Outline for today

1. Coalescent

2. Multispecies coalescent

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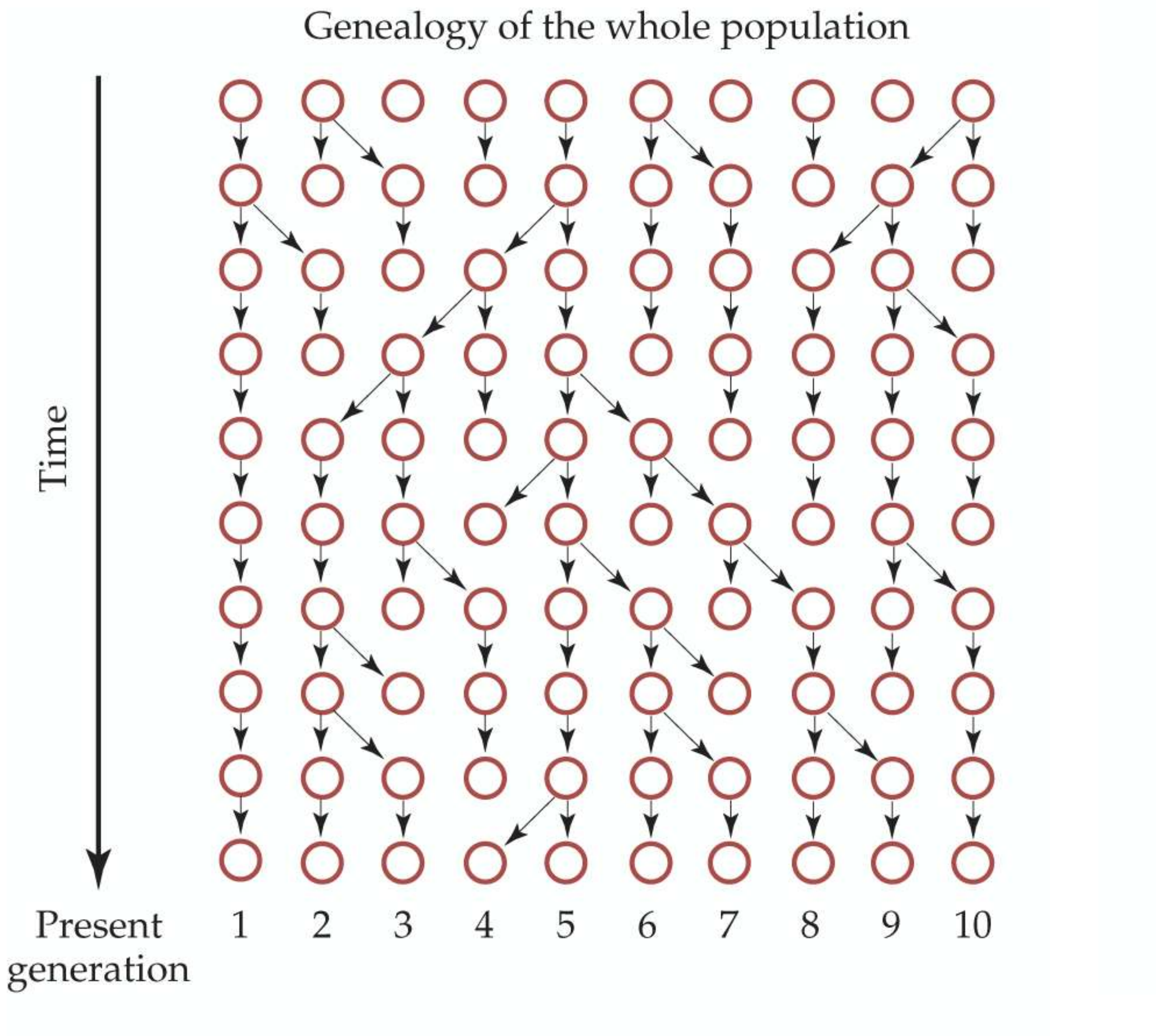
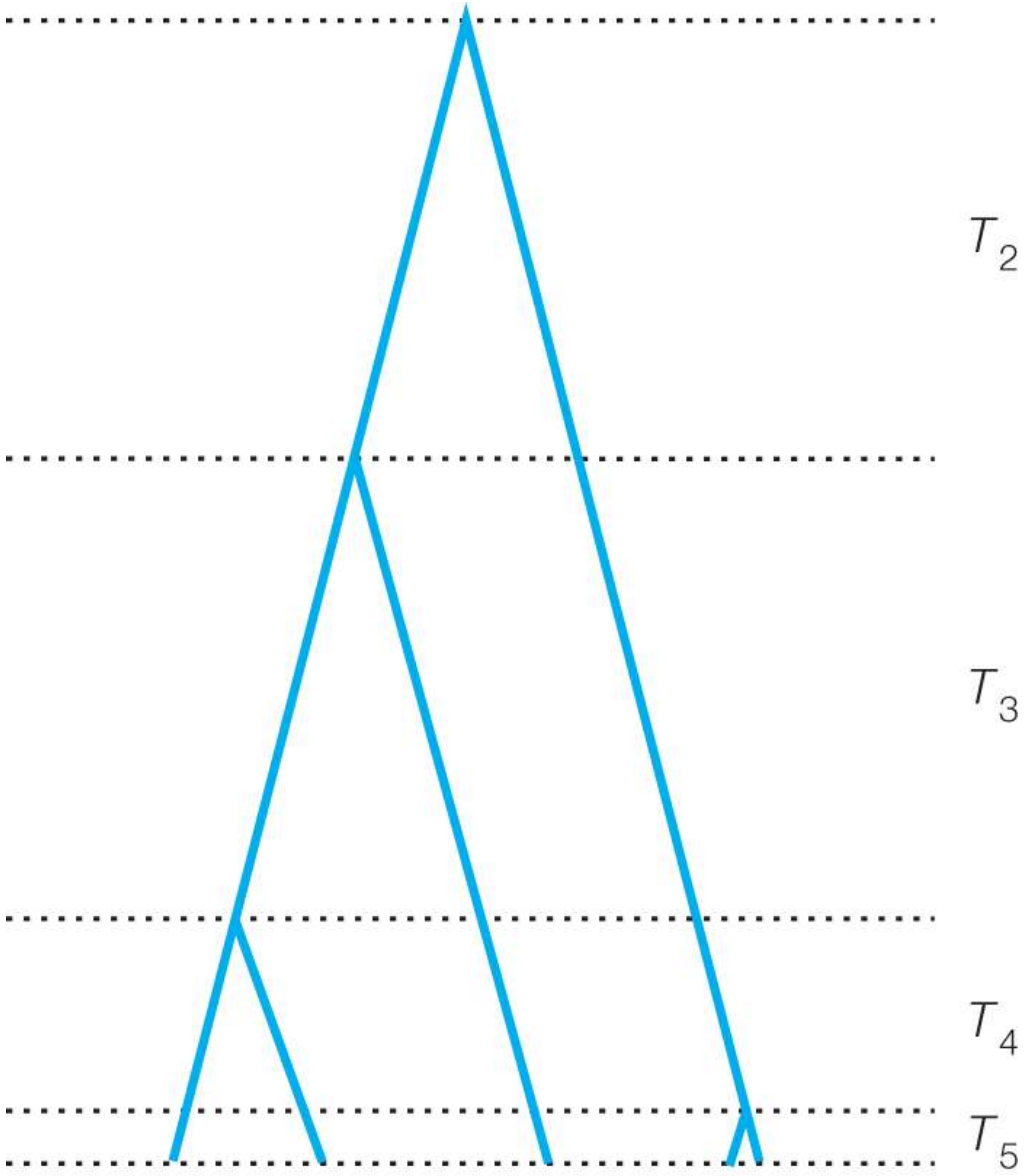
Why do we need the coalescent model?





Algorithm for generating a coalescent tree

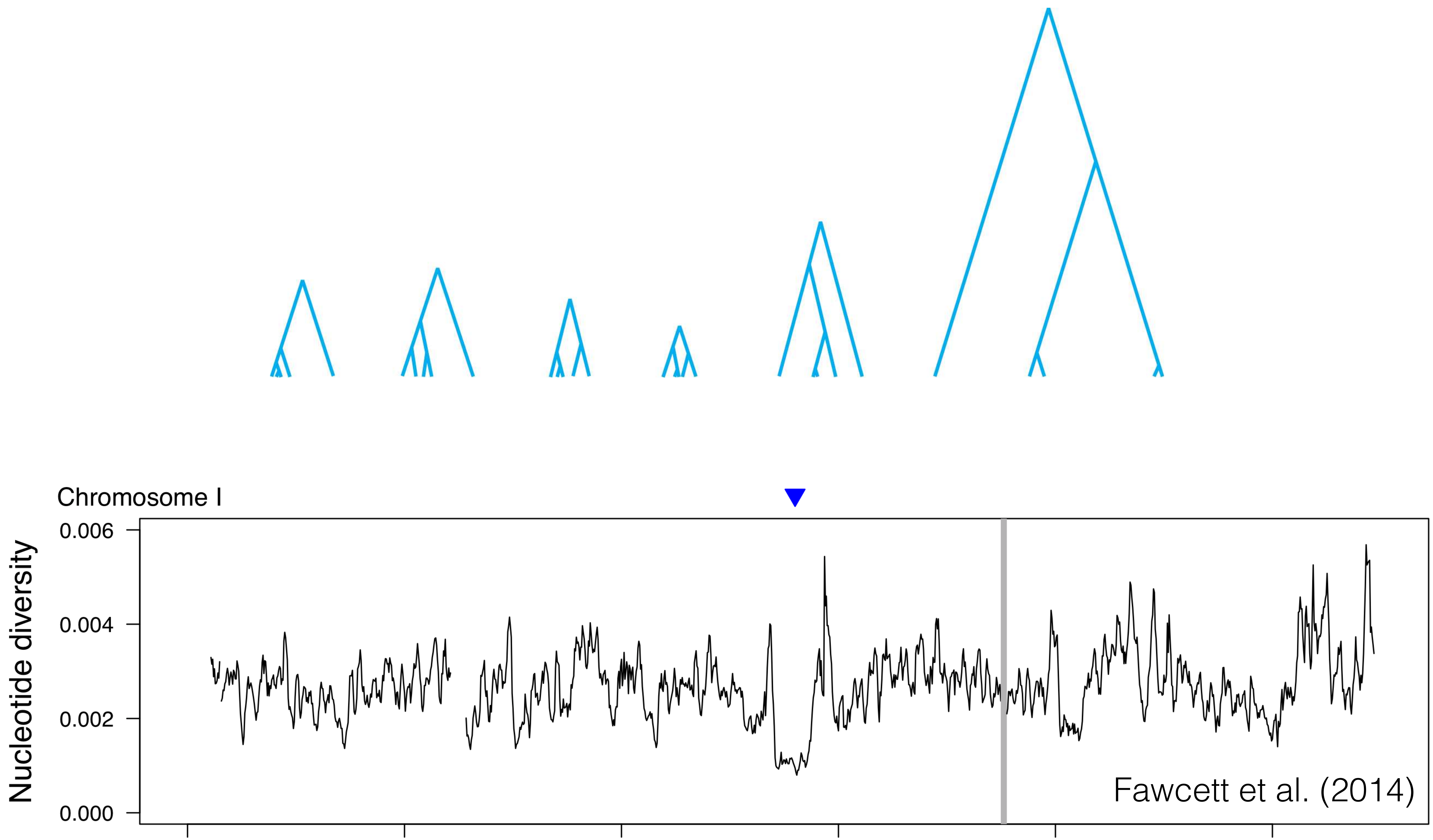
1. Start with i=n chromosomes

2. Choose a time until first coalescence from an exponential distribution with parameter x= i(i-1)/2

3. Choose two chromosomes at random to coalesce

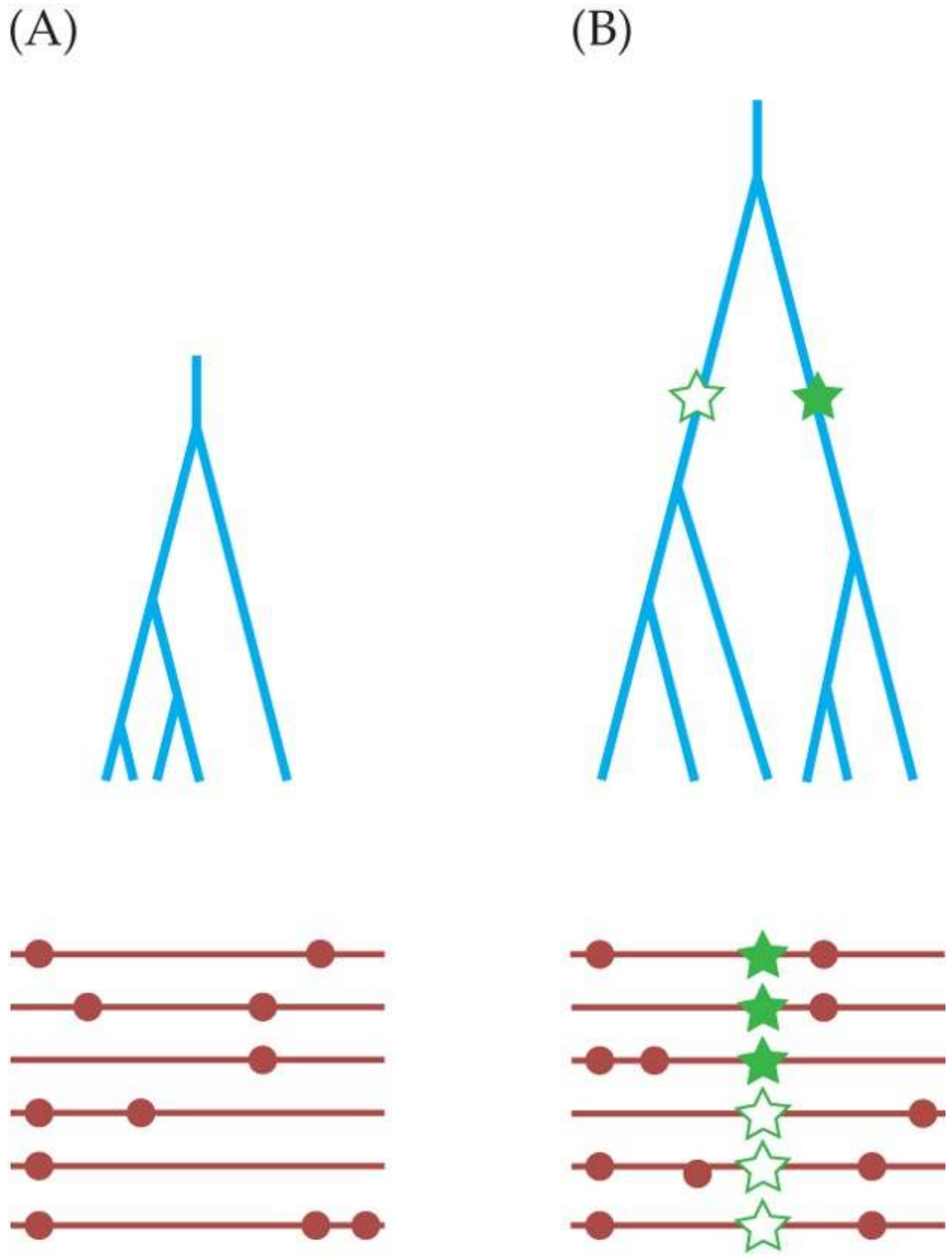
4. Merge the two lineages chosen, and have $i \rightarrow i$-1

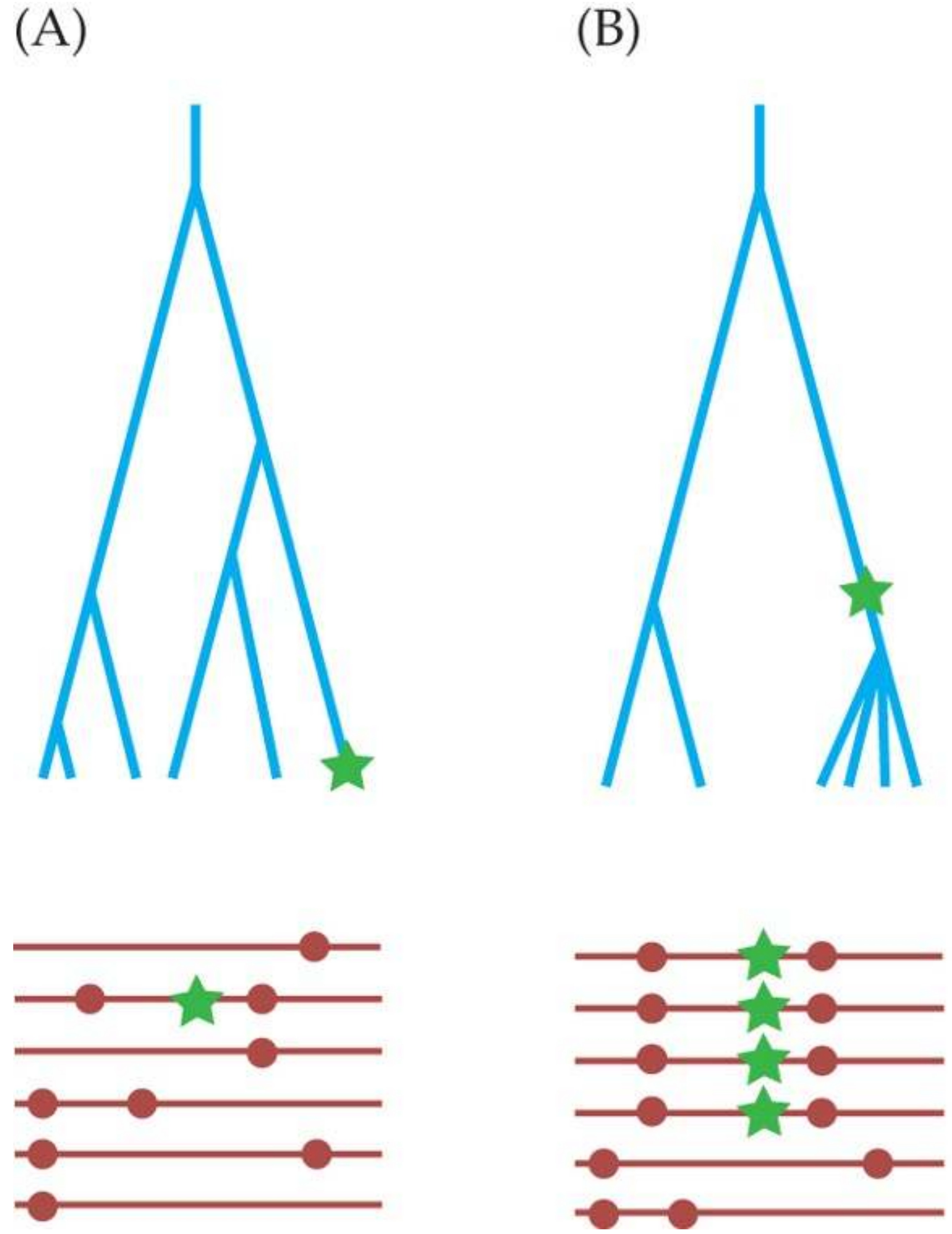
5. If i>1 go to 2; if not stop

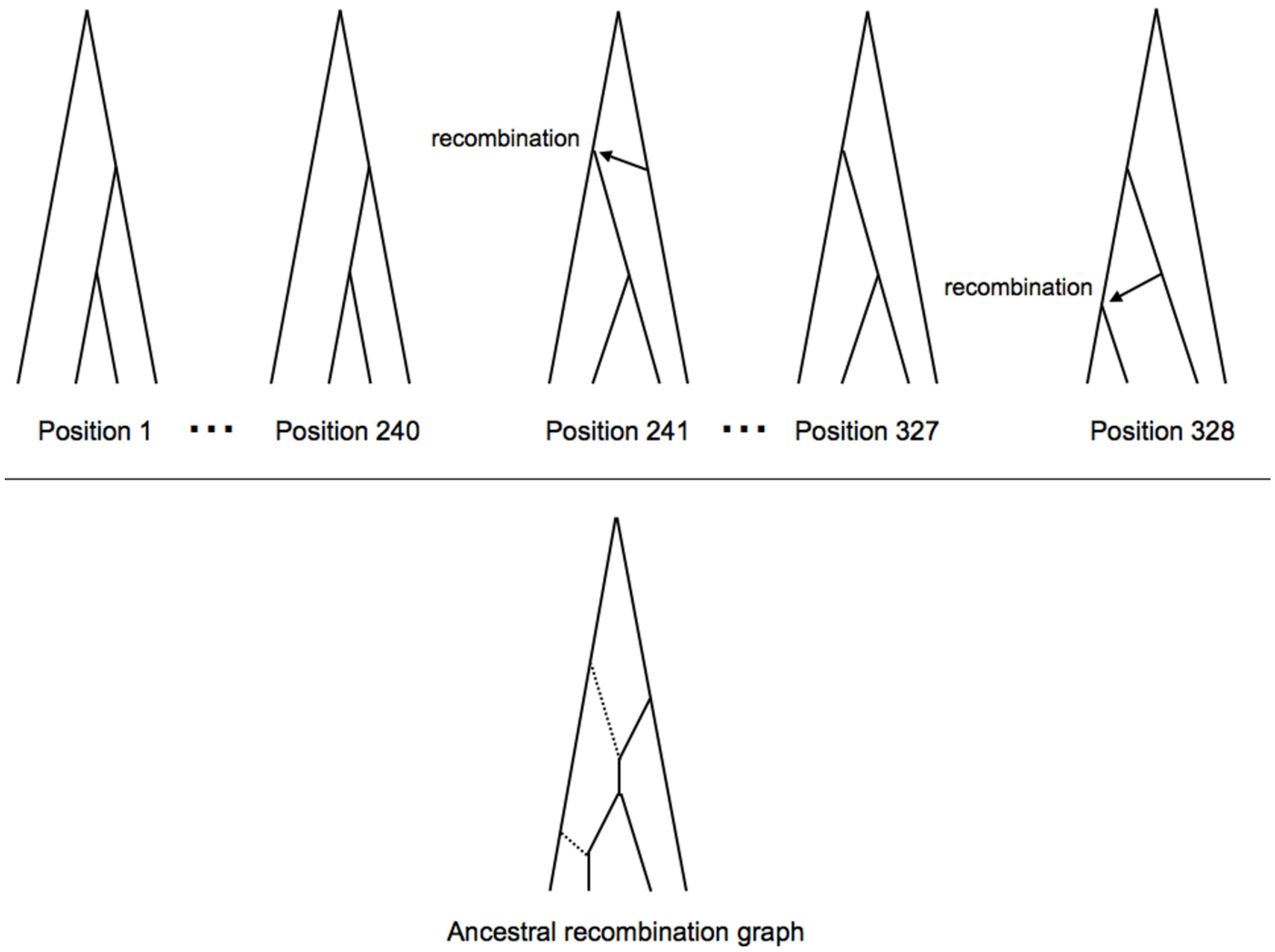


Chromosome I
Nucleotide diversity
0.006
0.004
0.002
0.000
Fawcett et al. (2014)

https://bedford.io/projects/coaltrace/

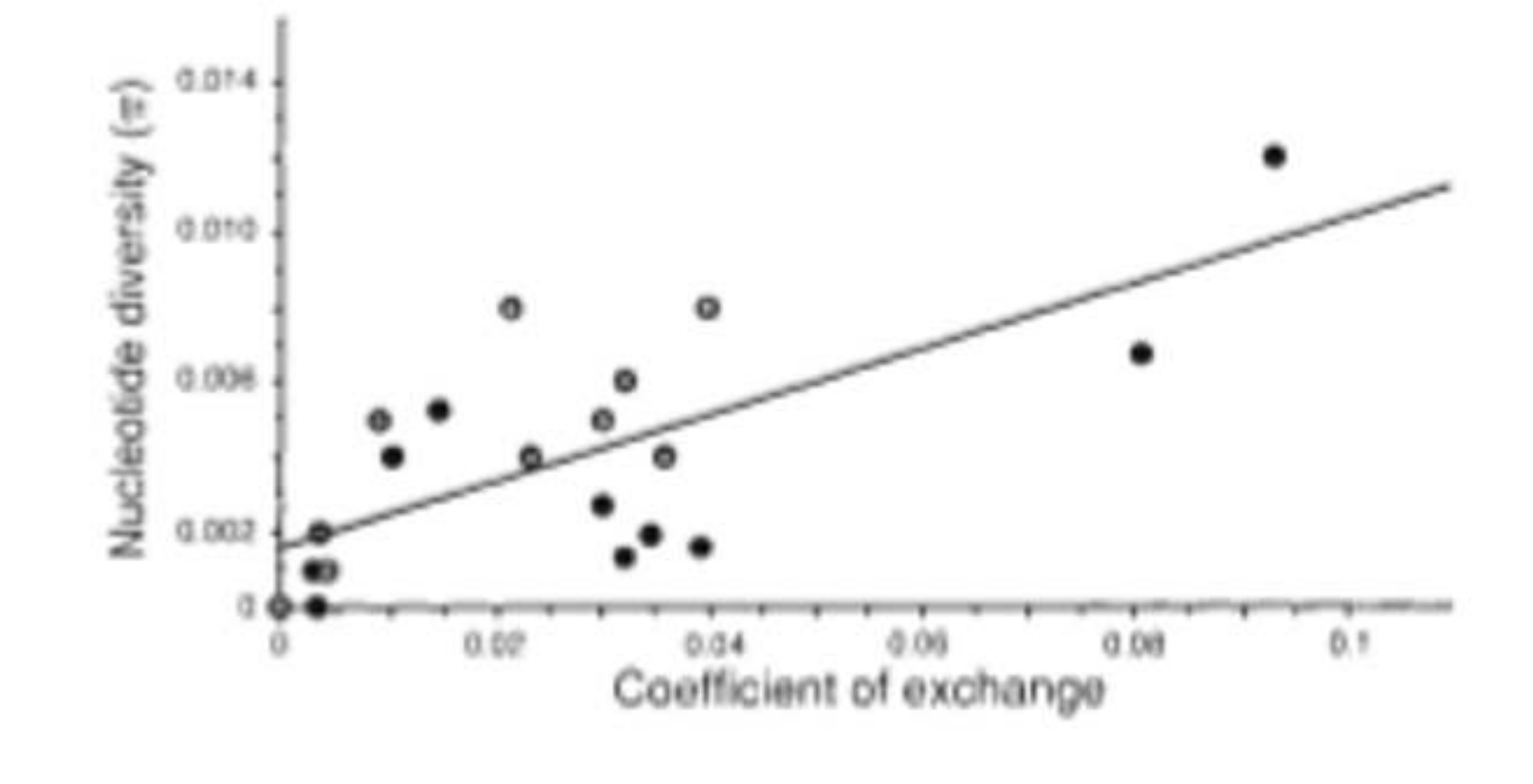

(A)
(B)


(A)
(B)

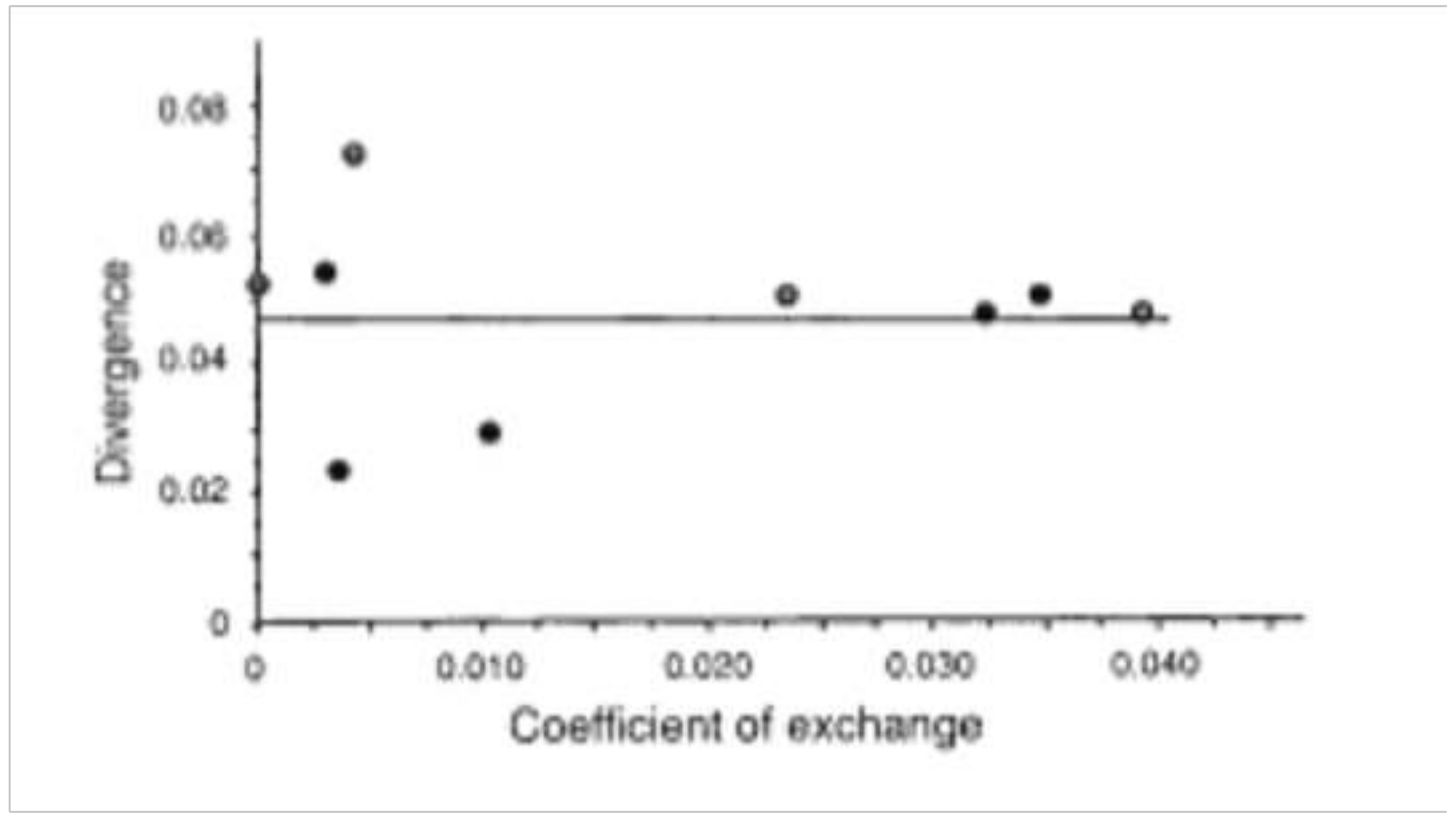


recombination
recombination
Position 1
Position 240
Position 241
Position 327
Position 328
Ancestral recombination graph

Polymorphism vs. recombination



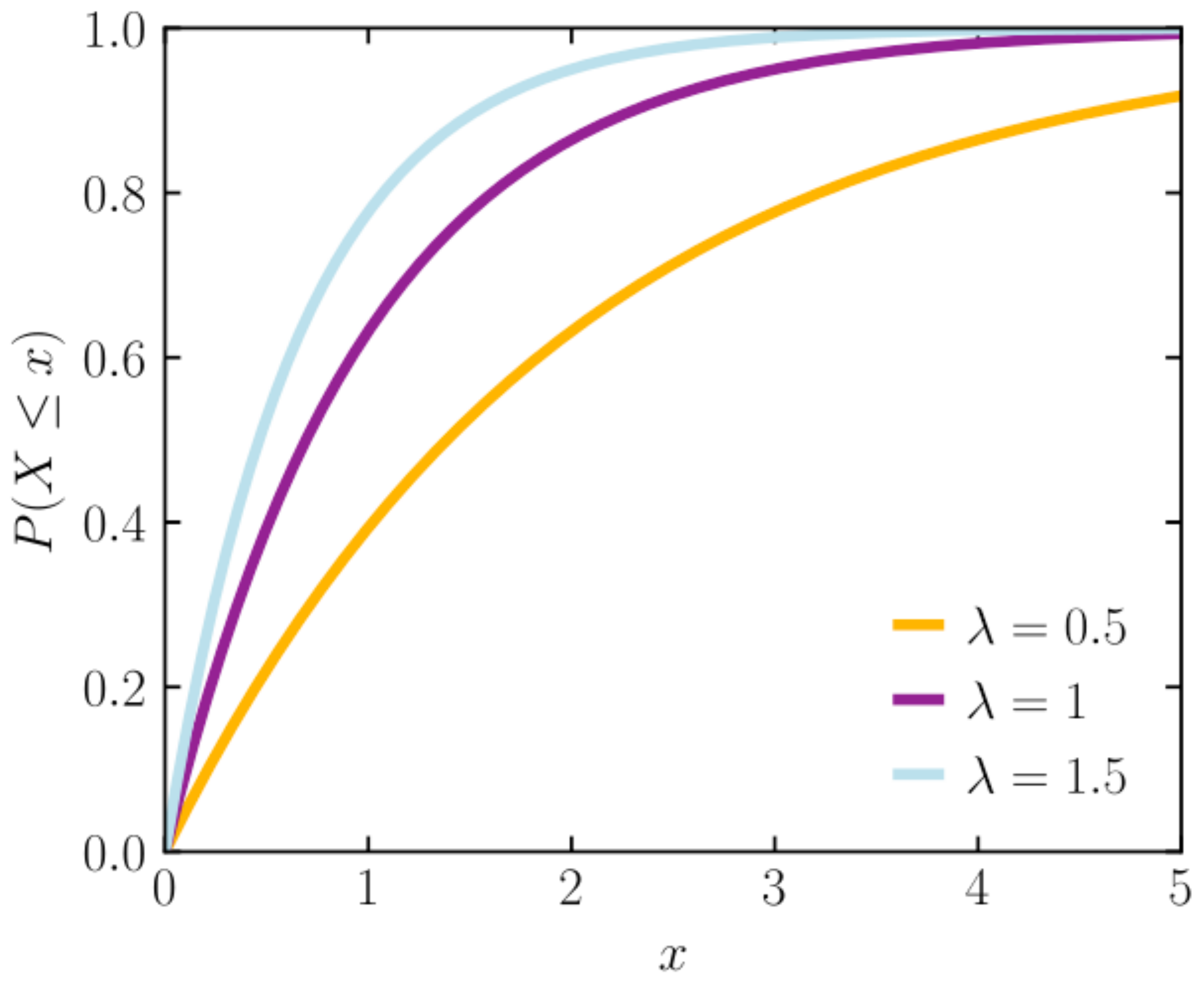
Divergence vs. recombination



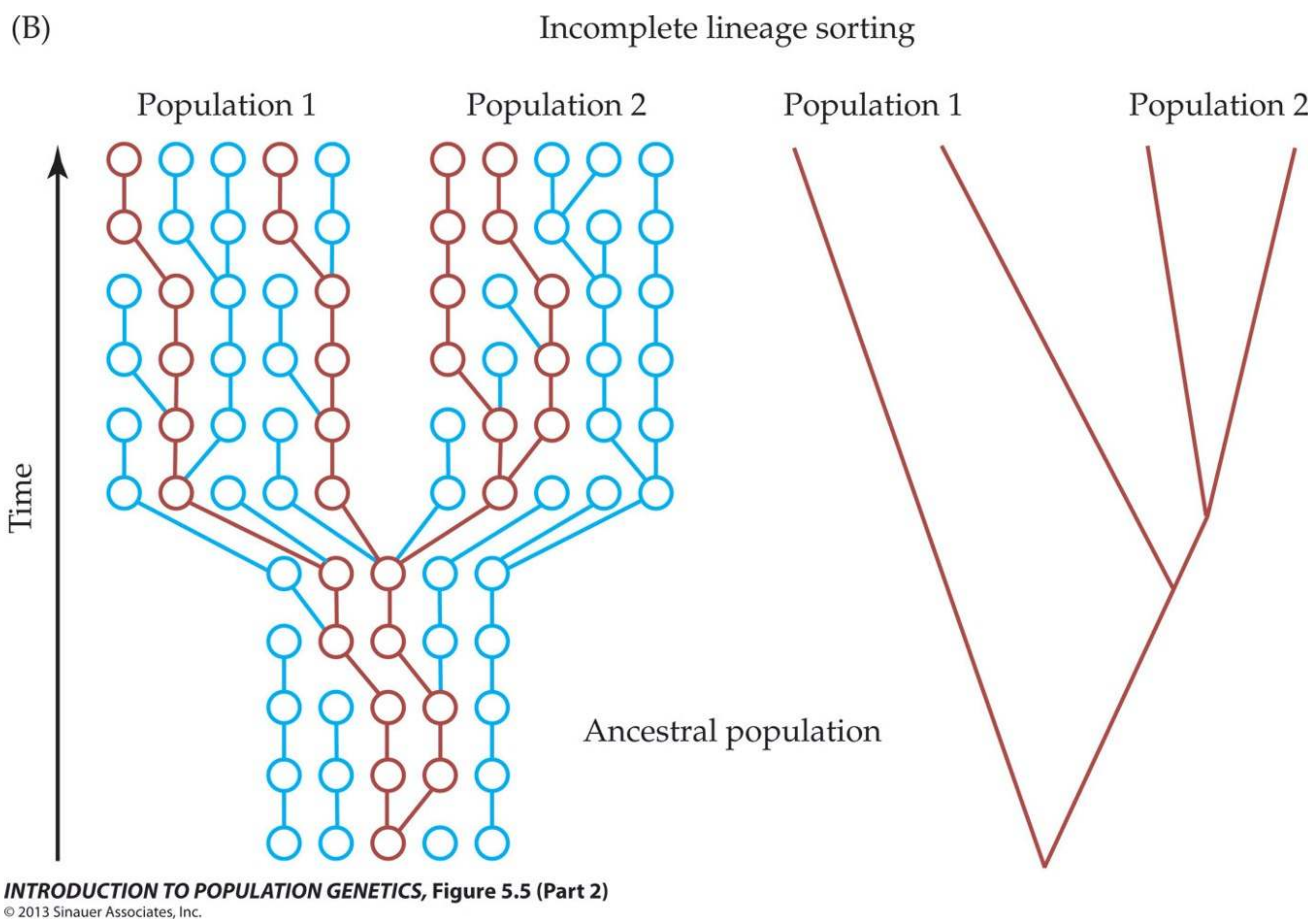
Begun and Aquadro (1992)

Cumulative distribution function of exponential: $1\text{-}e^{-\lambda x}$

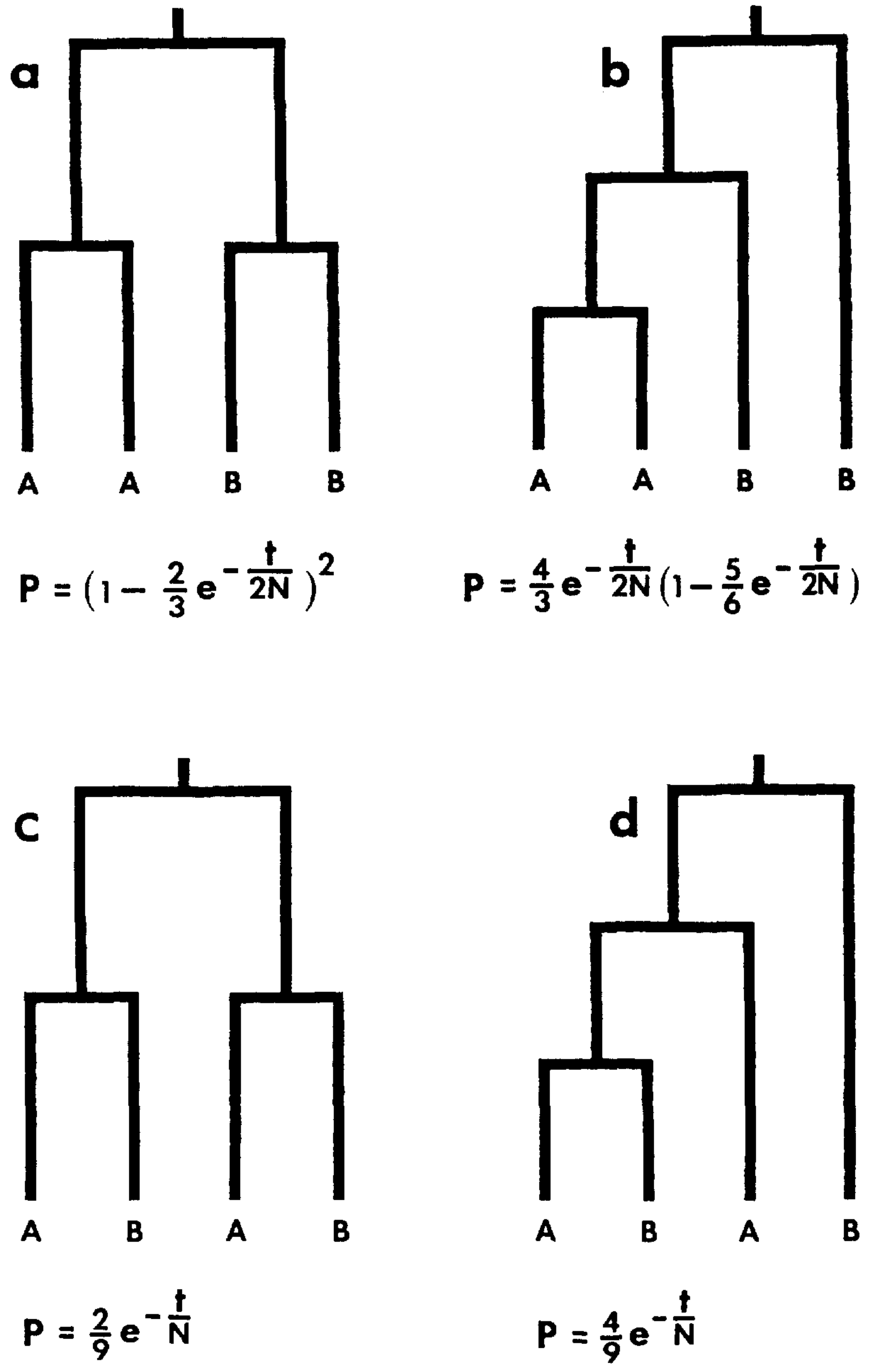
(For two lineages, lambda=1)



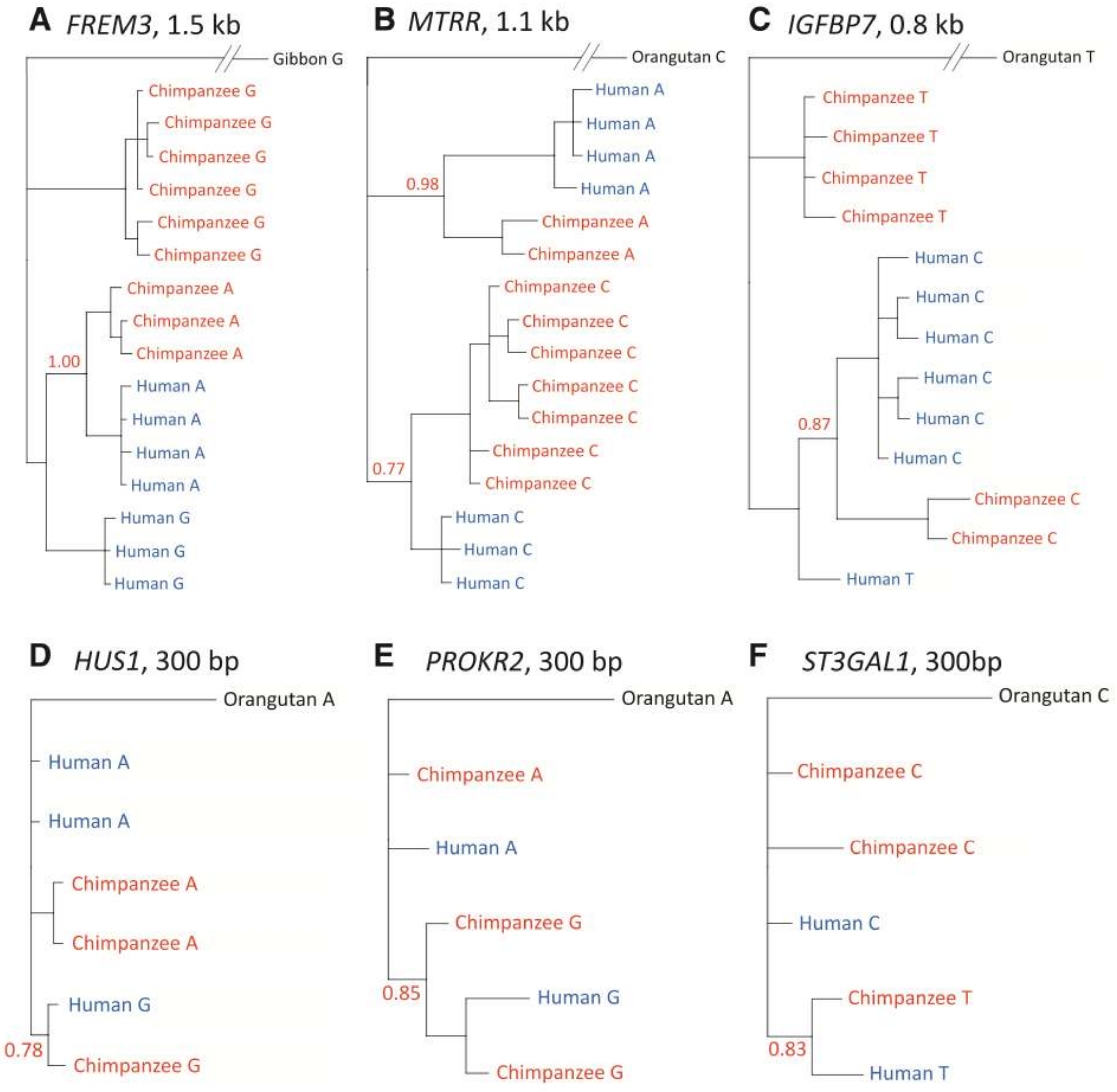
Wikimedia



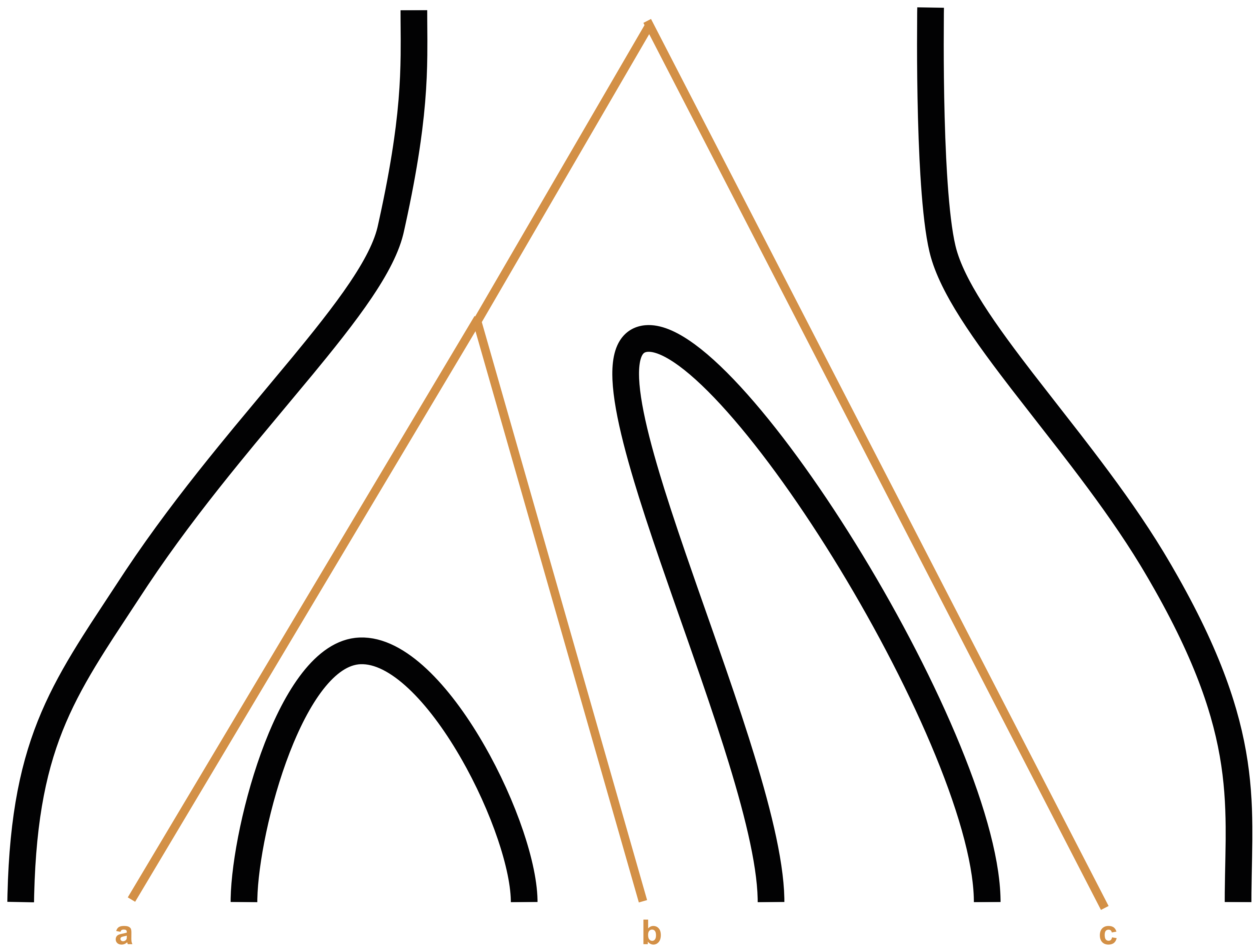
Nielsen and Slatkin (2013)

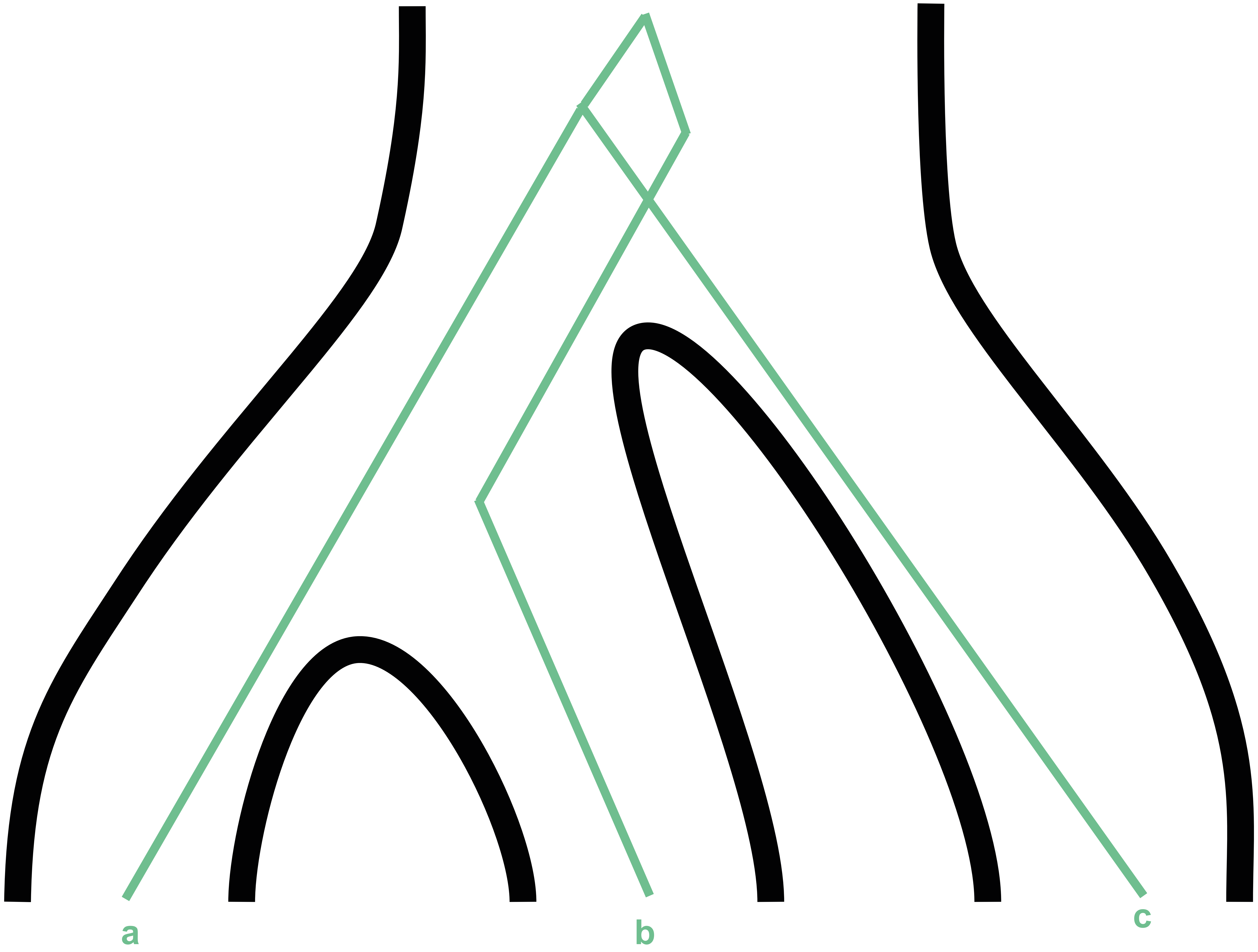

a
A A B B
$P = \left(1 - \frac{2}{3} e^{-\frac{t}{2N}}\right)^2$
b
A A B B
$P = \frac{4}{3} e^{-\frac{t}{2N}} \left(1 - \frac{5}{6} e^{-\frac{t}{2N}}\right)$
c
A B A B
$P = \frac{2}{9} e^{-\frac{t}{N}}$
d
A B A B
$P = \frac{4}{9} e^{-\frac{t}{N}}$

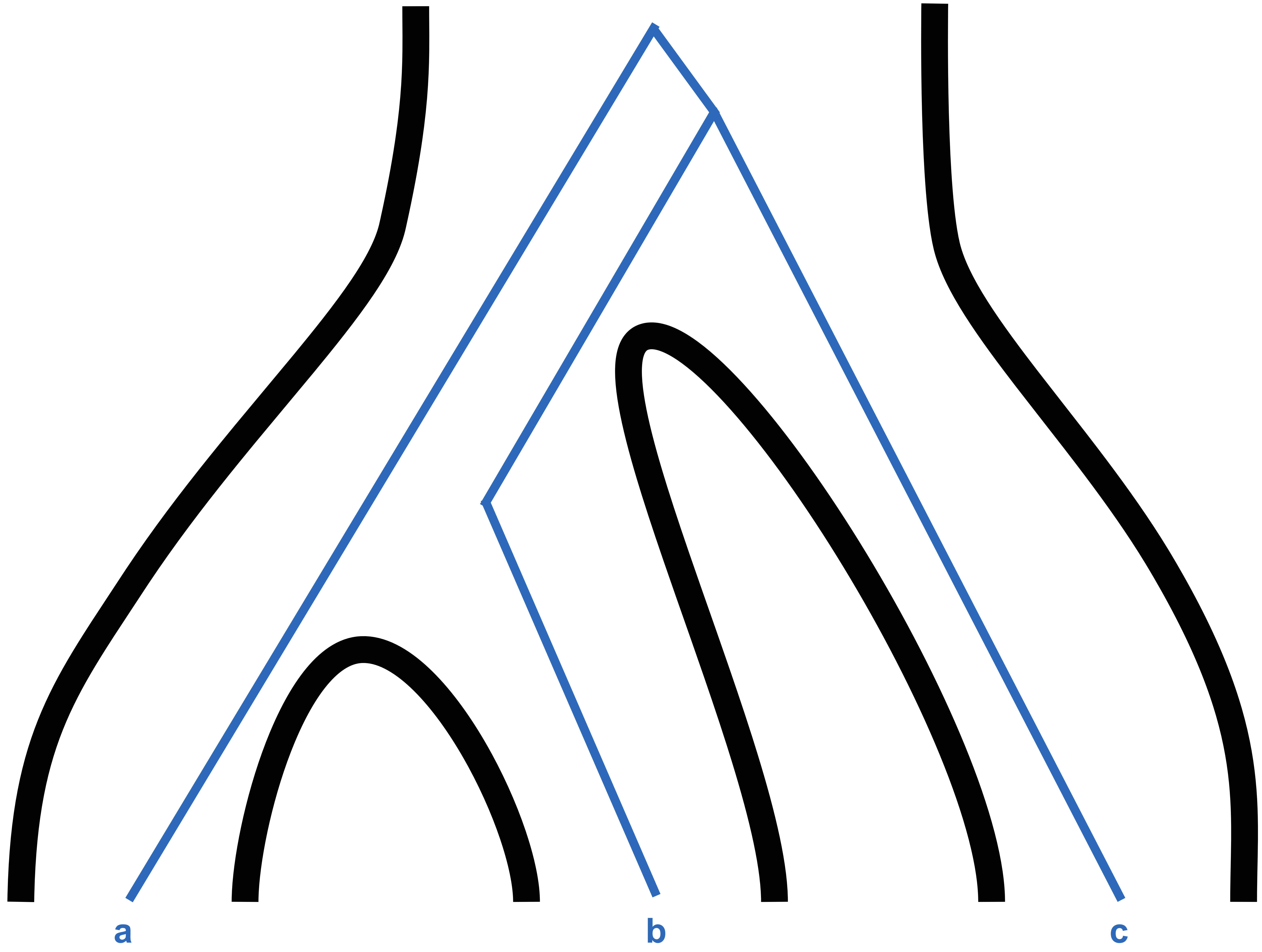
Tajima (1983)



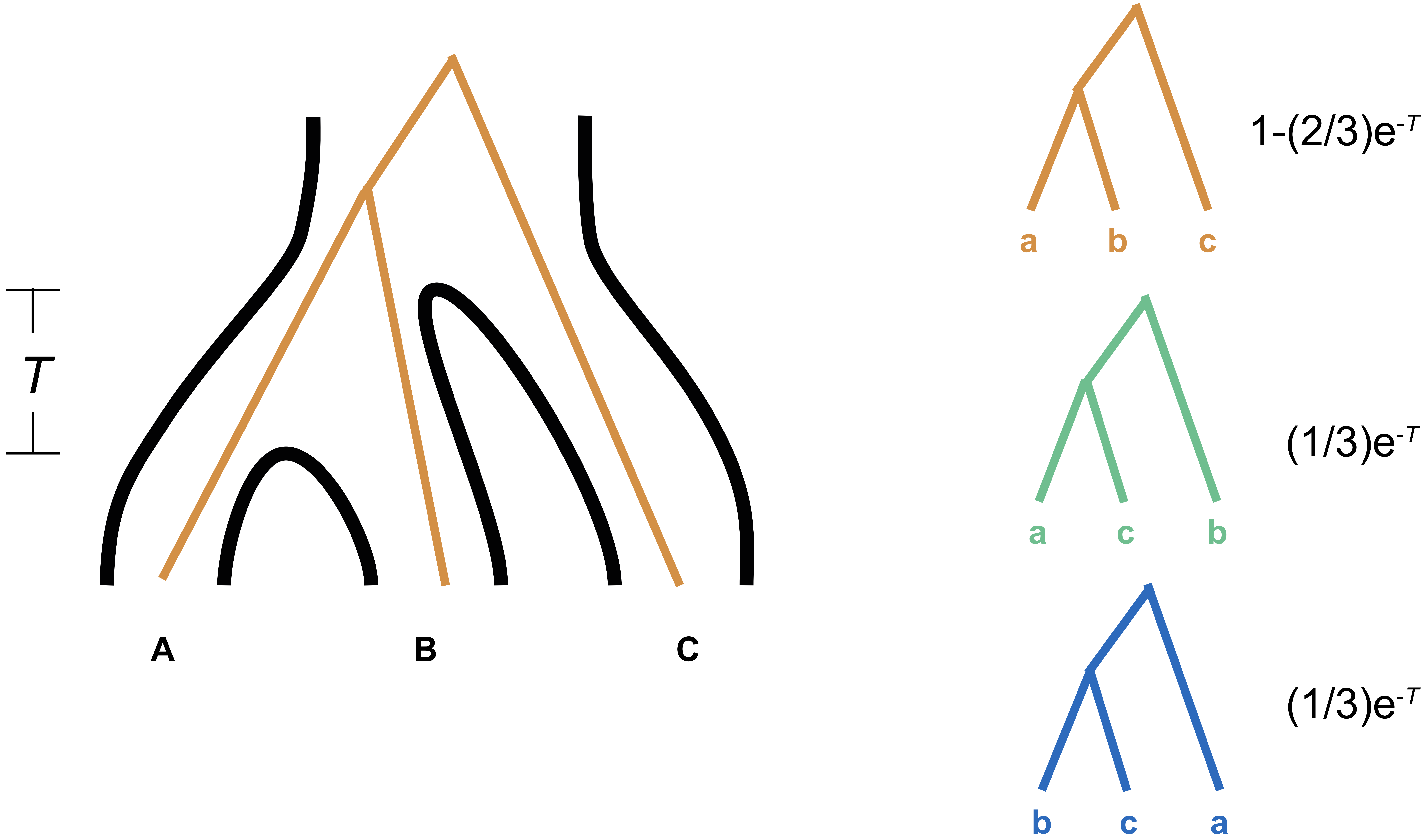
Leffler et al. (2013)

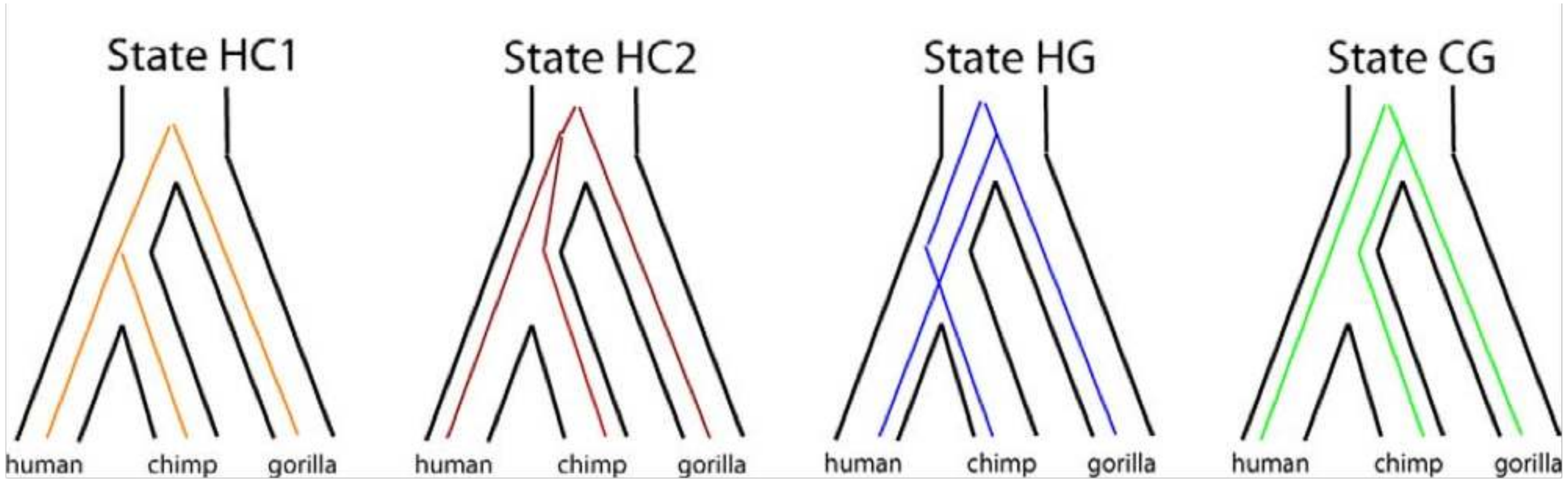

a
b
c

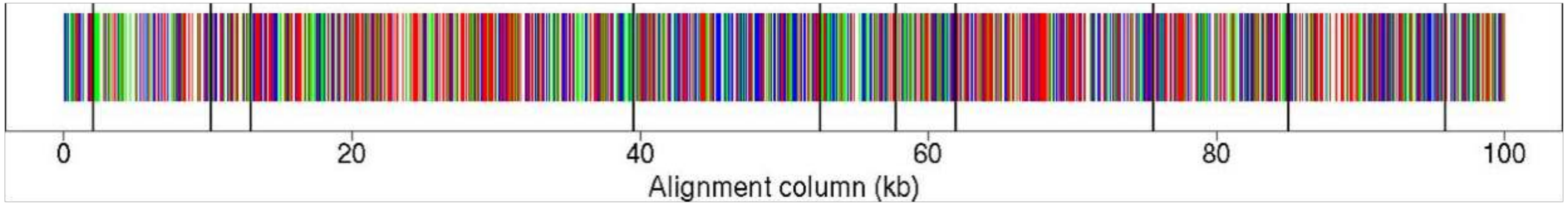

a
b
c


a
b
c

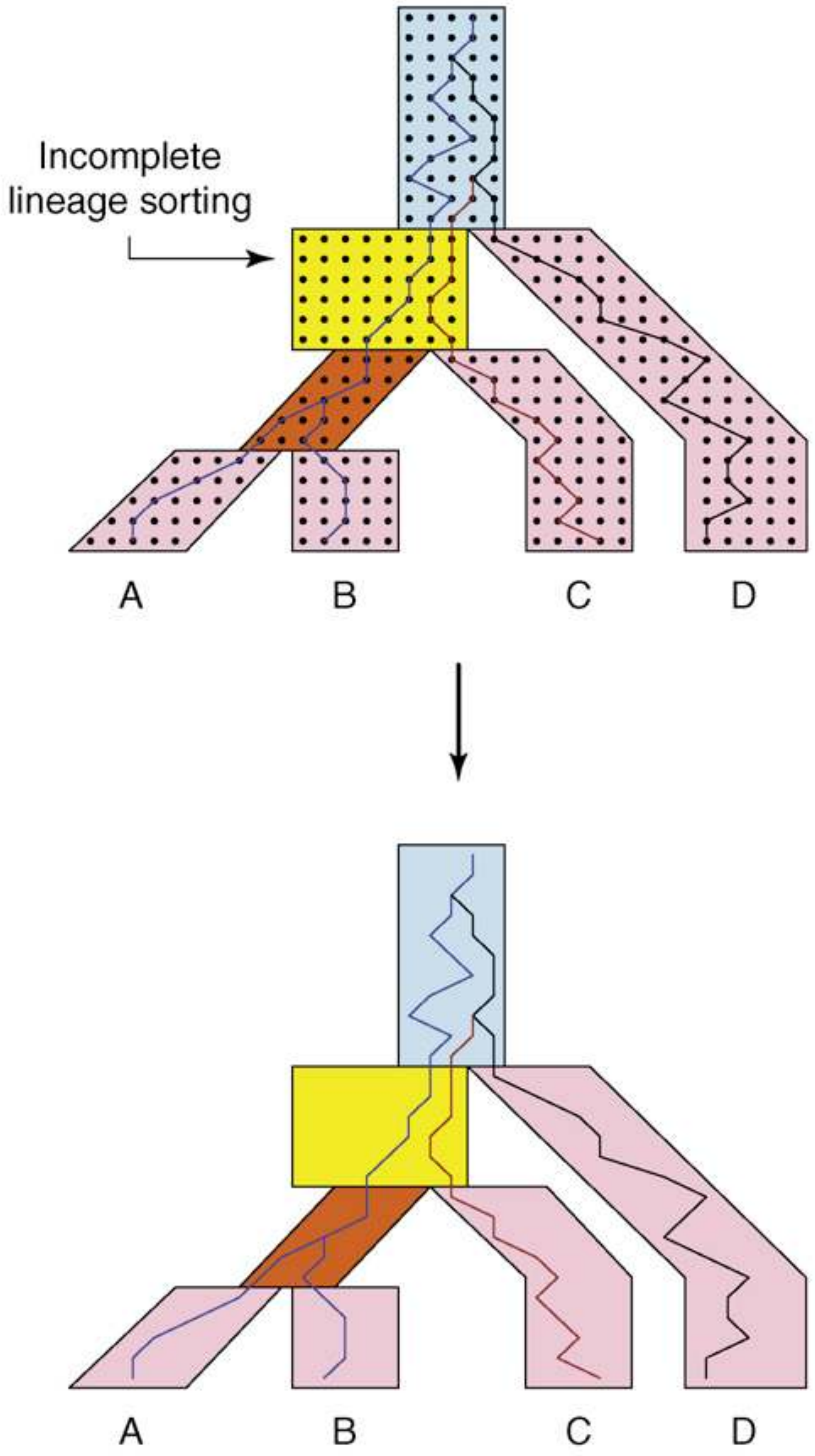
The multispecies coalescent model



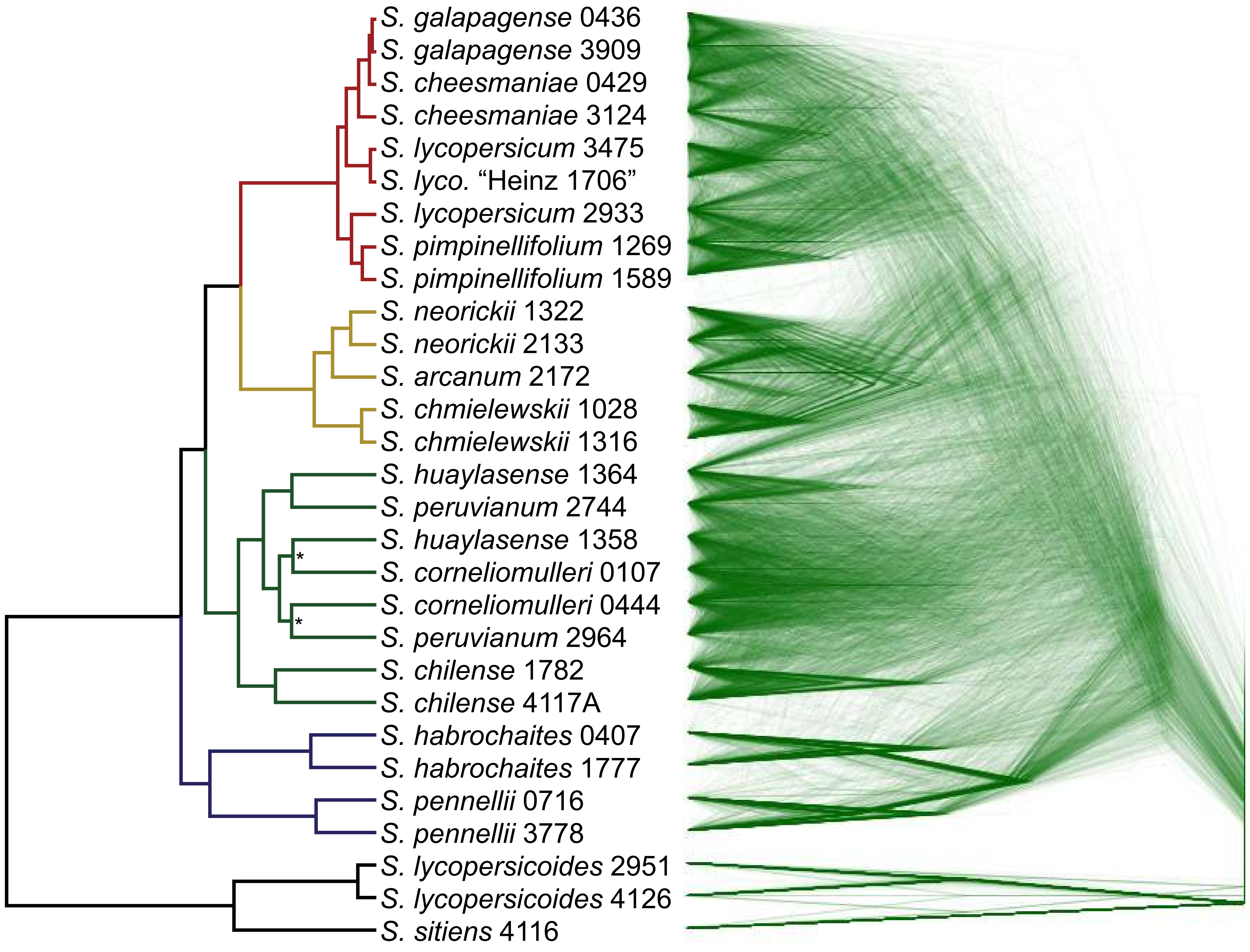




Hobolth et al. (2007)

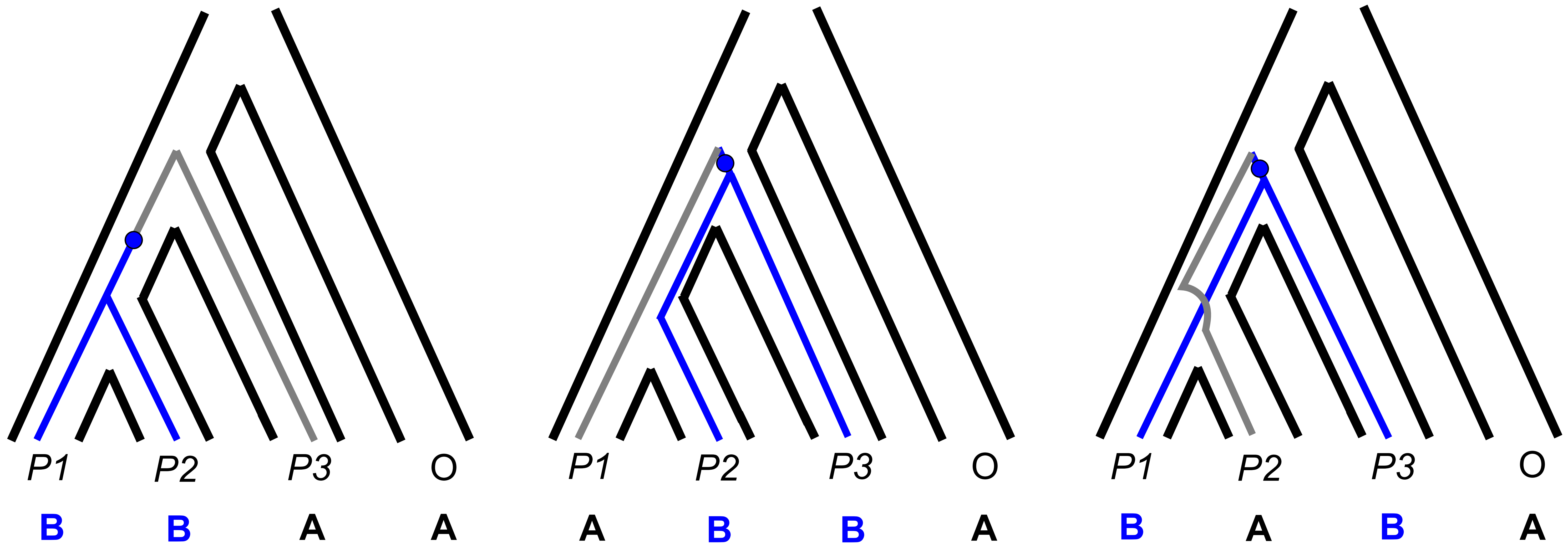


Degnan and Rosenberg (2009)



Pease et al. (2016)

ILS only:



ILS + introgression: