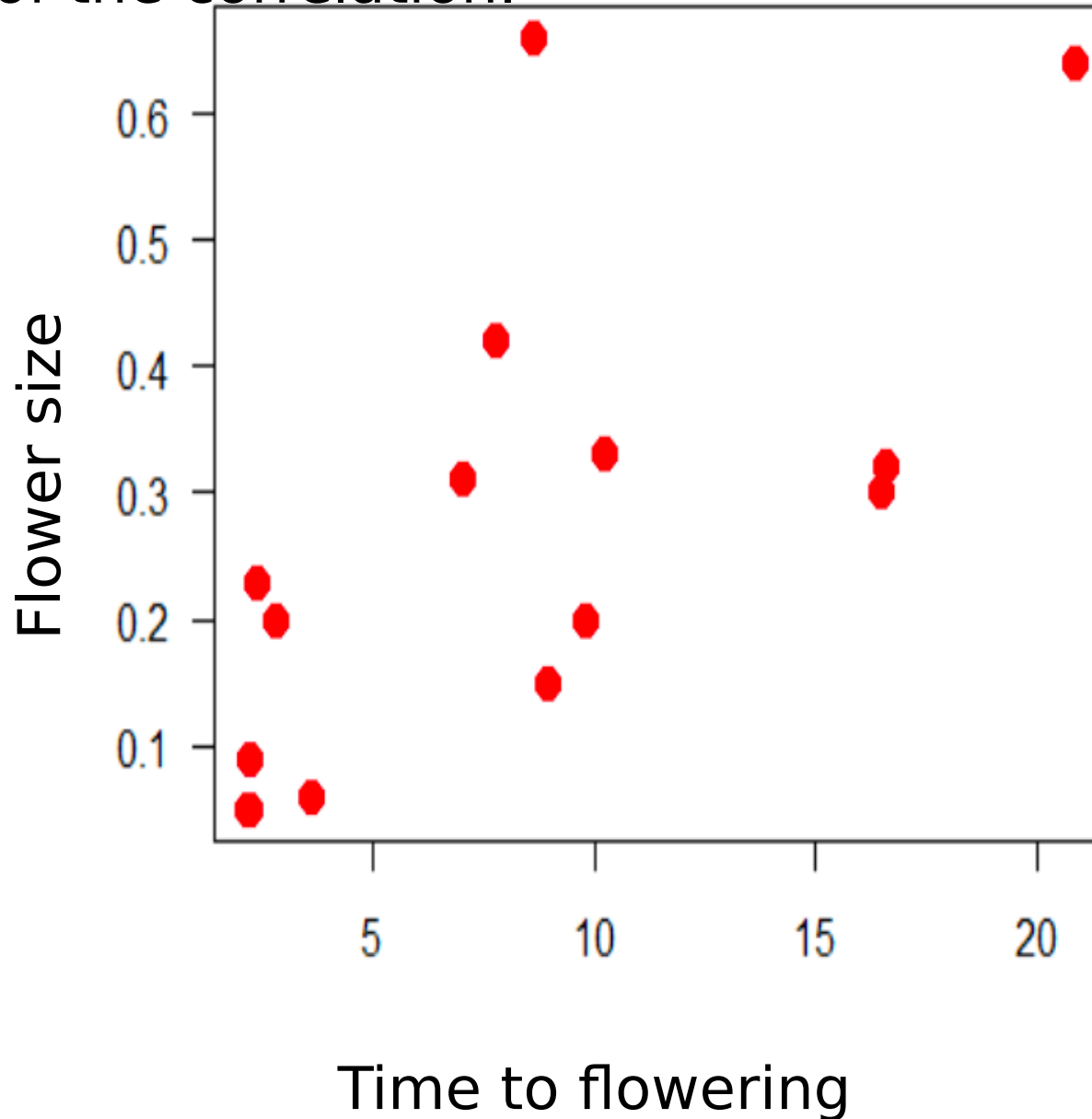


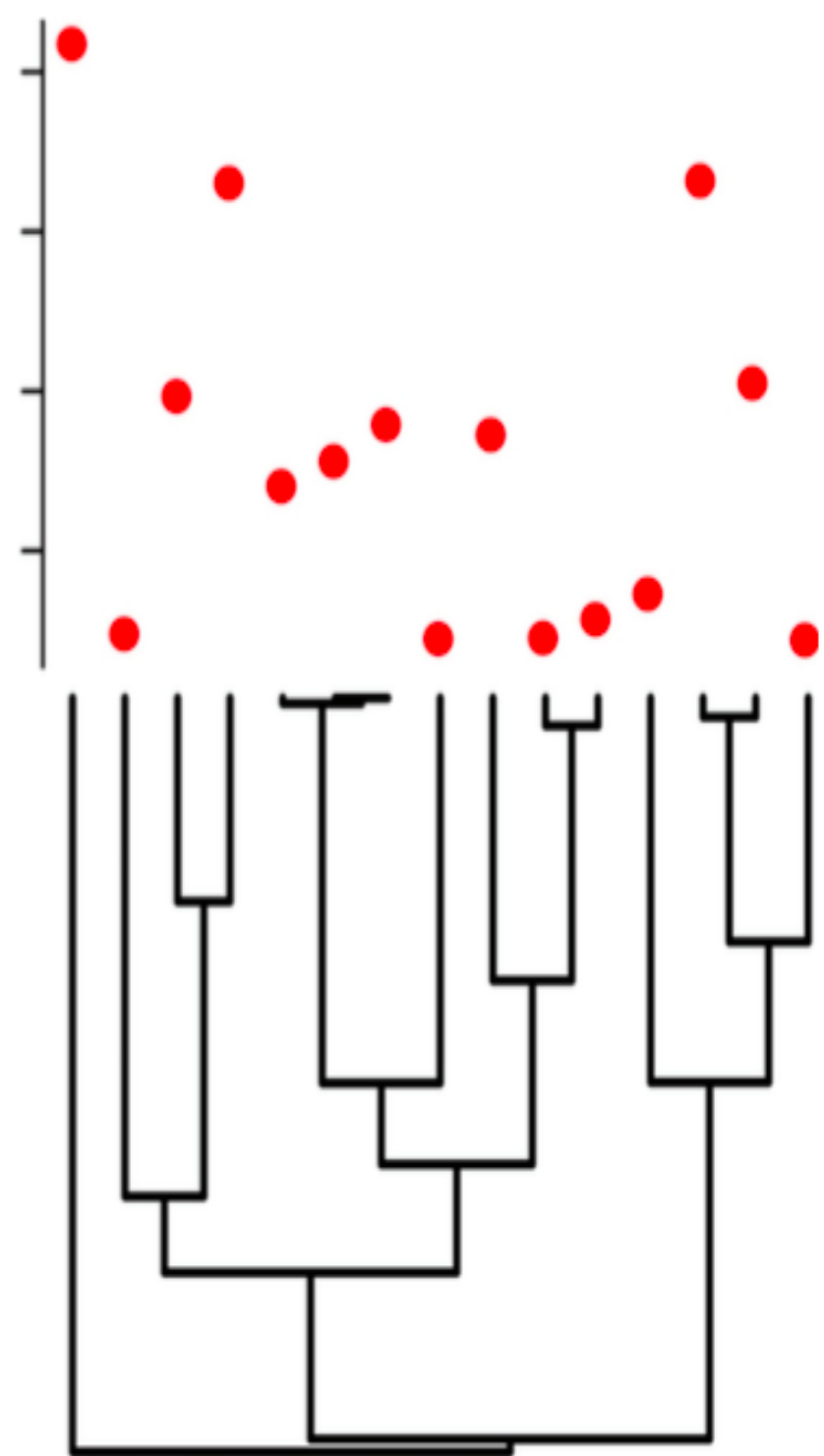
## An example of species data

Data reveal a positive association between the two variables. We would like to estimate the strength of the correlation.



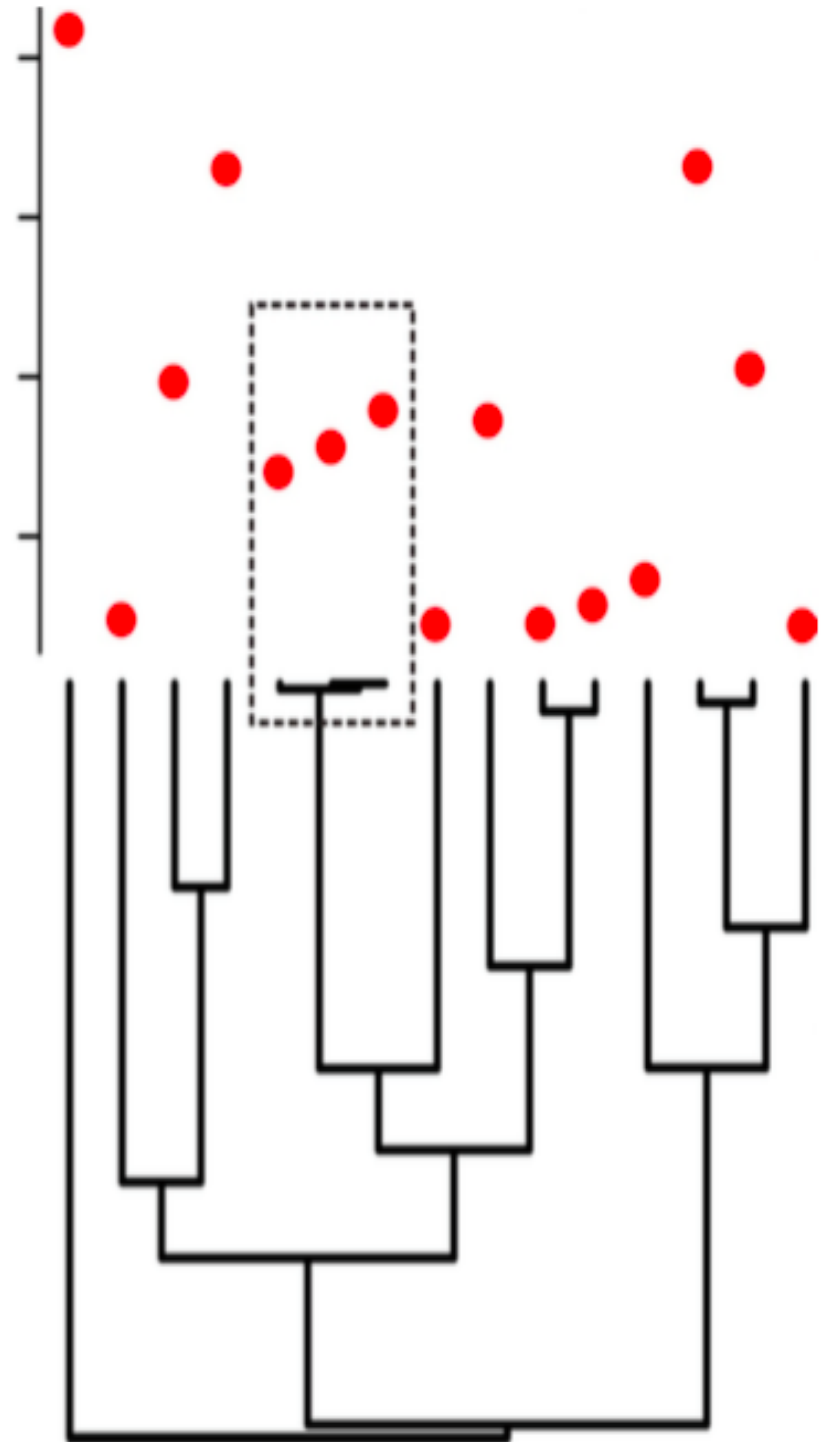
## The problem with species data

The data points (species) are not independent.



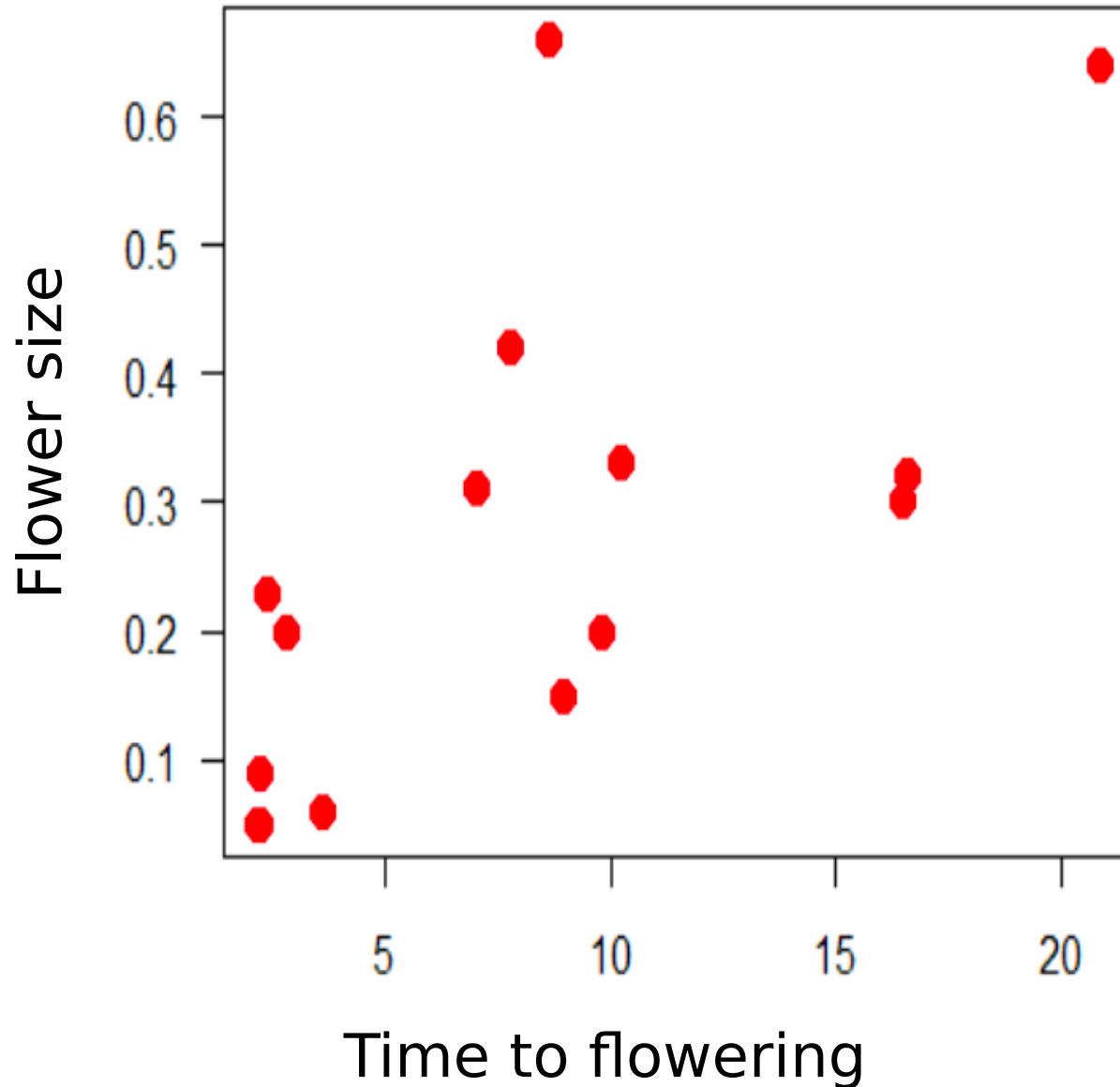
## The problem with species data

Closely related species tend to have similar trait values.



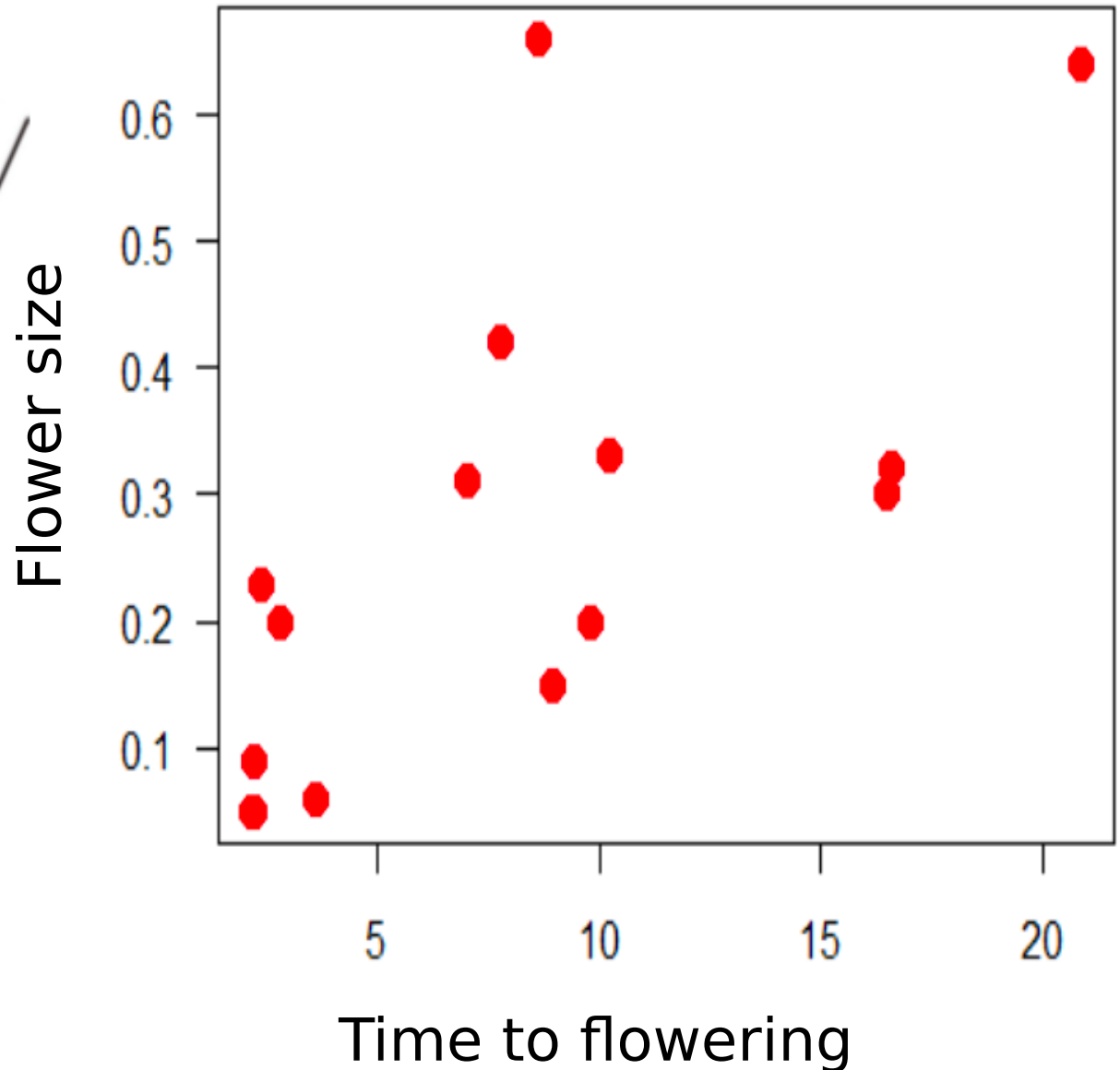
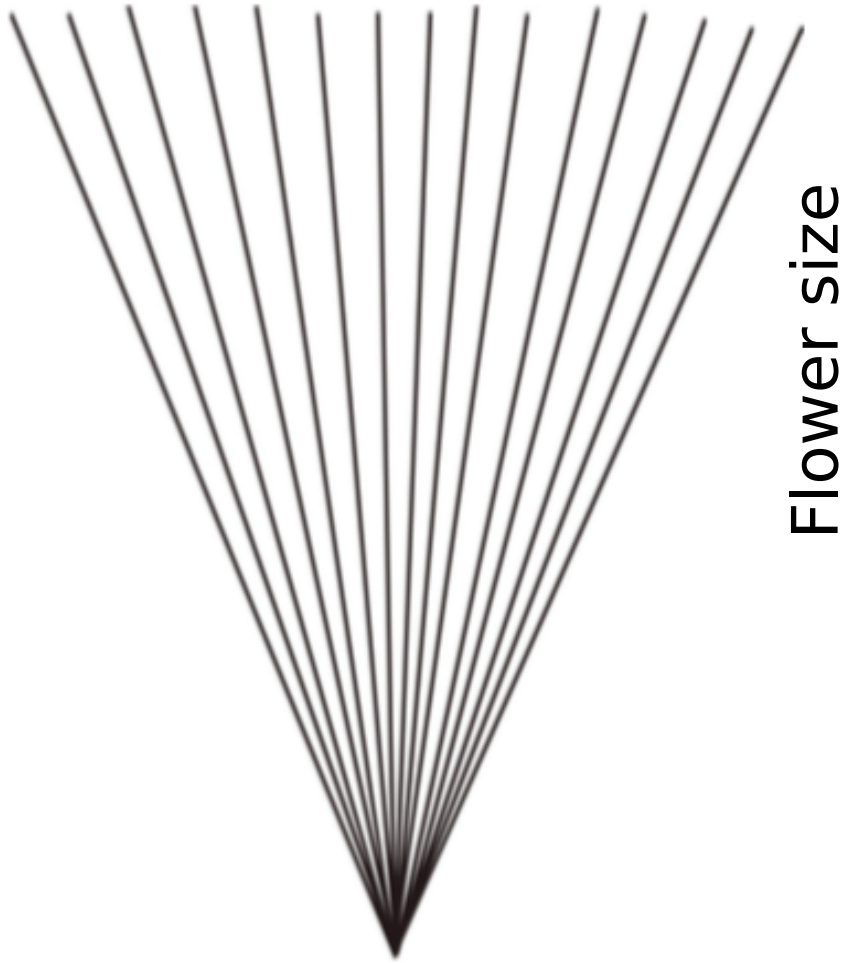
## The problem with species data

Non-independence of the species data points violates a major assumption of conventional statistical methods for data analysis.

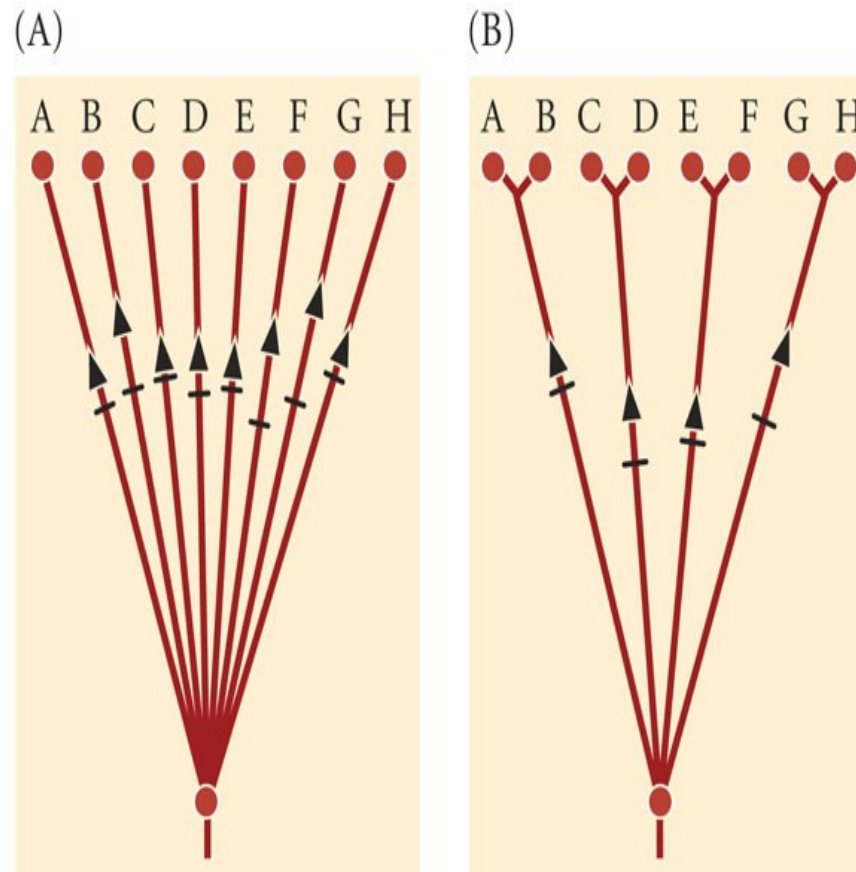


## What we are really assuming when we ignore phylogeny

That the species are related as in a “star” phylogeny, which leads to no phylogenetic signal.



# Independence assumption



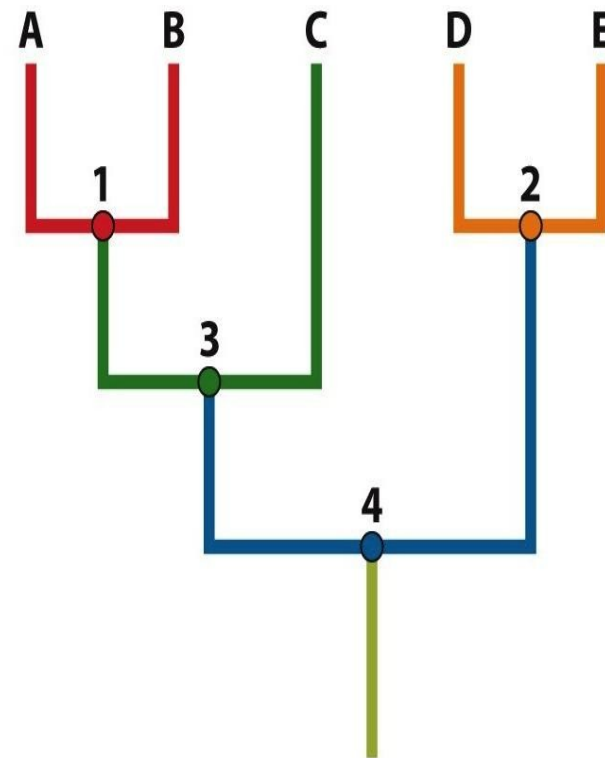
EVOLUTION, Figure 11.21 © 2005 Sinauer Associates, Inc.

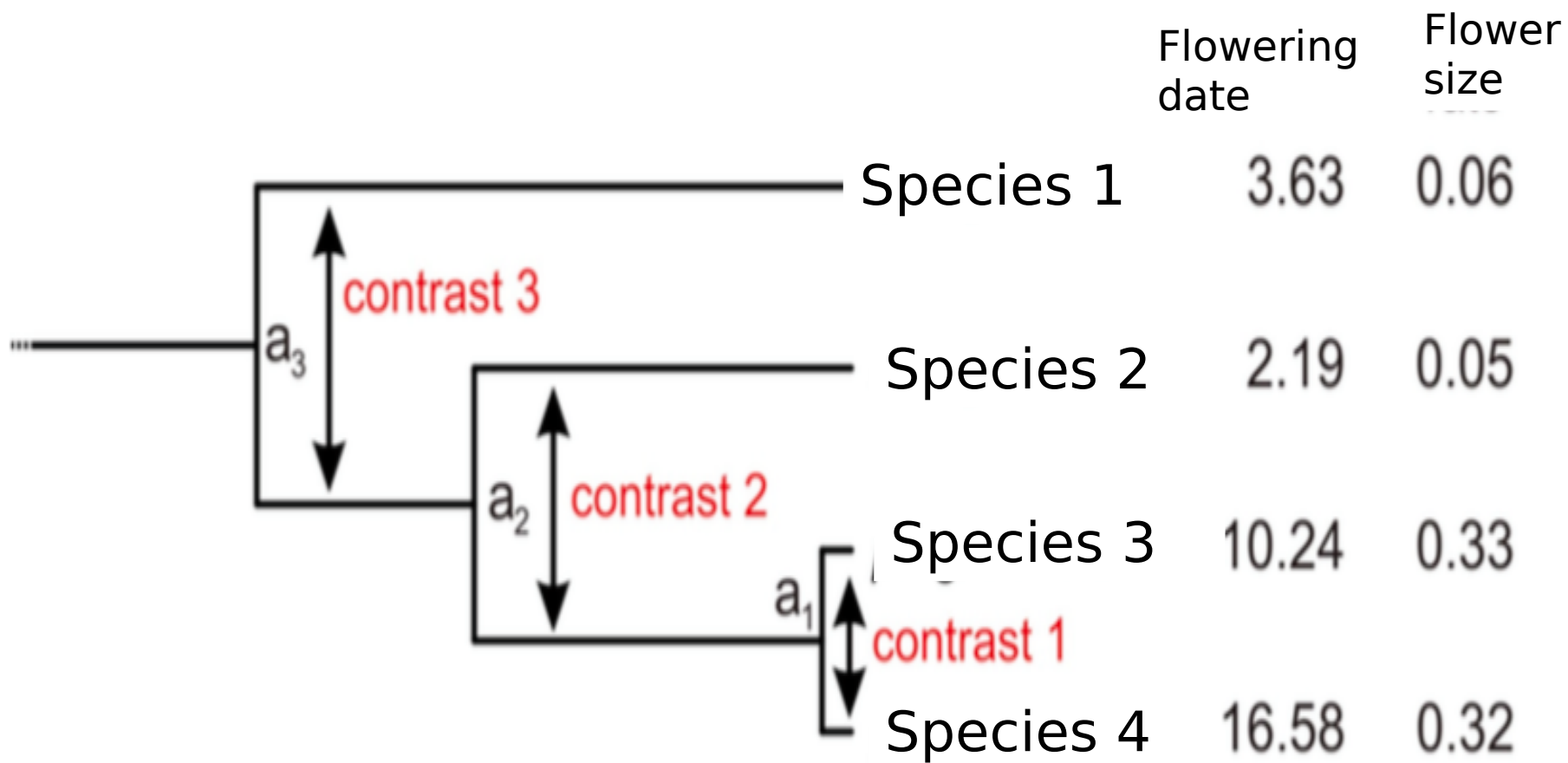
Characteristic evolved: 8 times  
4 times

Shared ancestry (branches) violates  
independence assumption!

# Phylogenetic Independent Contrasts (PIC)

- A method that accounts for the phylogeny when analyzing data from populations/species
- Take contrast (A-B) divided by branch length, then 1-C, 3-2, etc.
  - Each contrast is independent
  - Never “double count” branches!
- Analyze the contrasts rather than the tip data



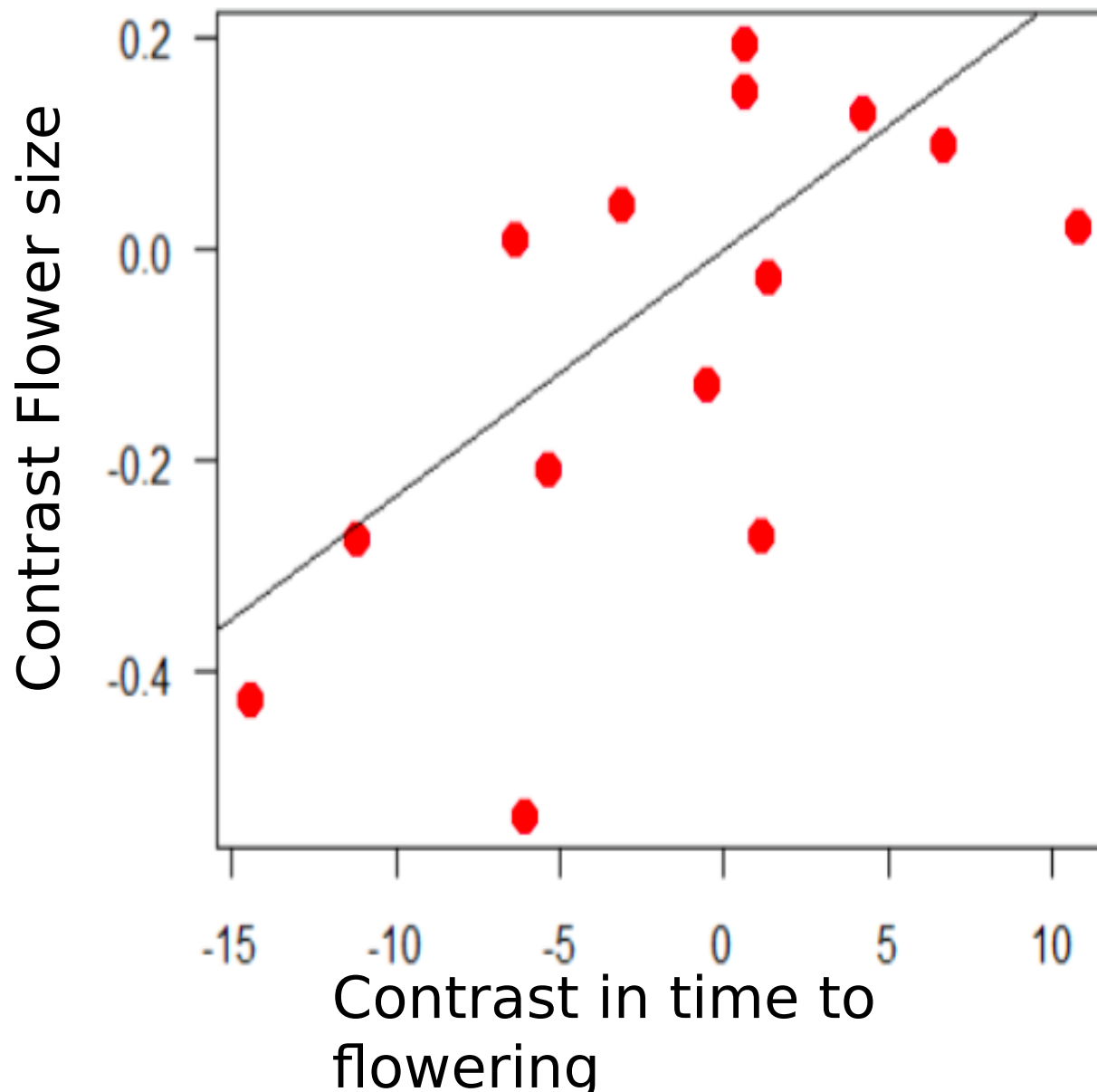




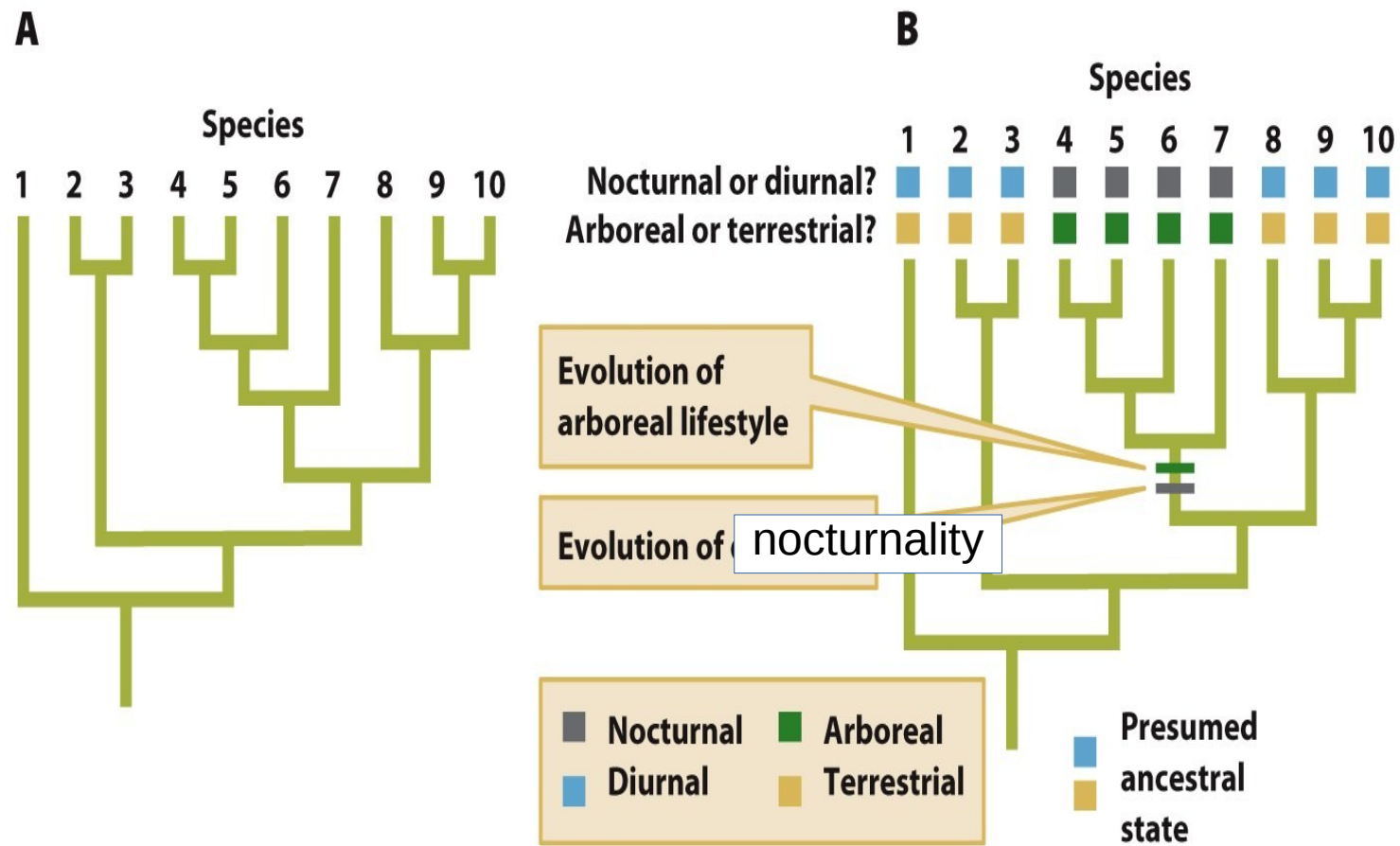
## Phylogenetically independent contrasts

Because the direction of the contrast is arbitrary, the correlation or regression using independent contrasts is forced through origin (0,0).

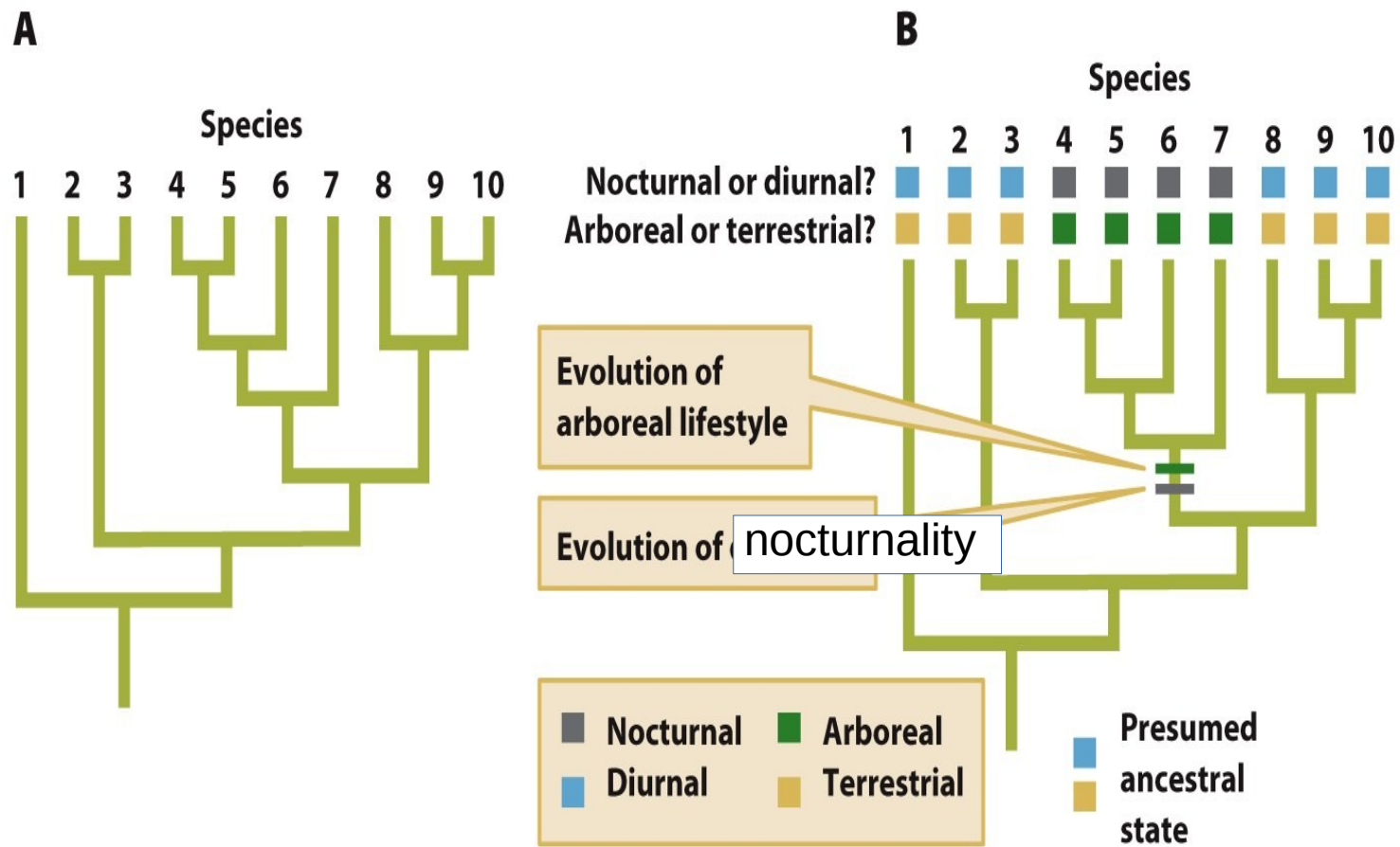
Positive correlation confirmed!



Did evolution of nocturnality select for an arboreal lifestyle?



Being nocturnal and arboreal evolved once  
 You have little statistical power to say that the two are  
 related



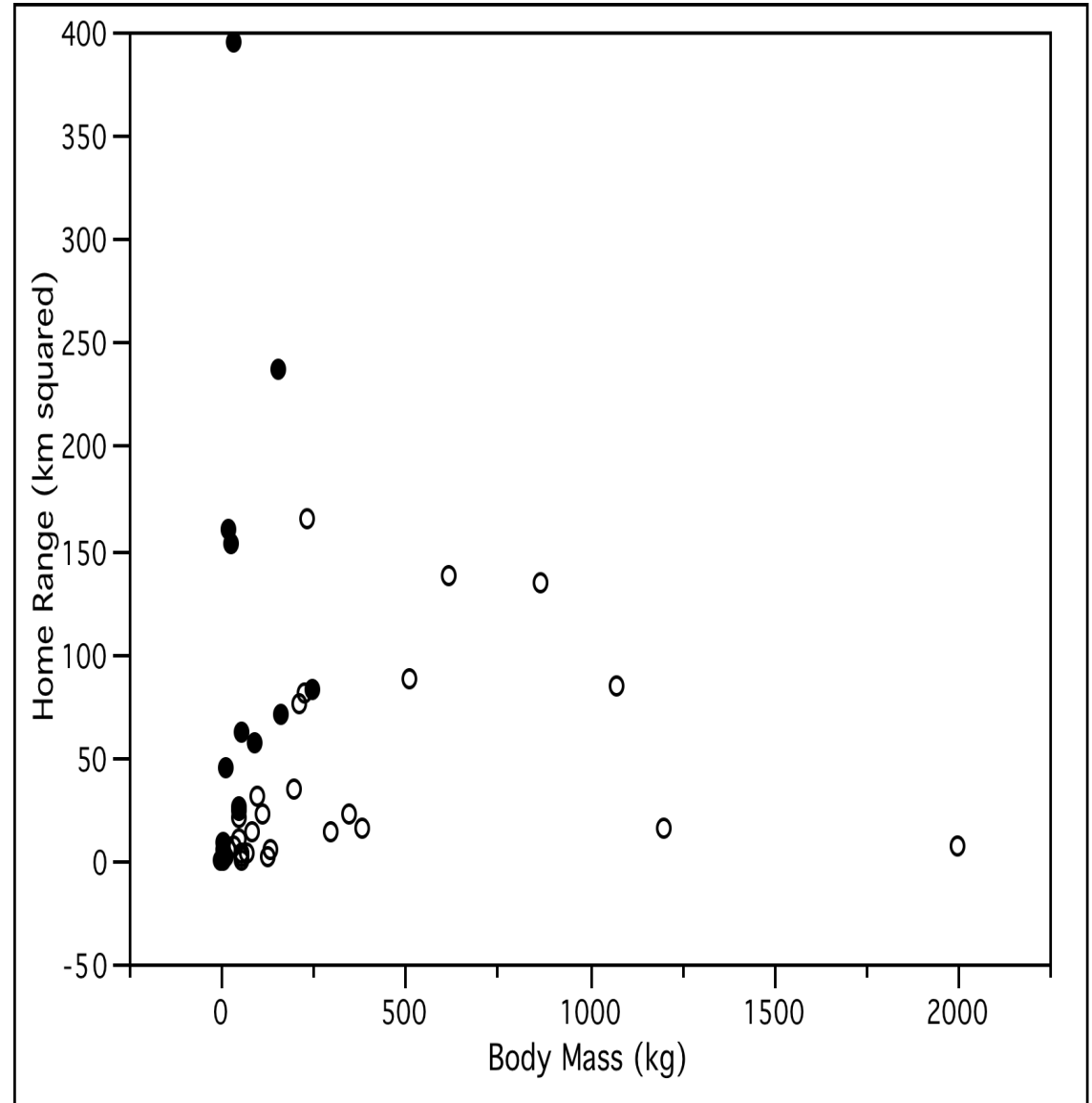
# PIC Example: Home Range Size

Carnivores



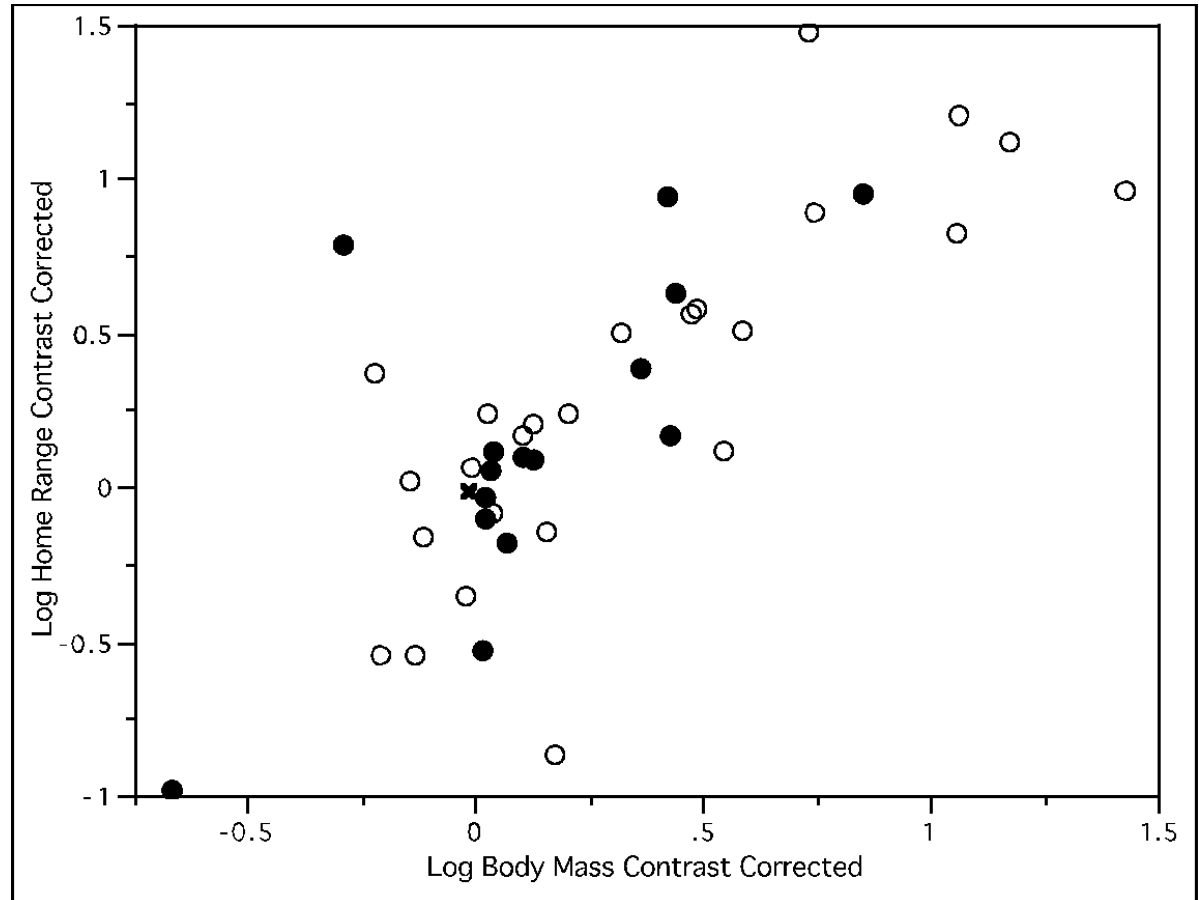
have larger home range sizes than

ungulates

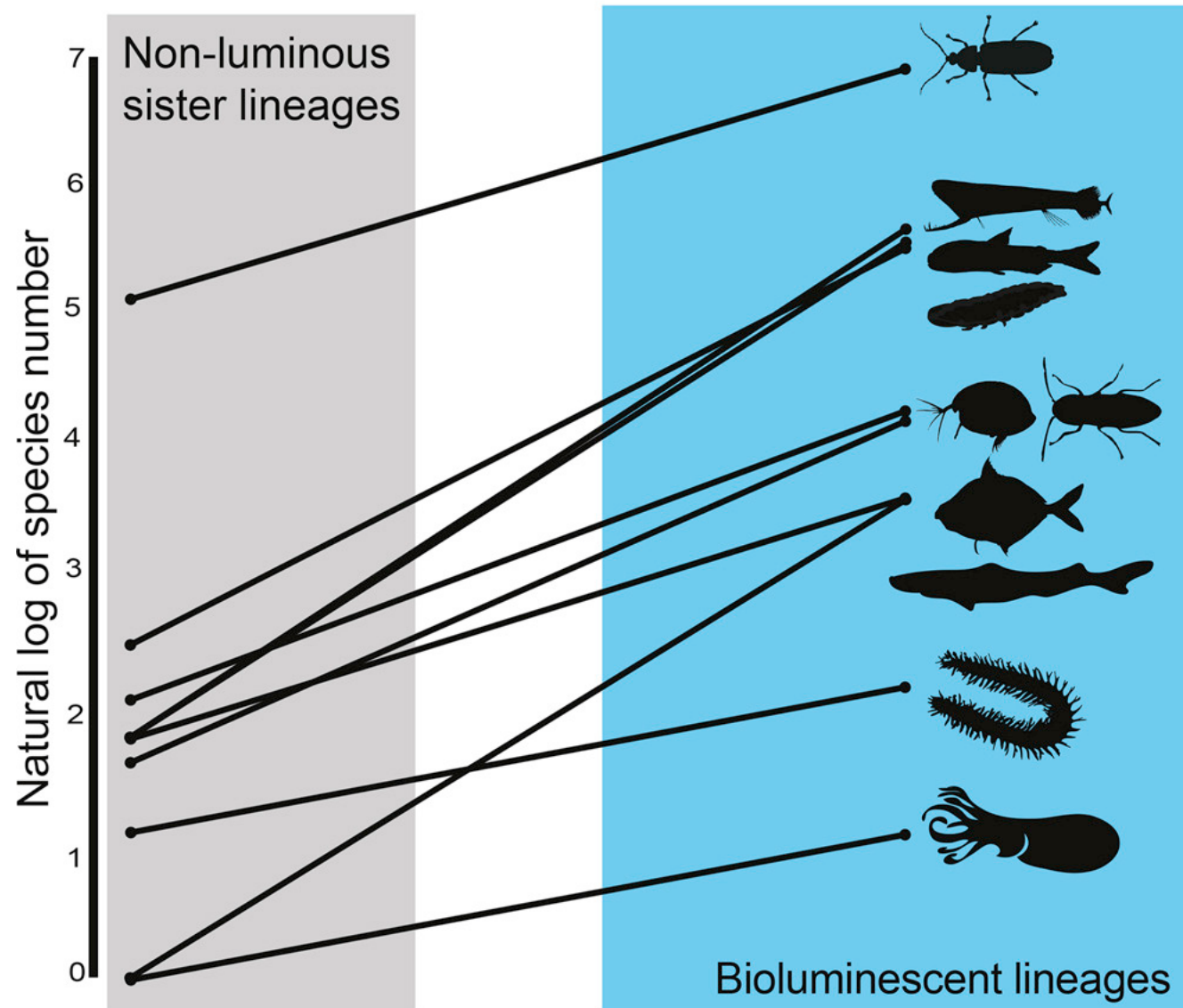


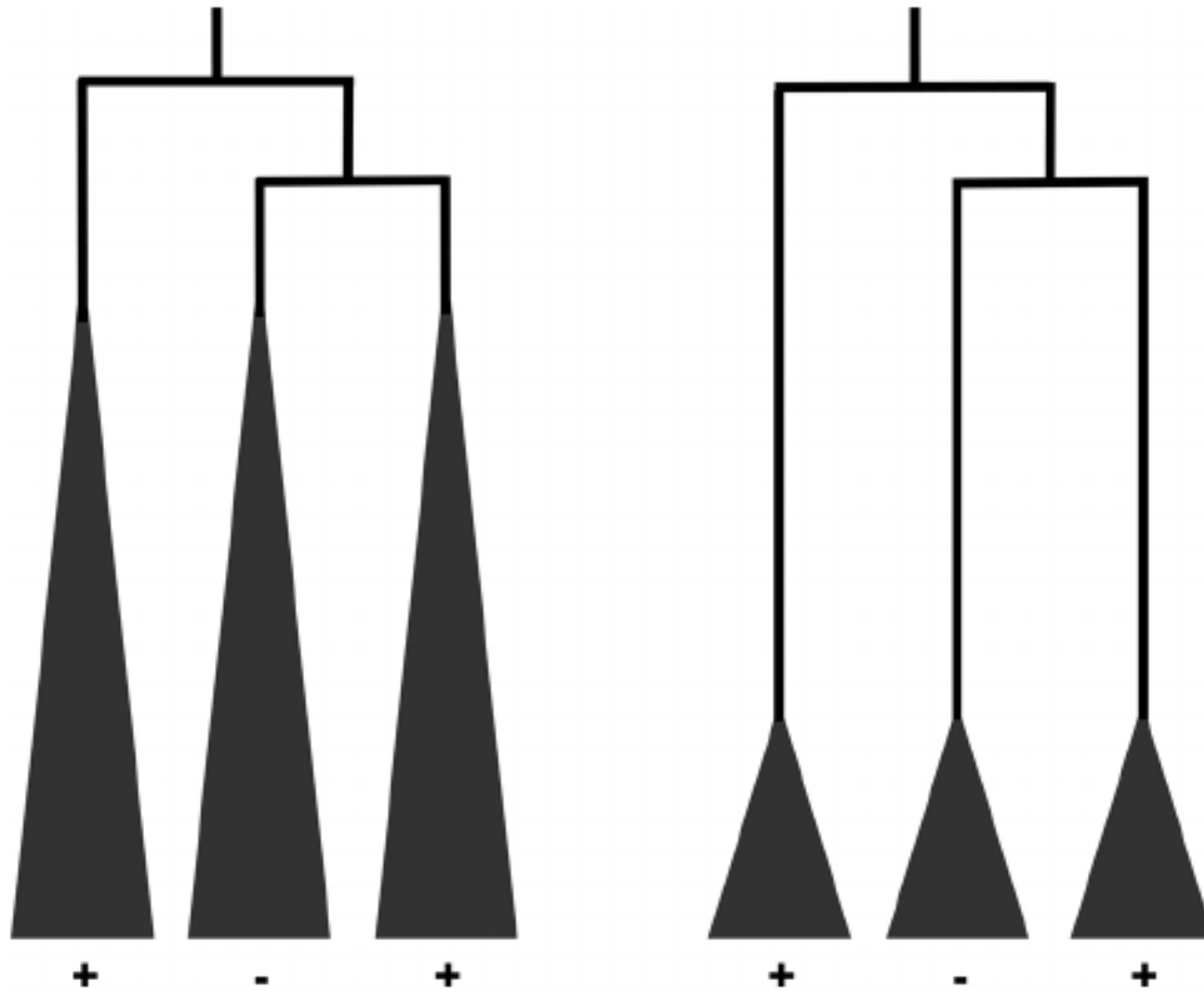
# PIC Example: Home Range Size

But not when you  
account for  
phylogeny!



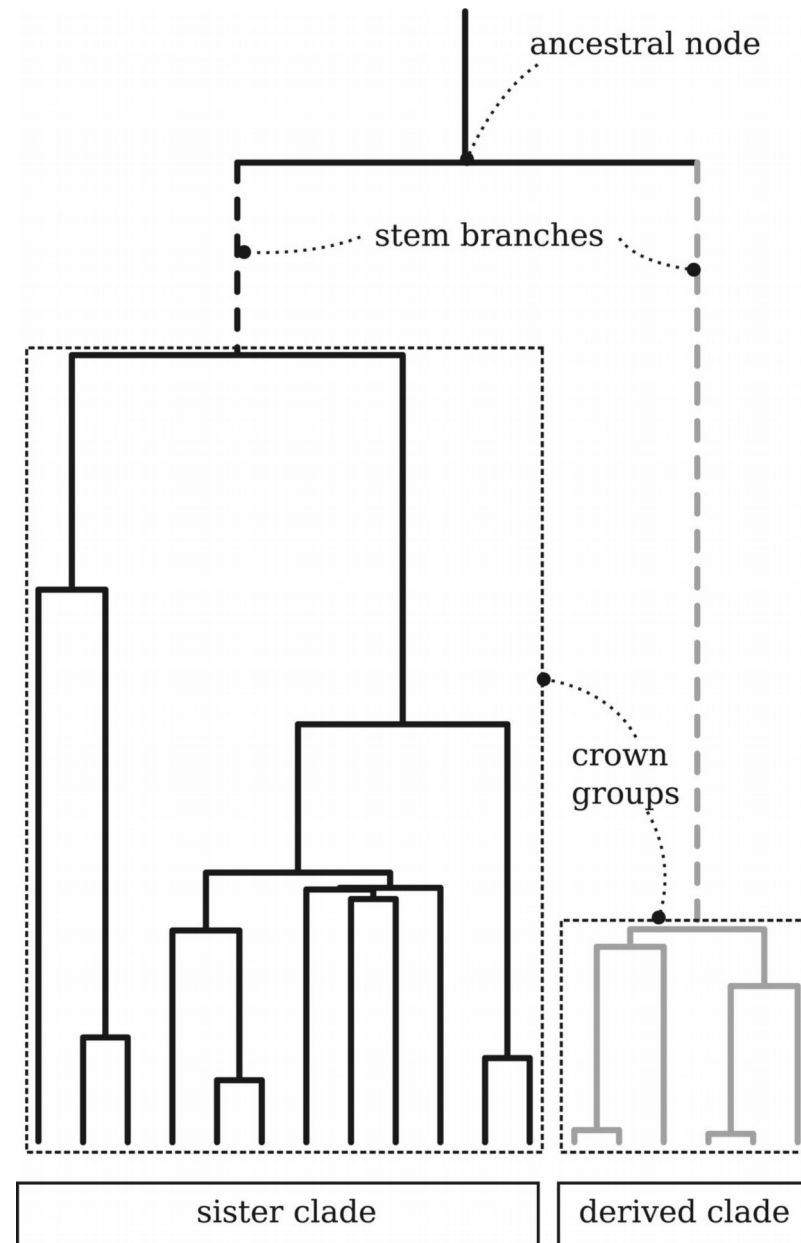
## Sexually-selected bioluminescence leads to more species





Which tree has a higher probability of convergence?

long branches provide  
more opportunity for trait  
evolution and less  
diversification



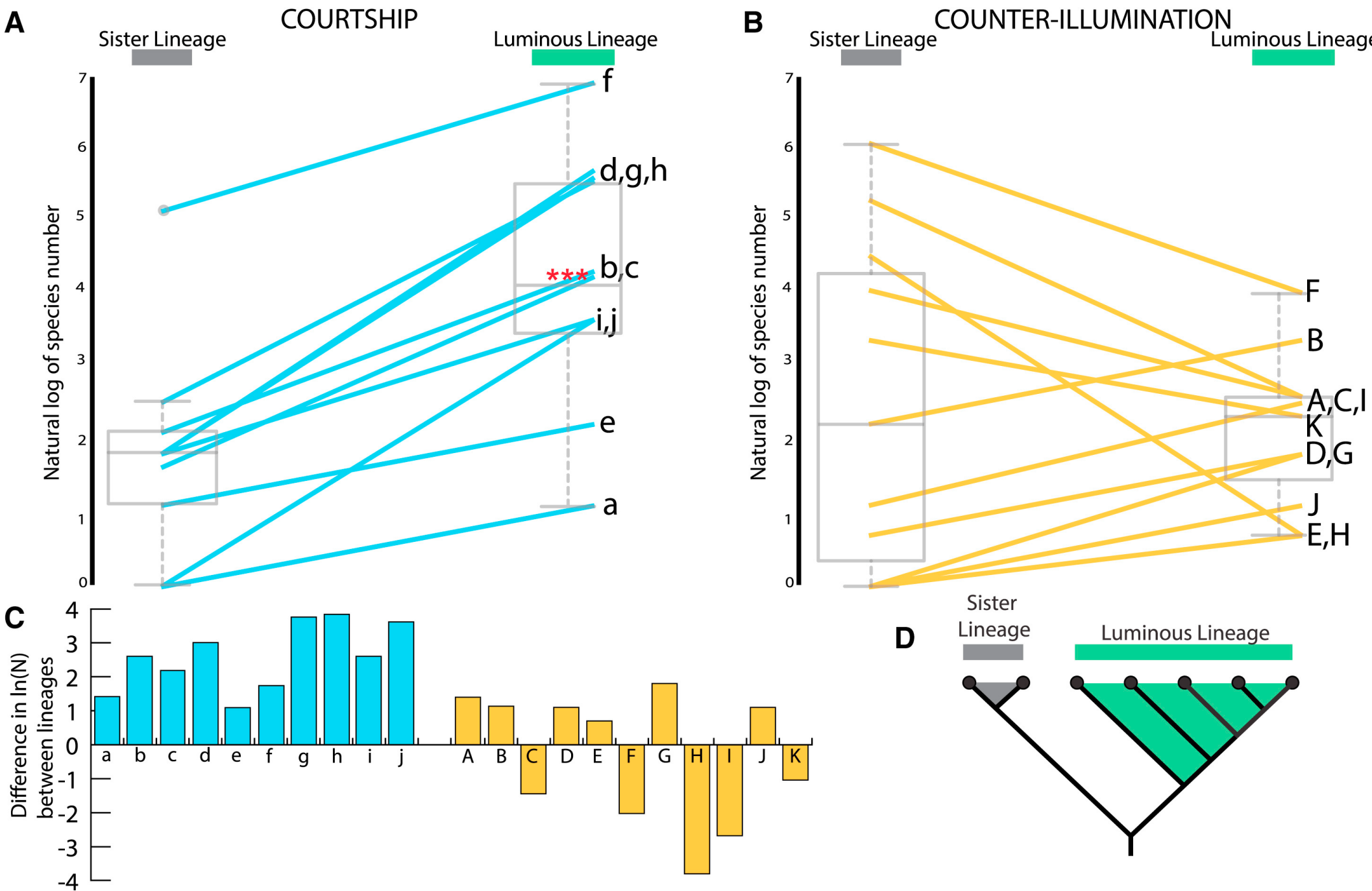
From: Standard Sister Clade Comparison Fails when Testing Derived Character States

Syst Biol. 2014;63(4):601-609. doi:10.1093/sysbio/syu024

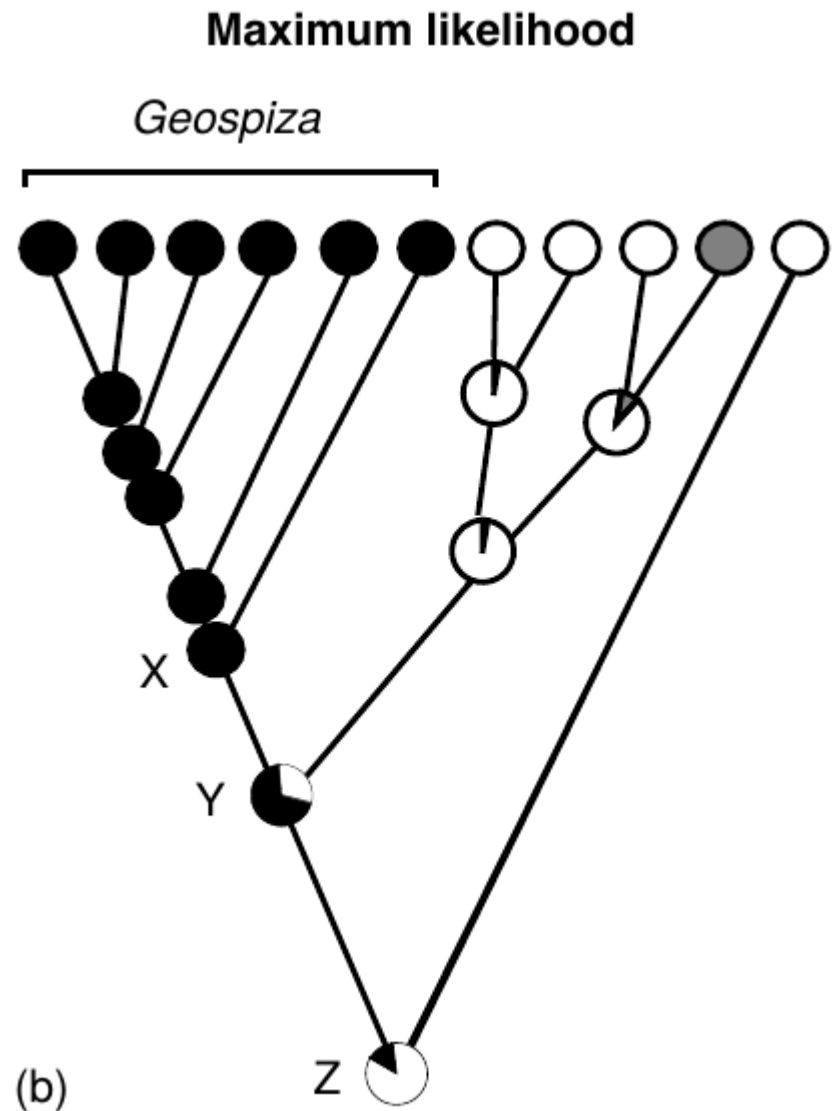
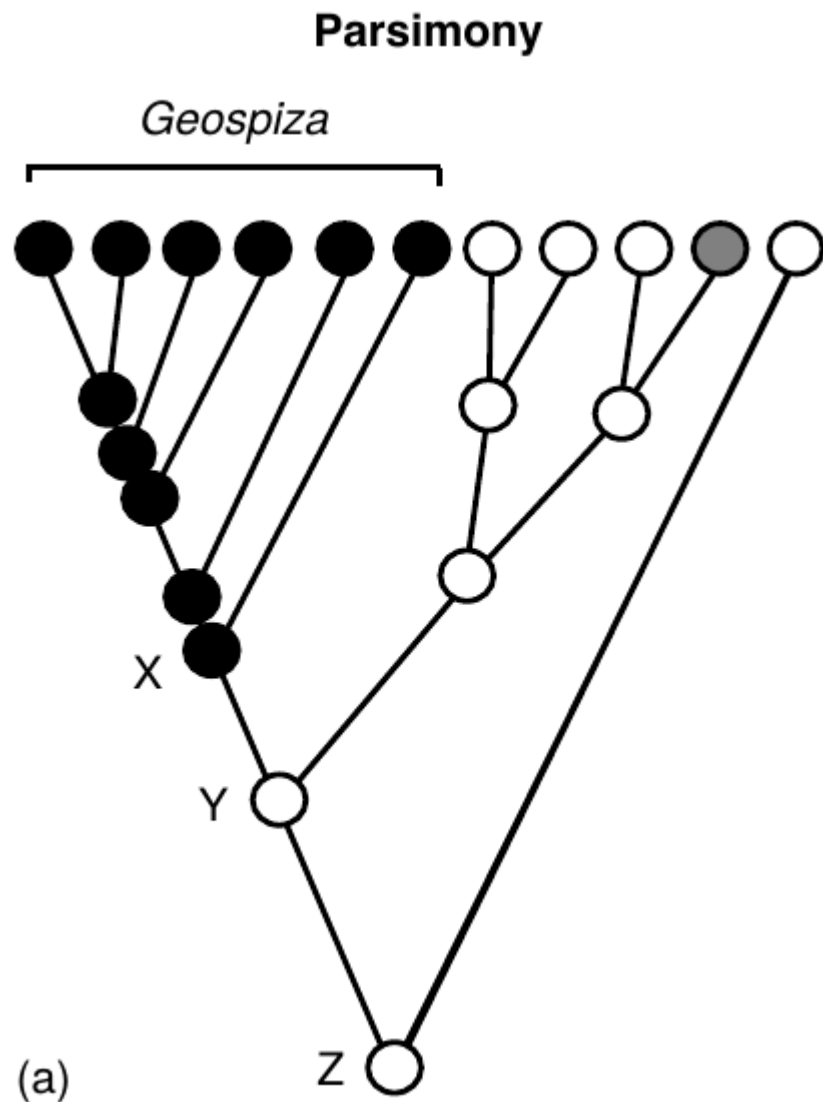
Syst Biol | © The Author(s) 2014. Published by Oxford University Press, on behalf of the Society of Systematic Biologists. All rights reserved.

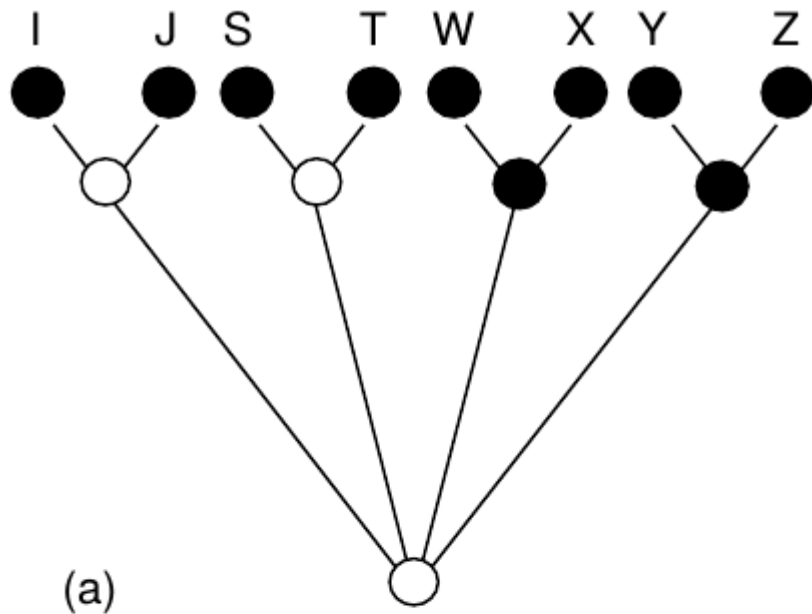
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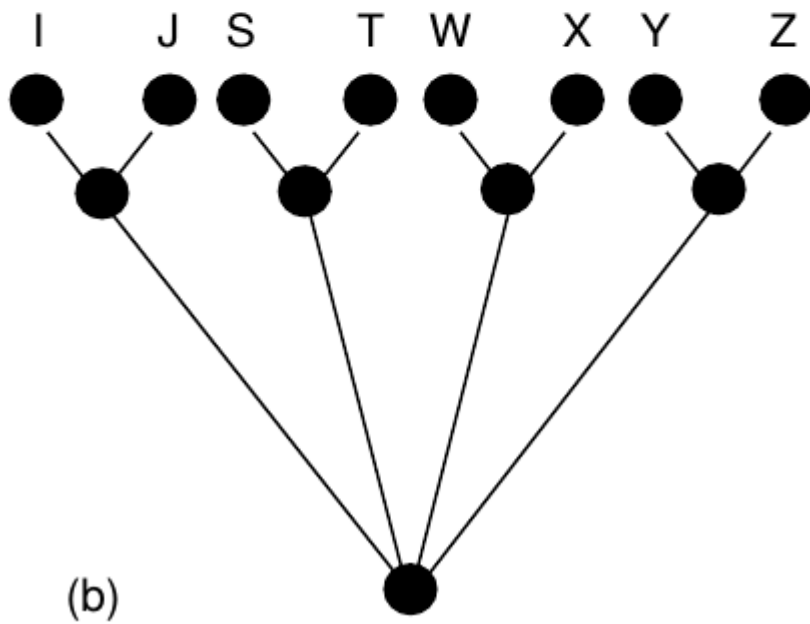


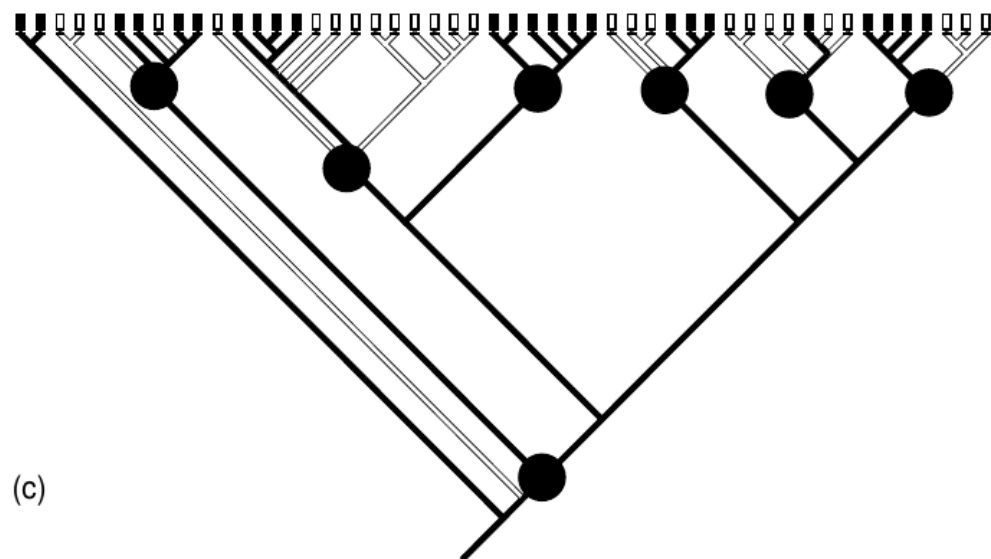
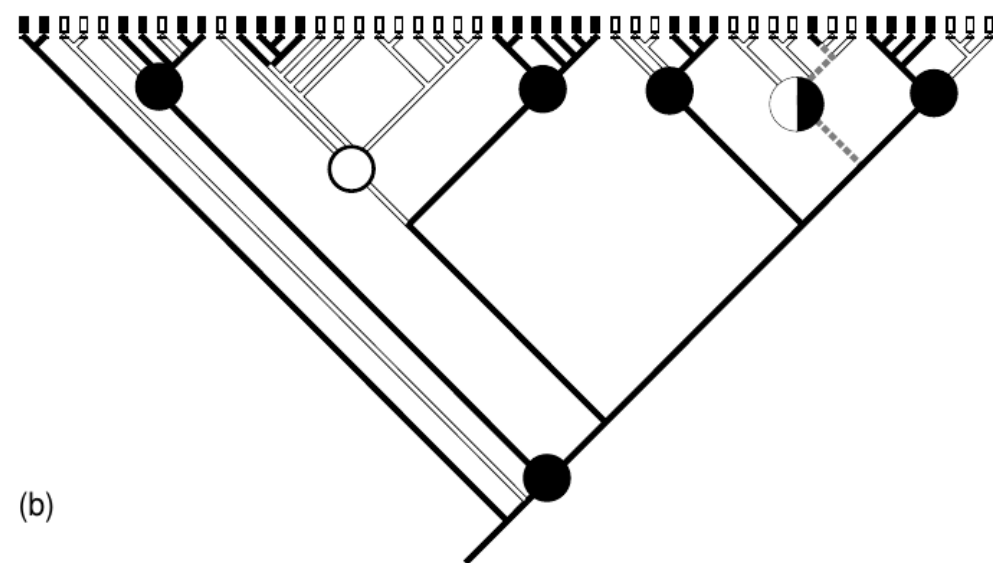
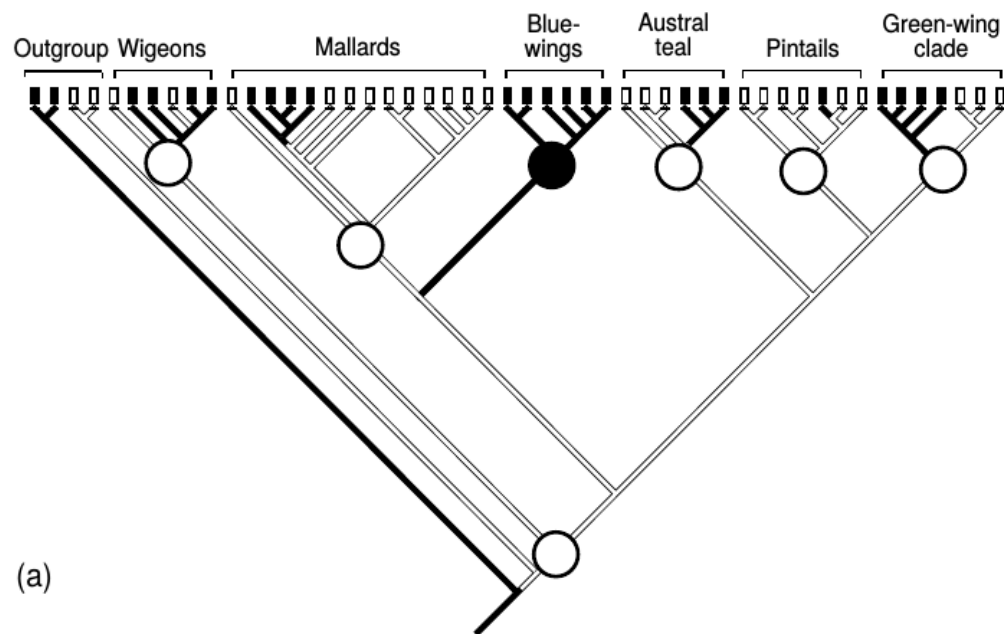
# Ancestral state reconstruction





relative rates matter

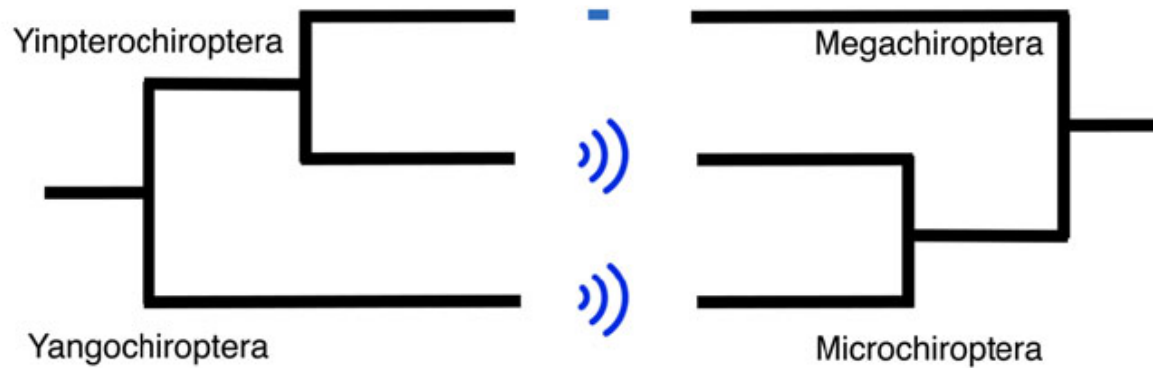




**Fig. 2.** Evolution of plumage dimorphism in dabbling ducks (*Anas*). White indicates monochromatic species, black indicates dichromatic, and grey broken lines indicate ambiguous reconstructions. (a) Parsimony reconstruction of ancestral character states. Reconstructed ancestral character states are shown in circles for the six main groups of dabbling ducks and for their common ancestor. Ancestral states for other nodes are indicated by shading within branches. Each terminal taxon is a species with its character state shown in the box at the top of the phylogeny. As with most parsimony reconstructions, this reconstruction allows equal weights for gains and losses. This reconstruction contradicts the widely held hypothesis that dichromatism has been lost many times. (b) When gains are three times more likely than losses, the number of independent origins of dichromatism decreases. (c) When gains are five times more likely than losses, the number of independent origins matches the widely held hypothesis. *Reproduced, with permission, from Ref. 16.*

what about the coalescent?

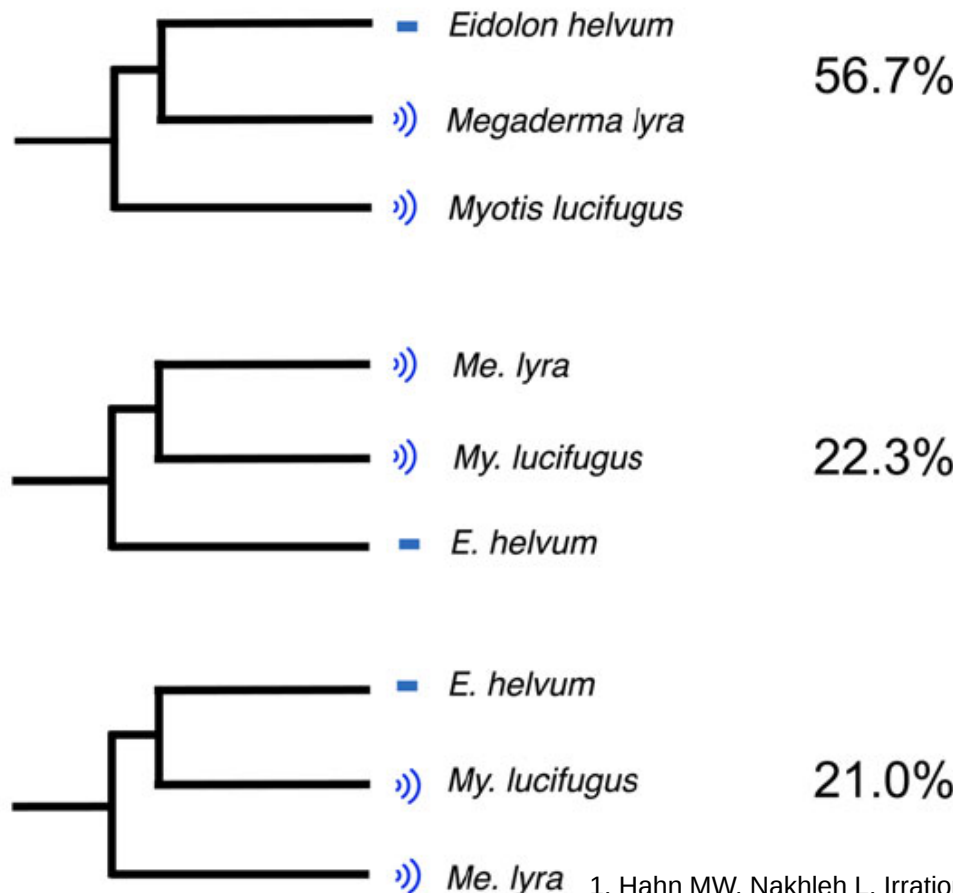
**A**



The evolution of echolocation in bats.

(A) Species relationships between echolocating and nonecholocating bats (after Teeling 2009). The left-hand species tree shows the relationships inferred from DNA sequence data, putting both echolocating and nonecholocating taxa in the suborder Yinpterochiroptera, with the other echolocating bats in the suborder Yangochiroptera. The right-hand tree shows the traditional species relationships inferred from morphological characters (and limited sequence data).

**B**



(B) Tree topologies inferred from 2083 genes using alignments from Tsagkogeorga et al. (2013) and Parker et al. (2013). Proportions shown are for the subset of genes (out of  $n = 2320$  total)