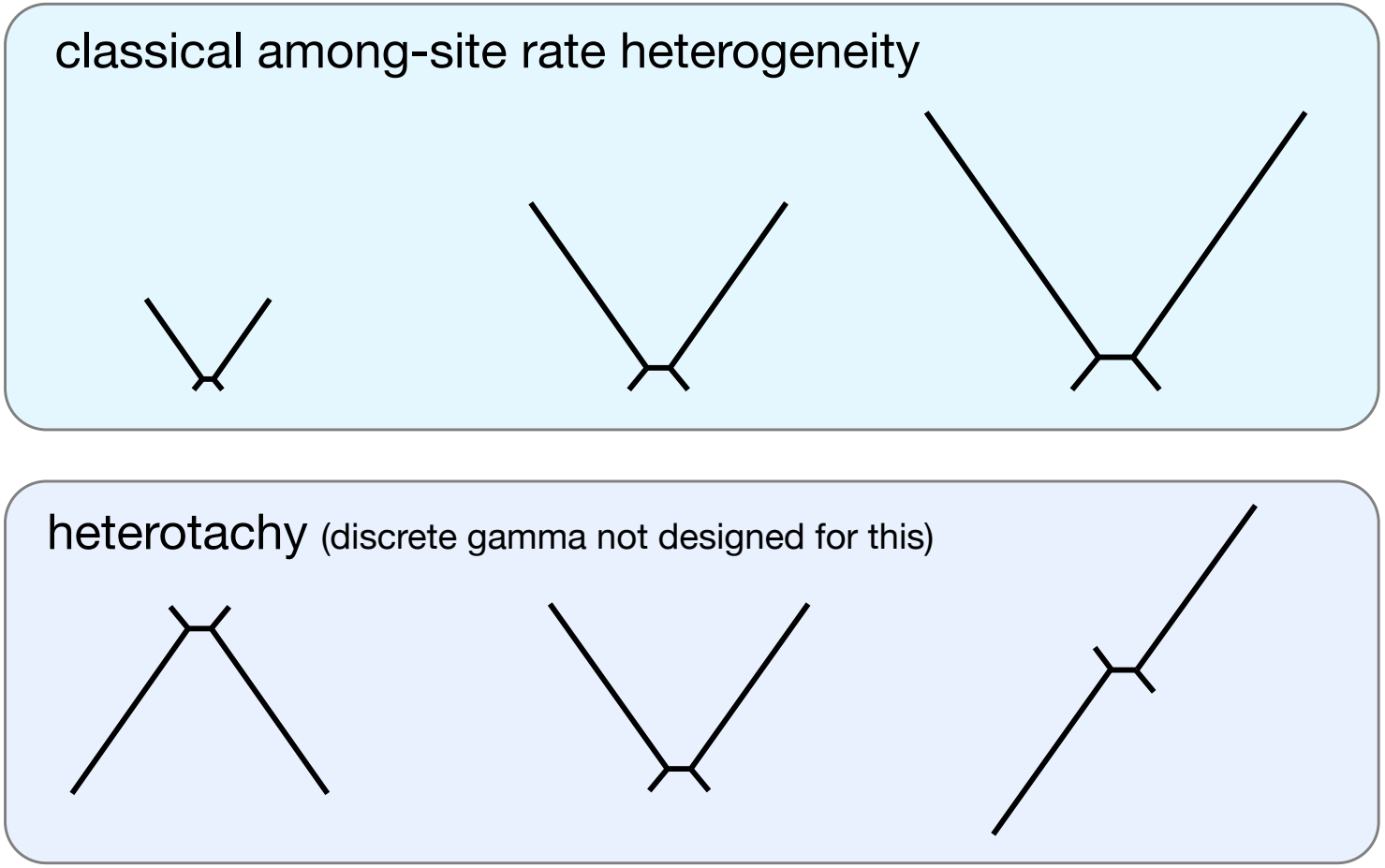
Heterotachy

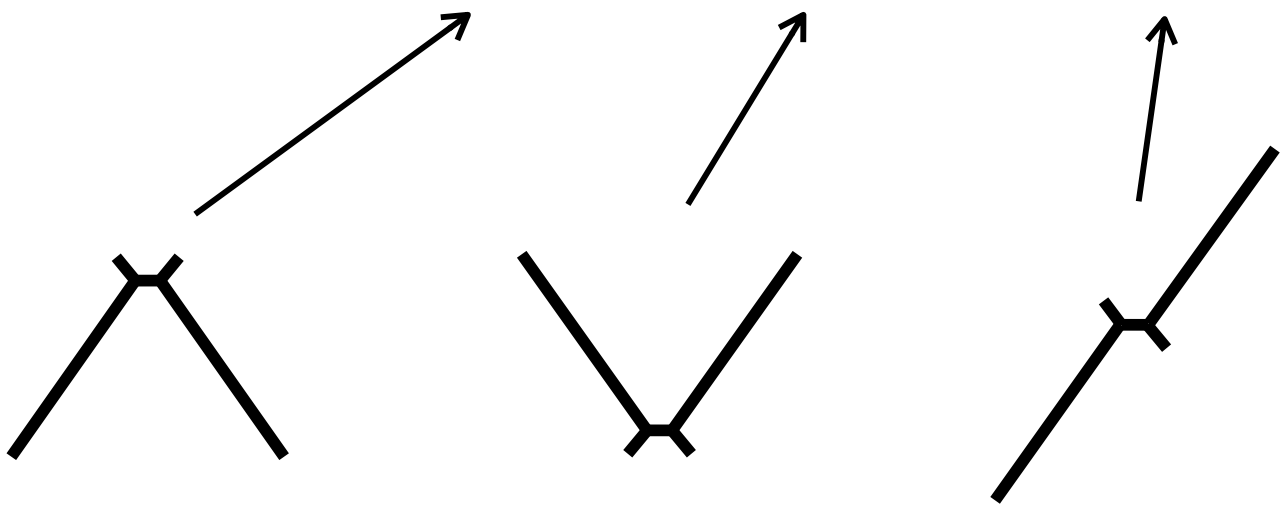
Heterotachy



Kolaczkowski and Thornton (2004)

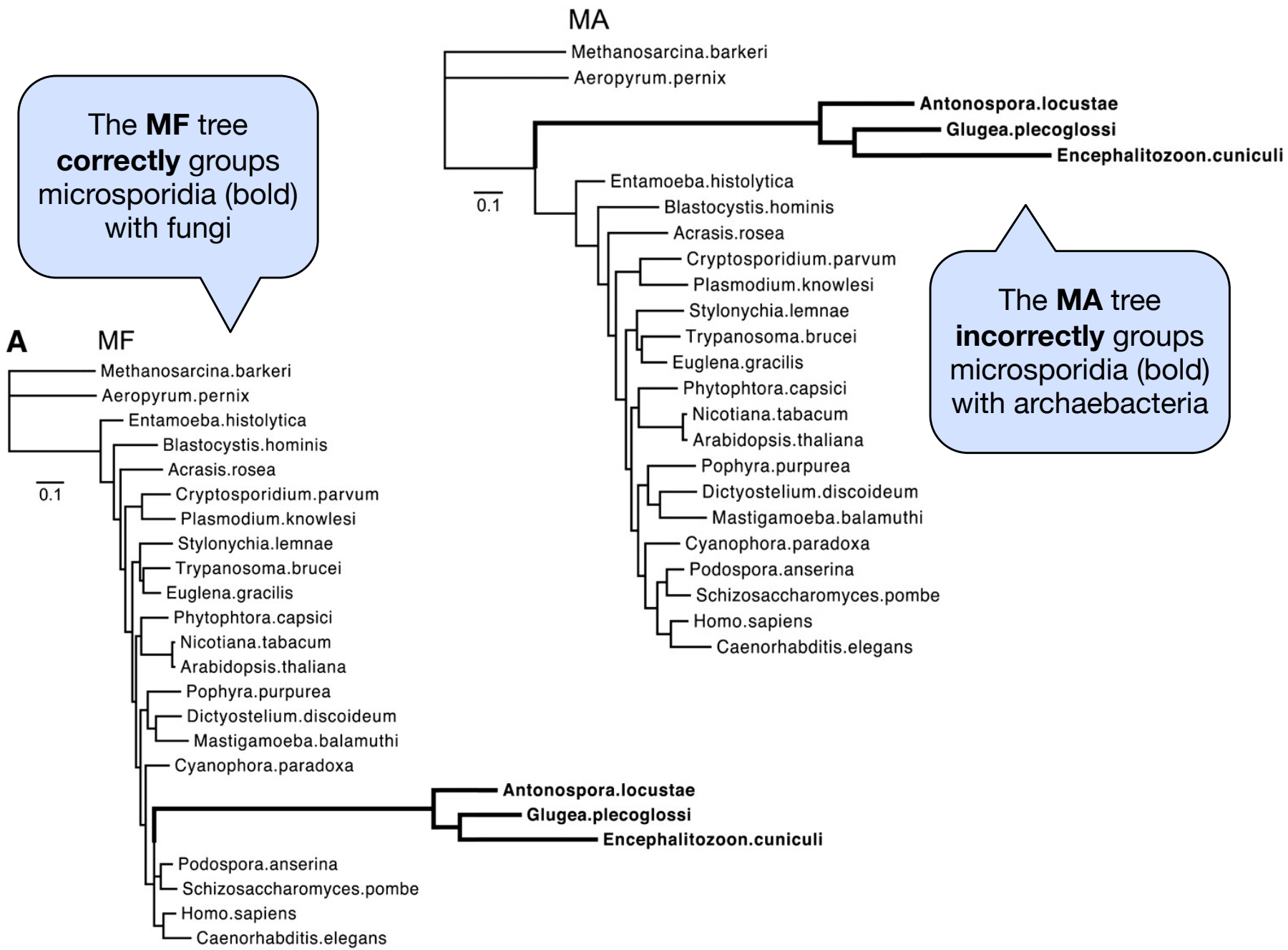
Kolaczkowski & Thornton's (2008) heterotachy model

$$L = w_1 L_{b_1} + w_2 L_{b_2} + w_3 L_{b_3}$$



Each b_i represents an *entire set* of 5 branch lengths.
This model potentially adds a *lot* of parameters (if the tree is large)

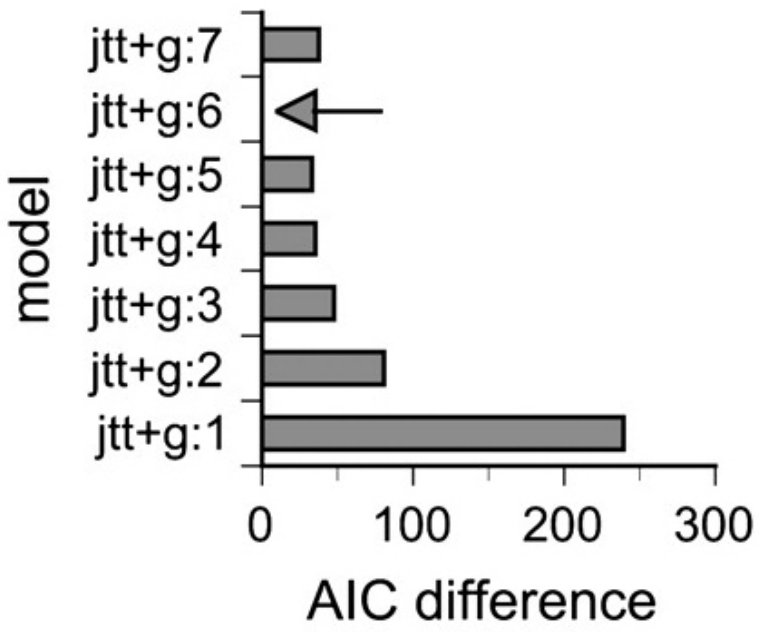
Kolaczkowski and Thornton (2008)

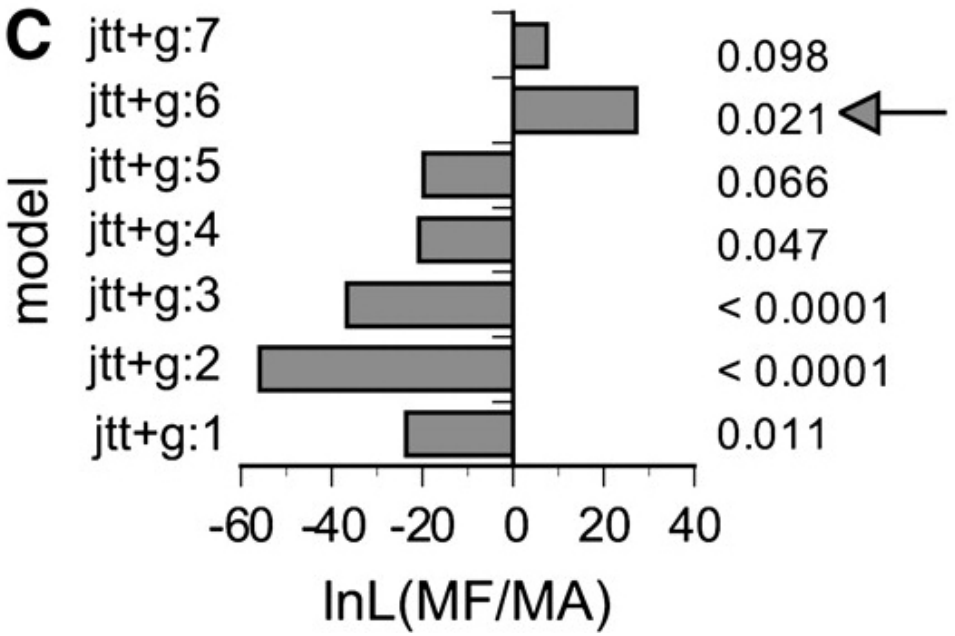


Kolaczkowski and Thornton (2008)

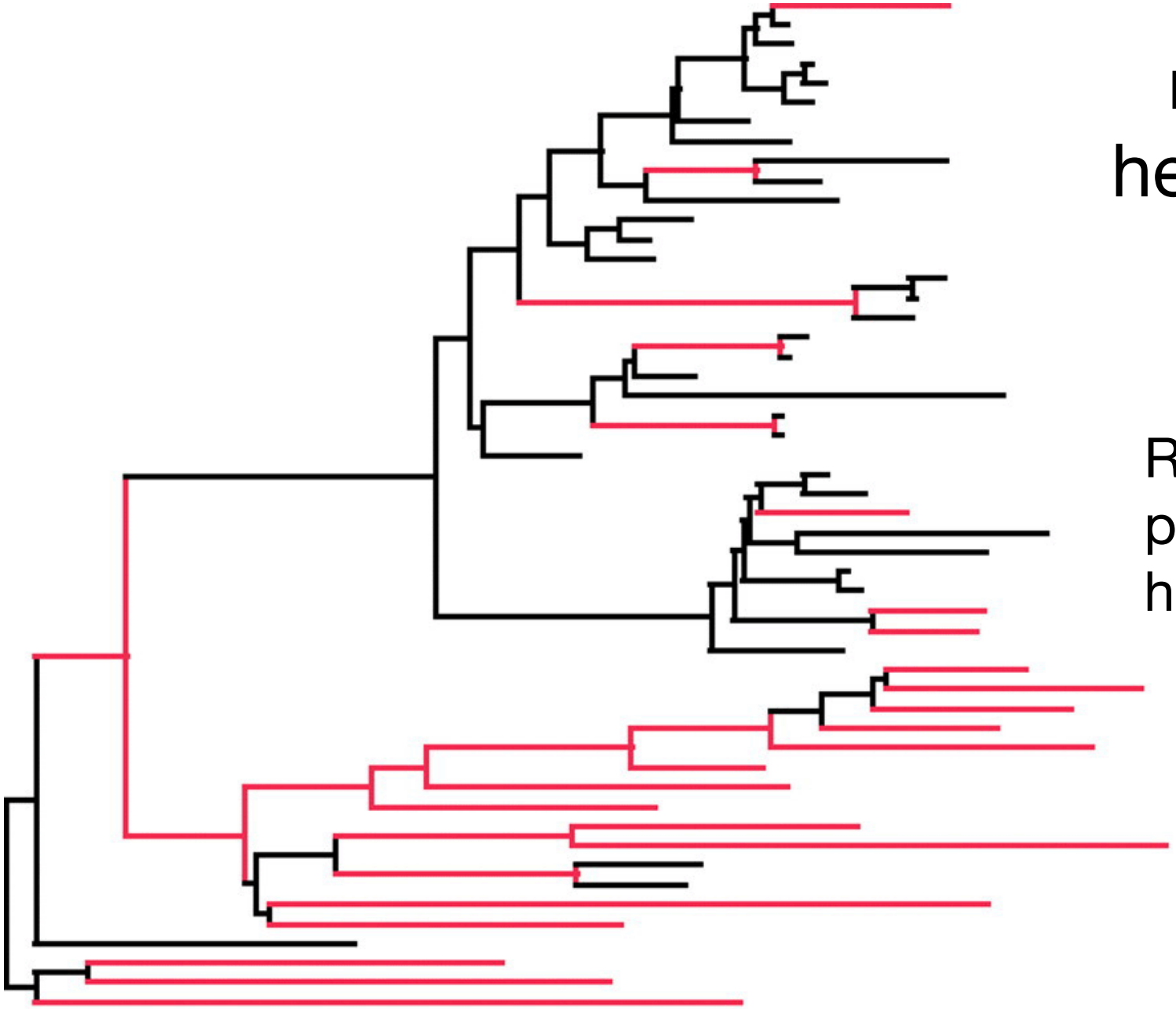
A mixture of 6 sets of branch lengths yields the minimum AIC score

A mixture of 6 sets of branch lengths yields maximum discrimination between the widely-recognized true tree (MF) and the artifactual tree (MA)





Kolaczkowski and Thornton (2008)

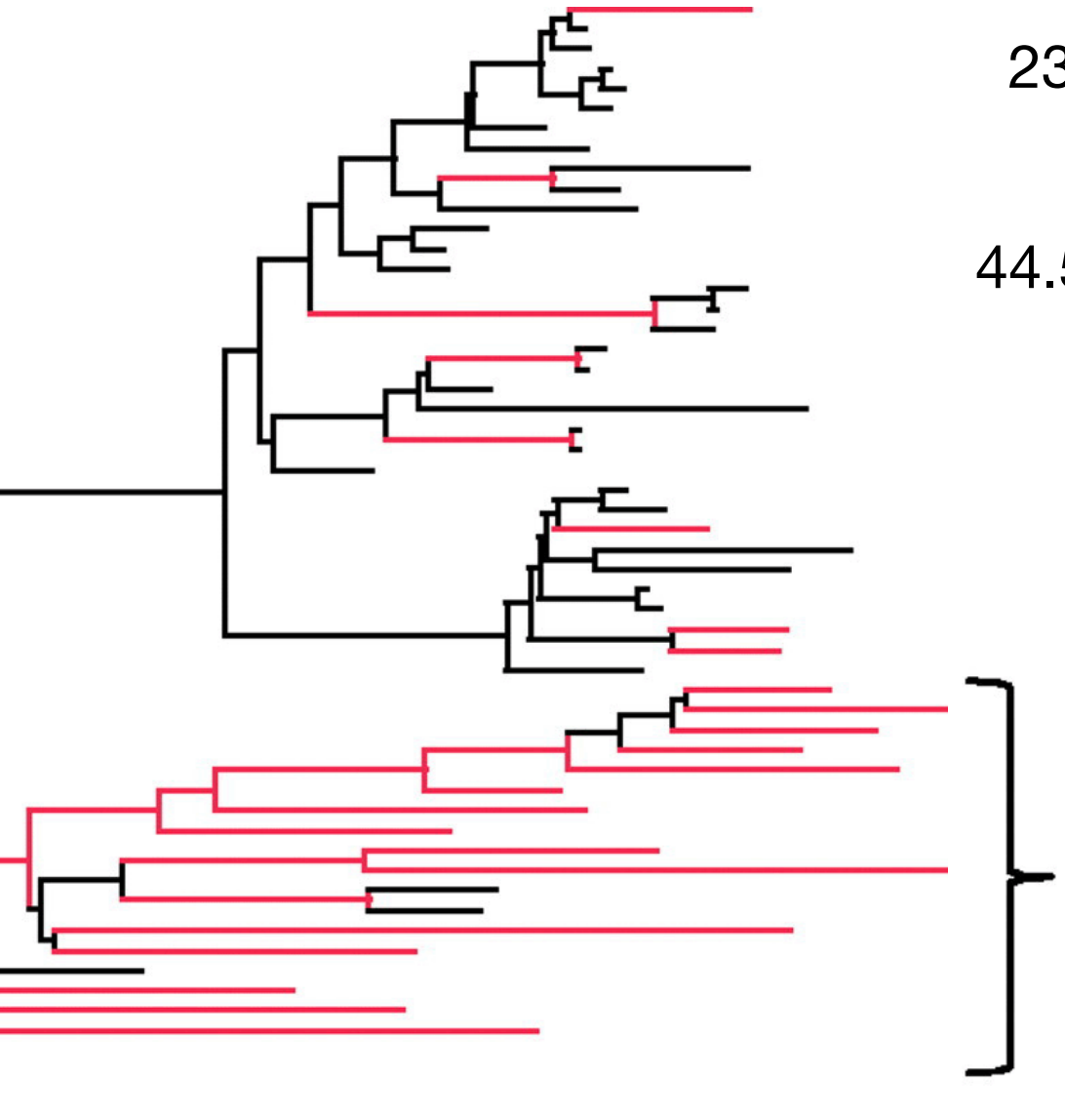


rjMCMC heterotachy model

Red edges have prob. > 0.5 of having 2 edges

Pagel and Meade (2008)

rjMCMC heterotachy model



236 primary edges (119 taxa)

44.5 extra edges

ribosomal genes evolve slowly in general (and also in this clade)

rbcL, atpB genes evolve quickly in this clade only

Software: http://www.evolution.reading.ac.uk/BayesPhyHeterotachy.html

Pagel and Meade (2008)

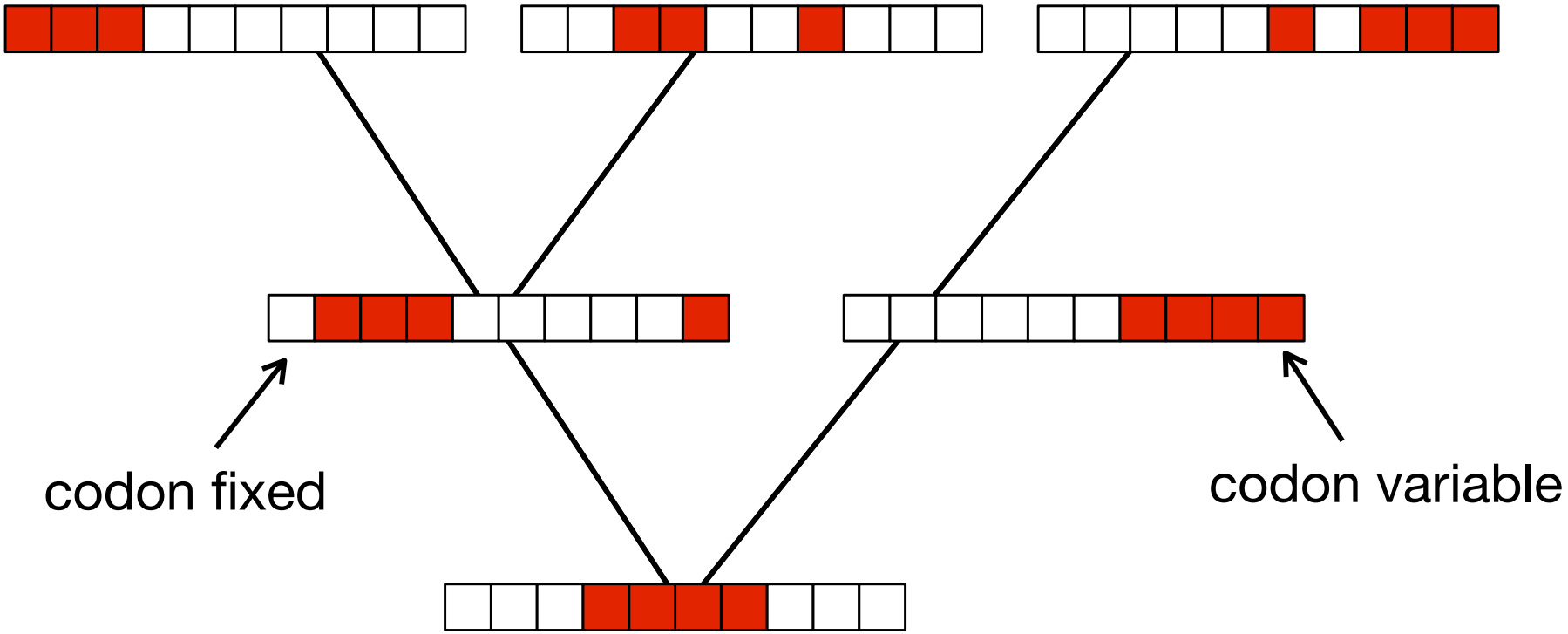
Covarion Models

Covarion Hypothesis

"*...at any one point in time only a very* ***restricted number of positions can fix mutations*** *but that as mutations are fixed the* ***positions capable of accepting mutations also change*** *so that examination of a wide range of species reveals a wide range of altered positions. We define this restricted group as the* ***concomitantly variable codons****.*"

Fitch and Markowitz (1970)

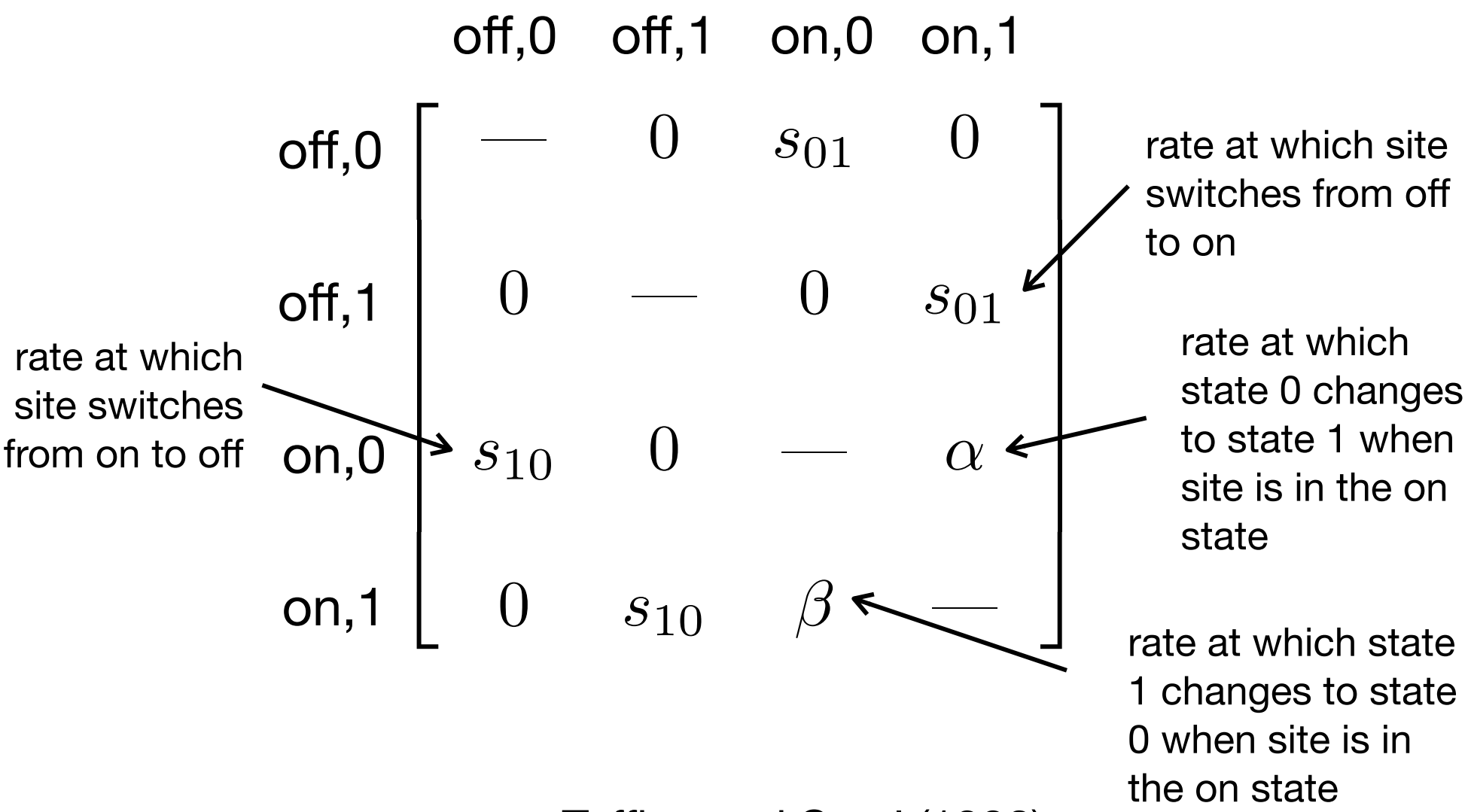
Covarion Hypothesis



Extreme form of heterotachy

Fitch and Markowitz (1970)

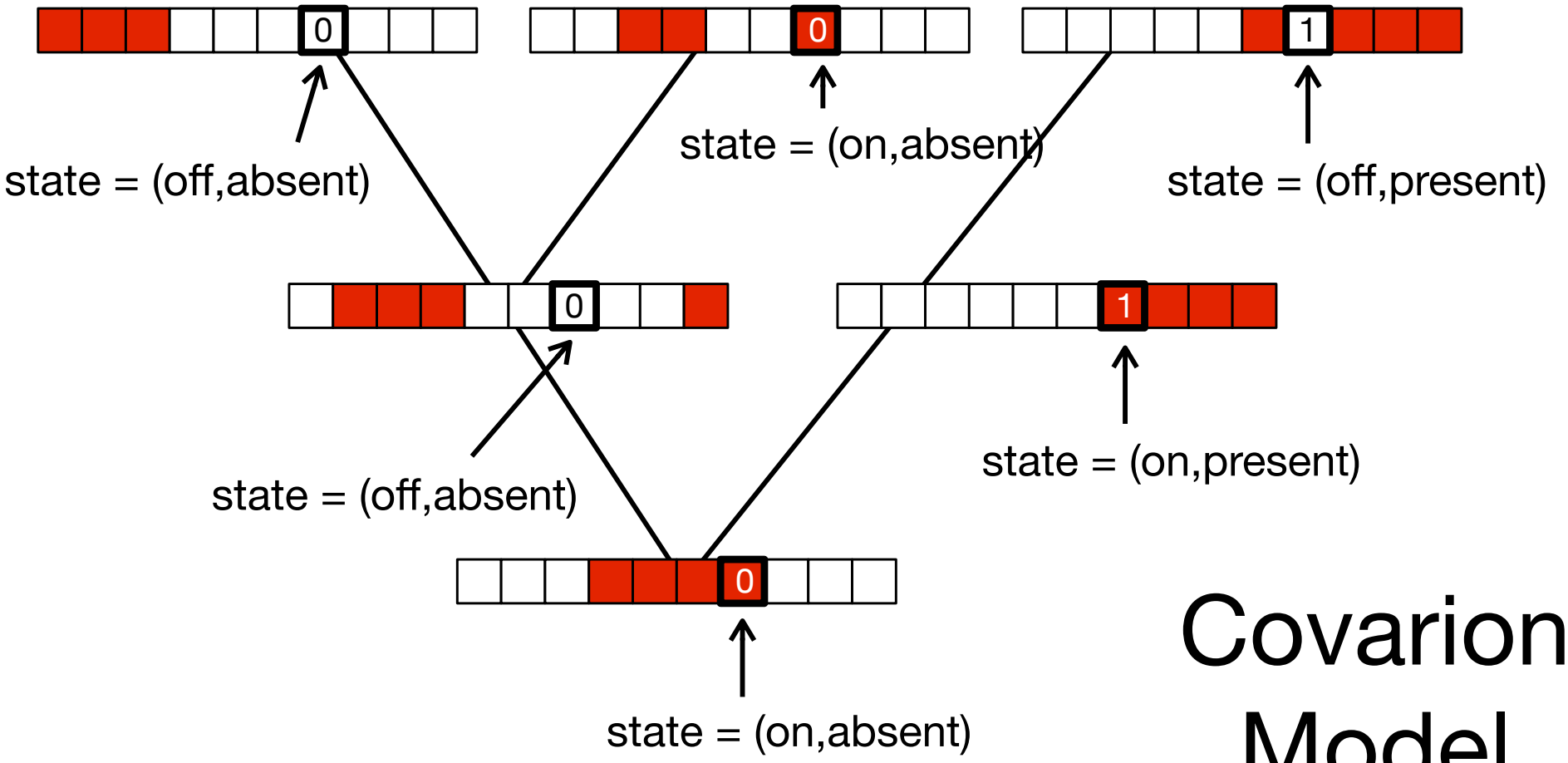
Covarion Model



Tuffley and Steel (1998)

Pretend there are 10 presence/absence characters, each of which can be in an on or off state at any point in time..

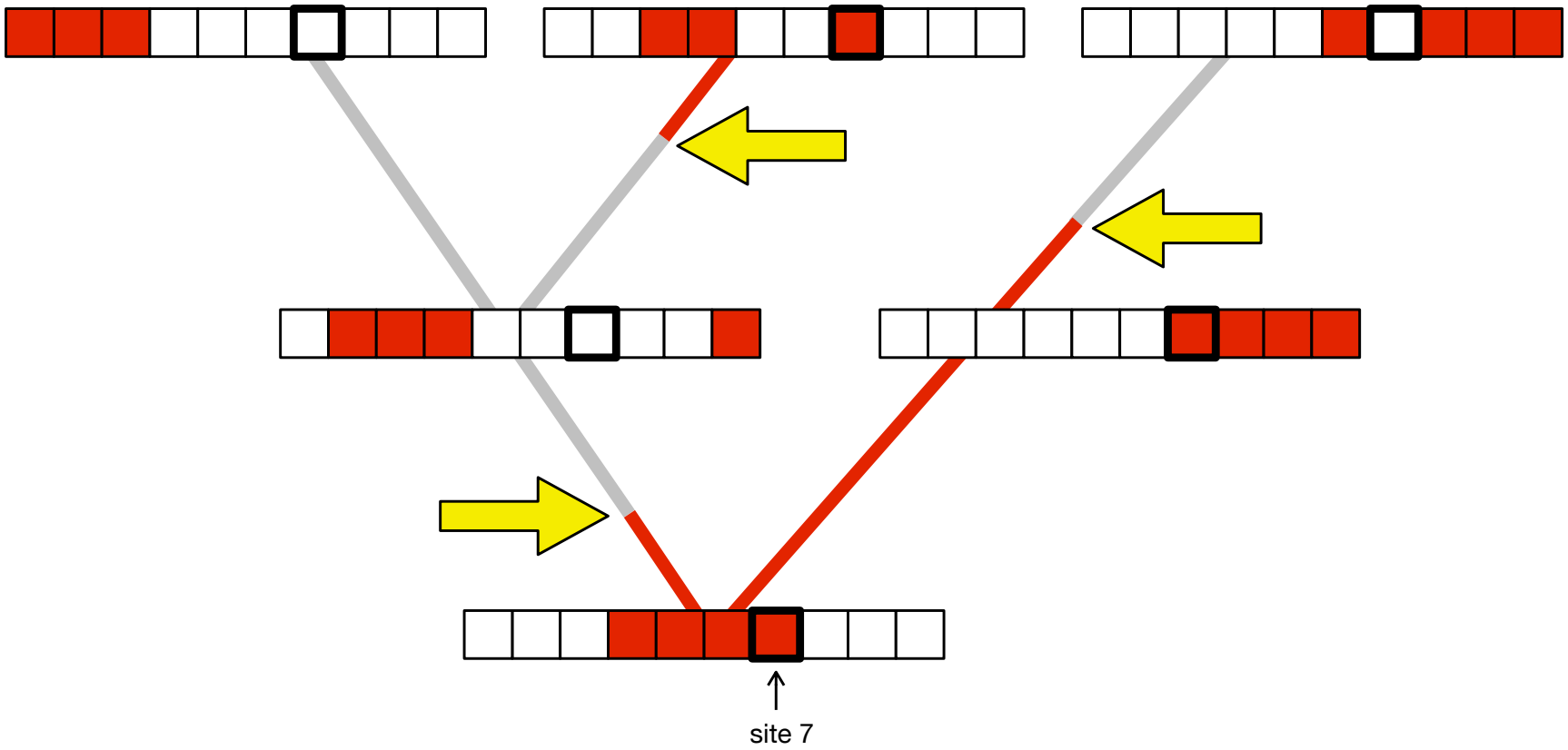
Consider only site 7 for the moment (bold boxes)...



Covarion Model

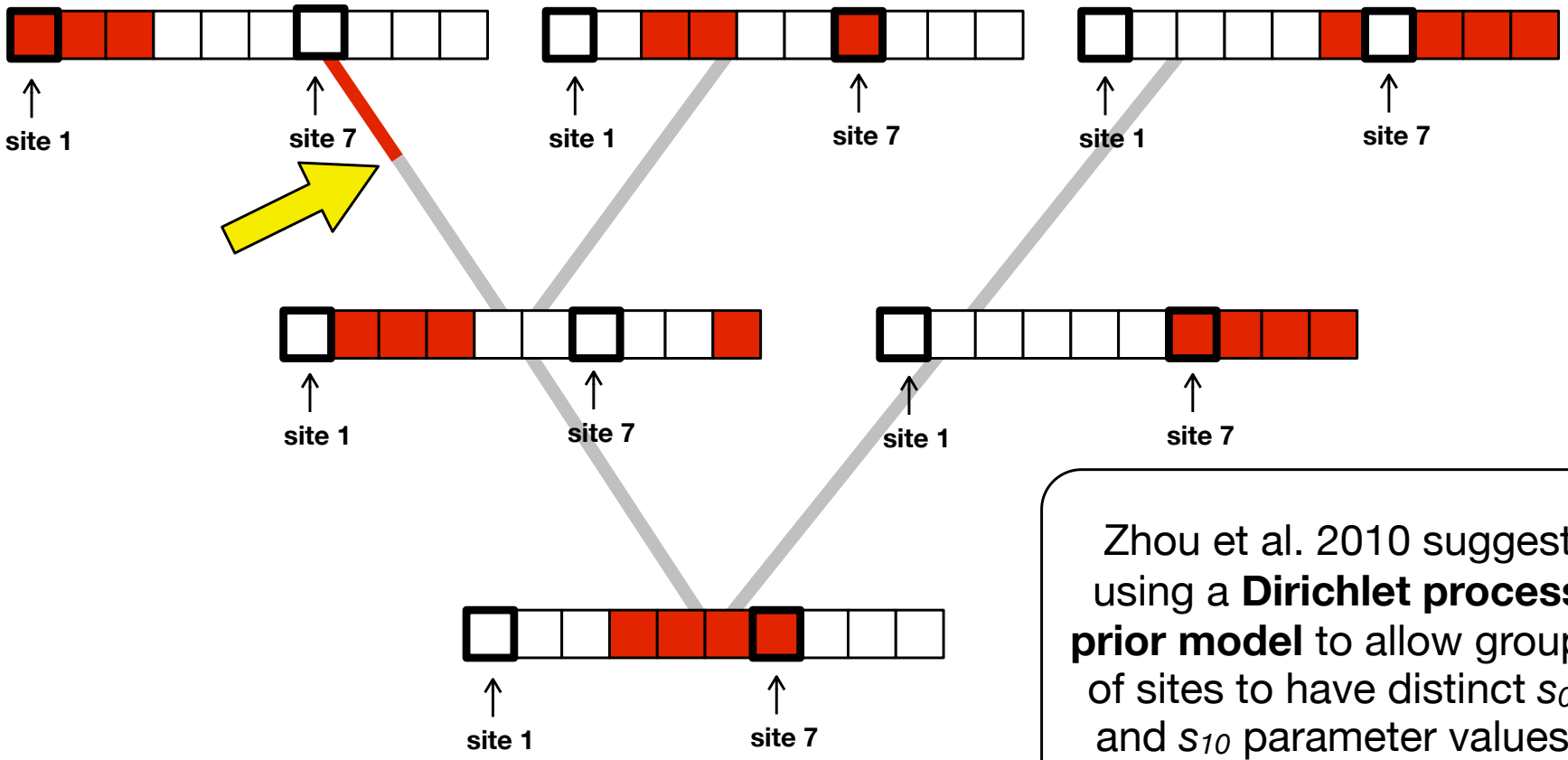
Covarion Mixture Model

Note that some sites switch from off to on (or vice versa) often (e.g. site 7)...



Covarion Mixture (CM) Model

...while other sites rarely switch (e.g. site 1).



Zhou et al. 2010 suggest using a **Dirichlet process prior model** to allow groups of sites to have distinct s_{01} and s_{10} parameter values.

Software:
http://www.phylobayes.org/

Zhou et al. (2010)