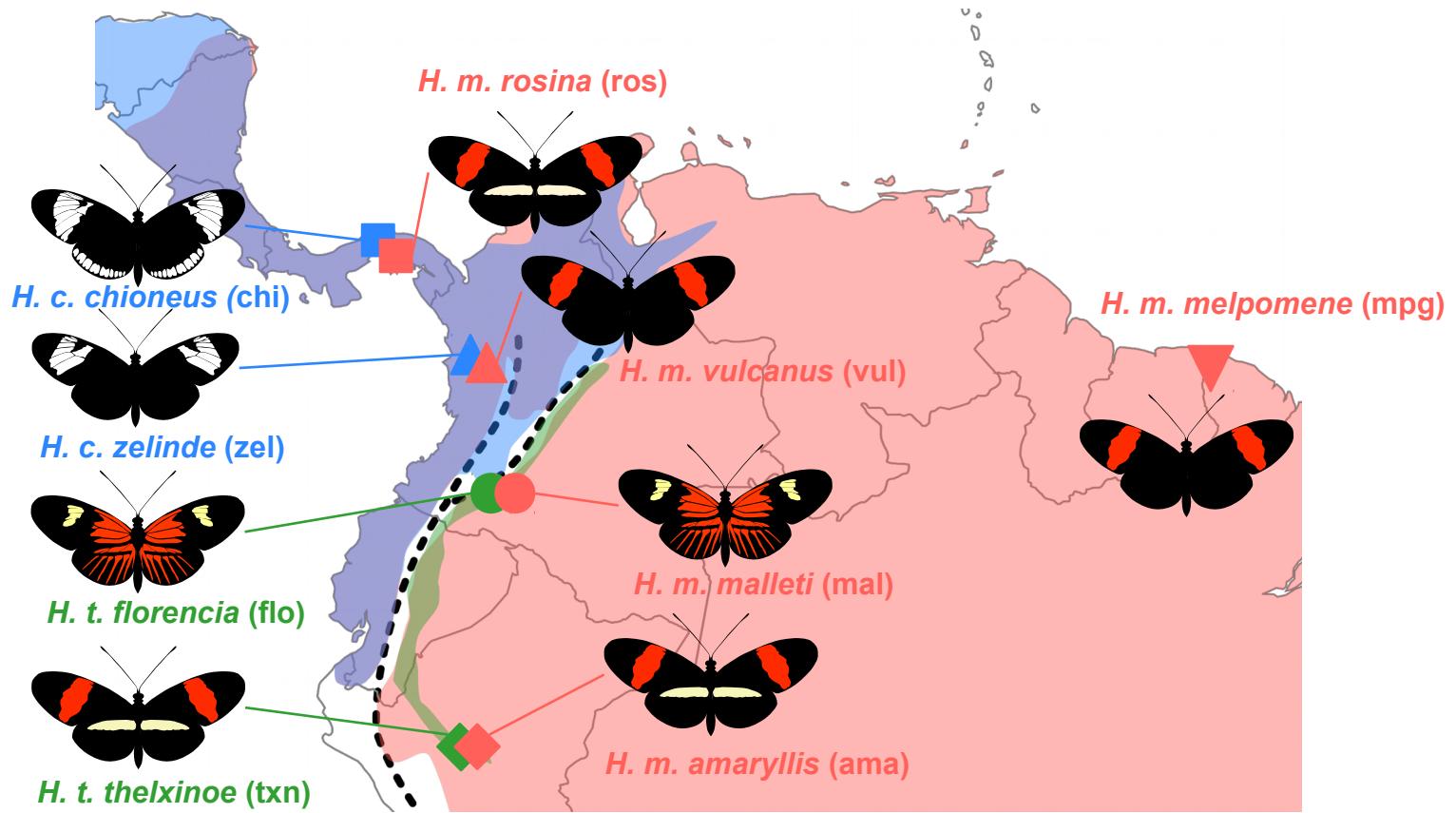
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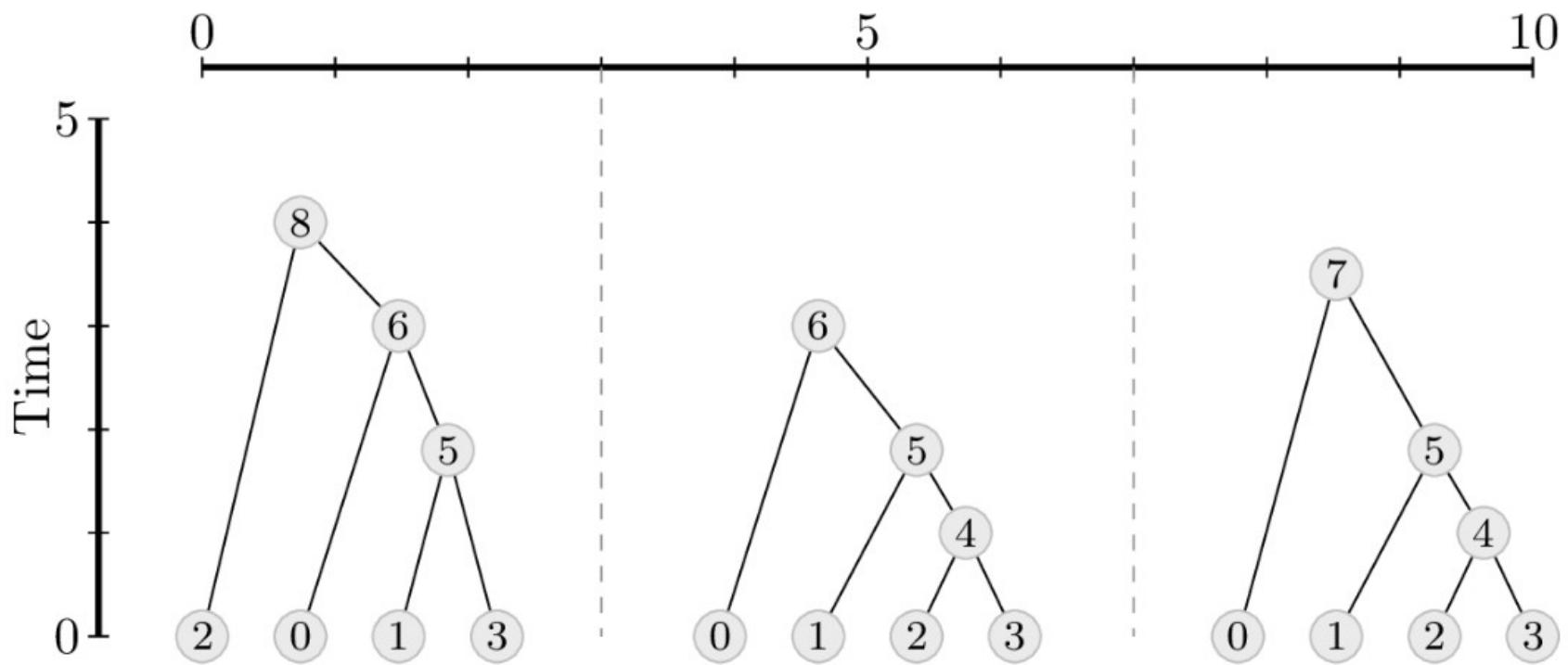






Nodes		Edges			
id	time	left	right	parent	child
0	0.0	3.0	10.0	4	2
1	0.0	3.0	10.0	4	3
2	0.0	0.0	10.0	5	1
3	0.0	0.0	3.0	5	3
4	1.1	3.0	10.0	5	4
5	1.8	0.0	7.0	6	0
6	3.0	0.0	7.0	6	5
7	3.5	7.0	10.0	7	0
8	4.0	7.0	10.0	7	5
		0.0	3.0	8	2
		0.0	3.0	8	6

Chromosomal coordinates



Edges			
left	right	parent	child
3.0	10.0	4	2
3.0	10.0	4	3
0.0	10.0	5	1
0.0	3.0	5	3
3.0	10.0	5	4
0.0	7.0	6	0
0.0	7.0	6	5
7.0	10.0	7	0
7.0	10.0	7	5
0.0	3.0	8	2
0.0	3.0	8	6

Chromosomal coordinates

