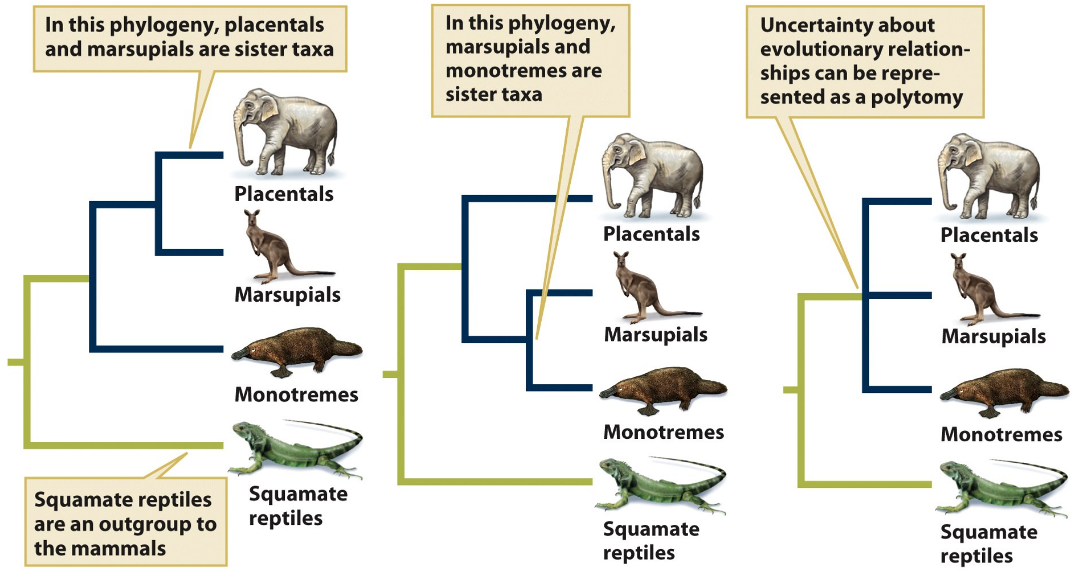
Anatomy of a tree



Evolution, 1/e Figure 4.9a

Evolution, 1/e Figure 4.9b

Evolution, 1/e Figure 4.9c

outgroup: an early branching relative of the interest groups

sister taxa: taxa derived from the same recent ancestor

polytomy: >2 taxa emerge from a node

Anatomy of a tree

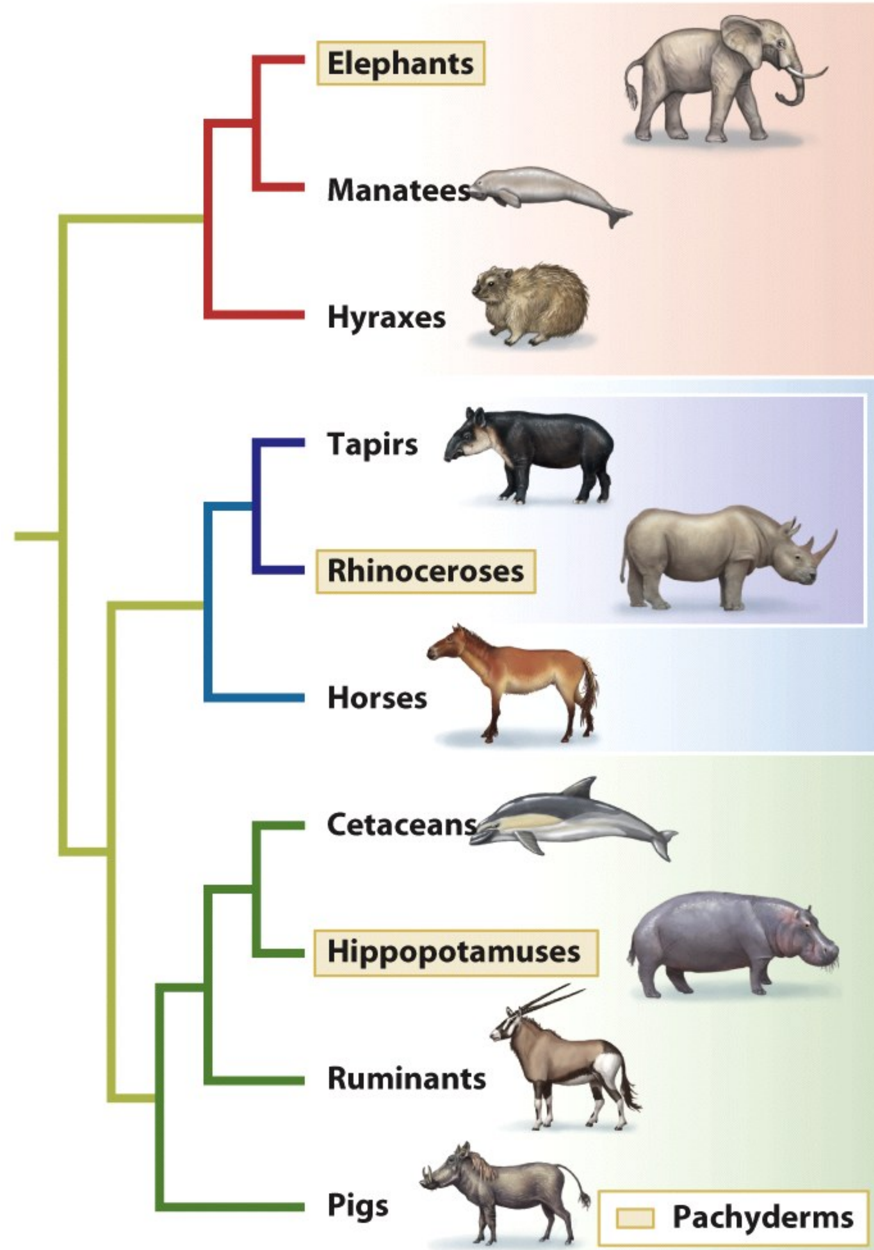
clade is group of organisms with a shared ancestor

a **monophyletic** group shares a single common ancestor

= tapirs-rhinos-horses

a **polypheletic** group includes members that lack a recent common ancestor

=pachyderms



Evolution, 1/e Figure 4.11

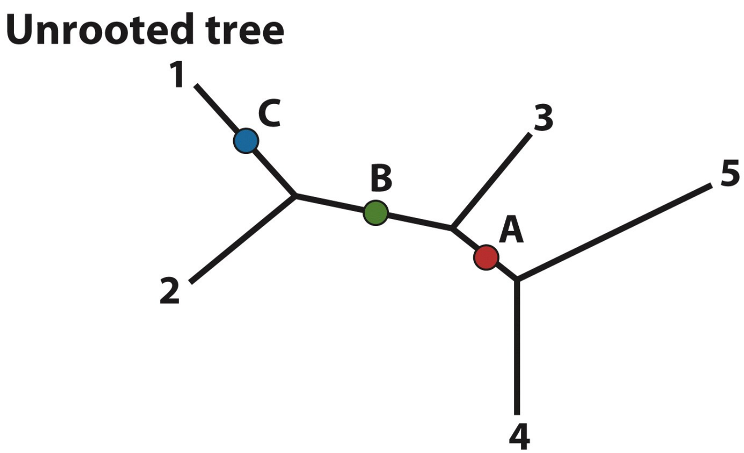
To root or not to root

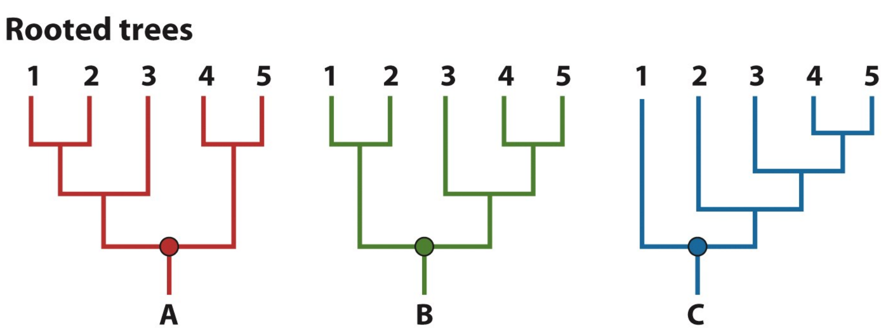
Rooted trees indicate a common line of descent through time

Unrooted trees do not strictly illustrate evolutionary relationships

-represent many rooted trees

-root can decide what clades are monophyletic





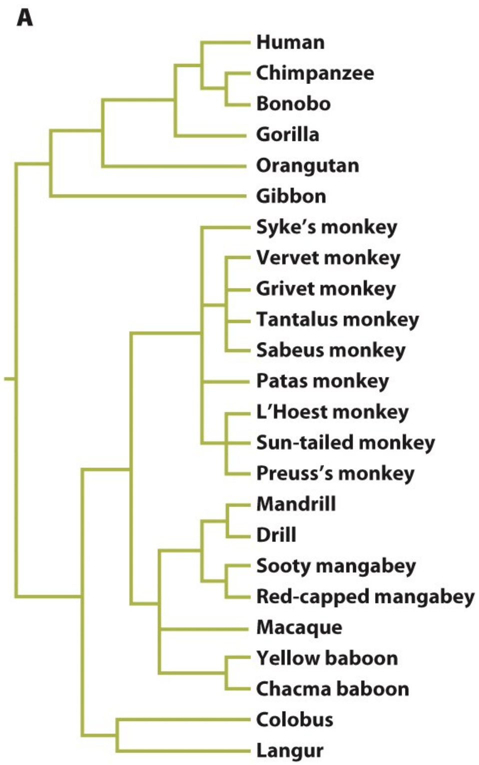
Types of trees

Cladograms only evolutionary relationships

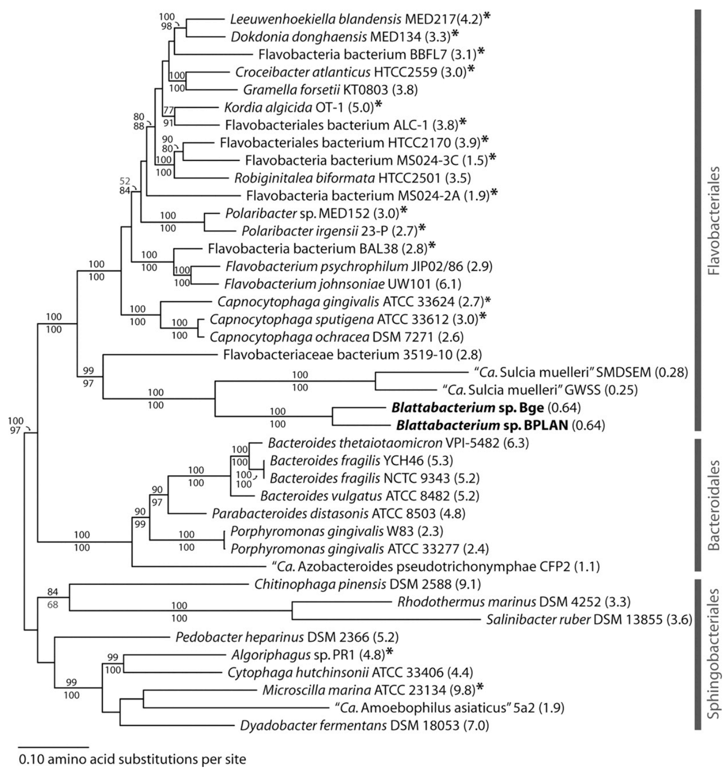
Phylograms evol. relationships and changes over time (branch lengths)

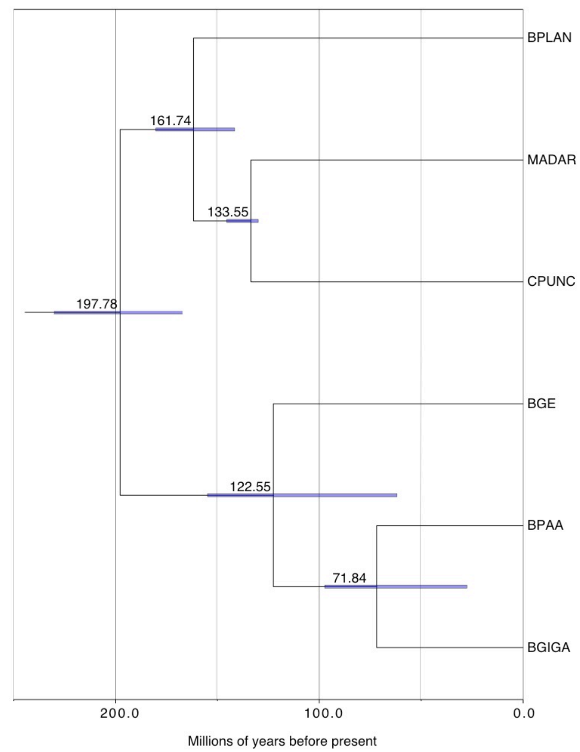
-longer branches = more changes

Chronogram relationships, changes calibrated to actual time



Evolution, 1/e Figure 4.15





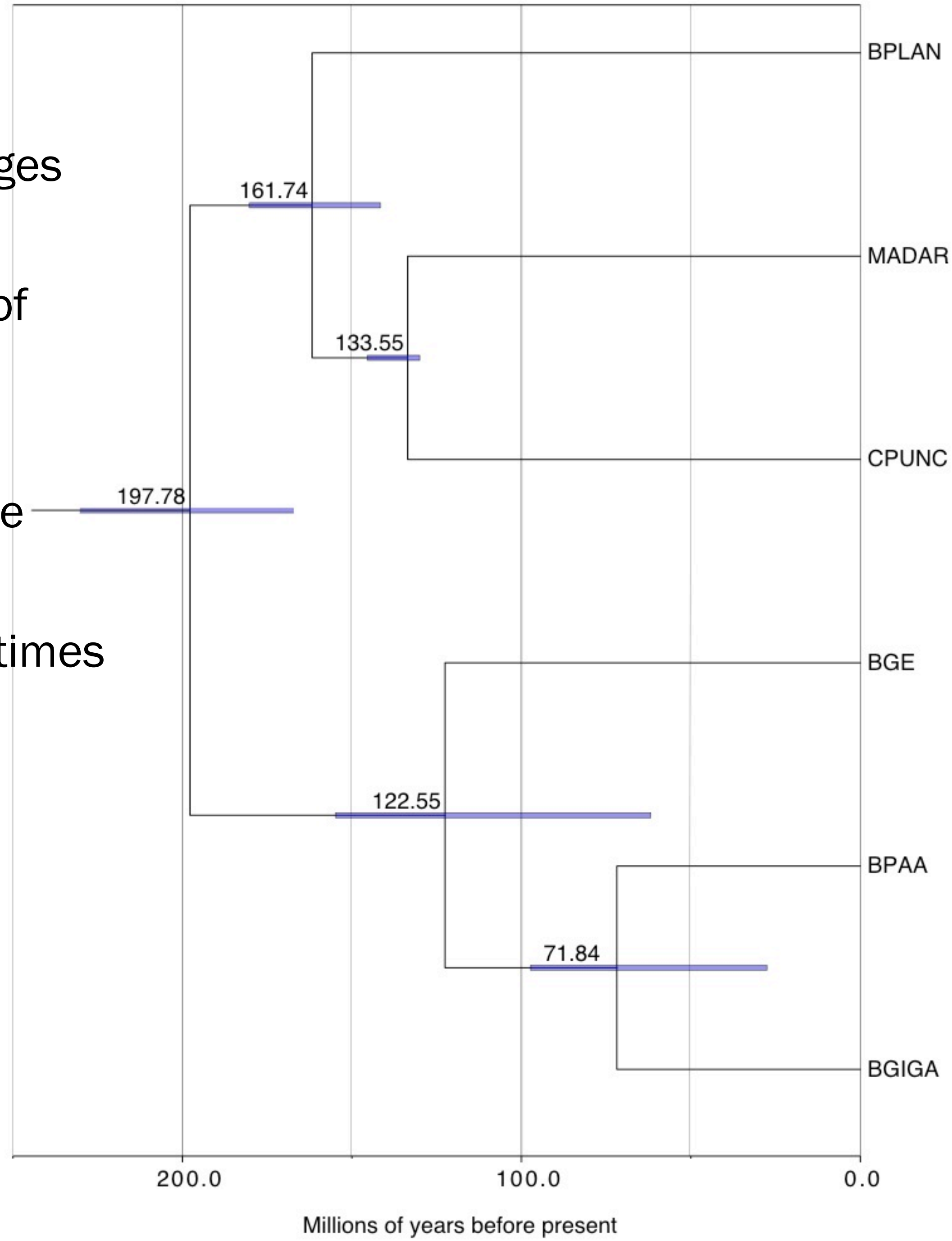
Types of trees

Chronogram relationships, changes calibrated to actual time

-fossil record or extant samples of known ages and elemental (e.g. 13C) dating methods

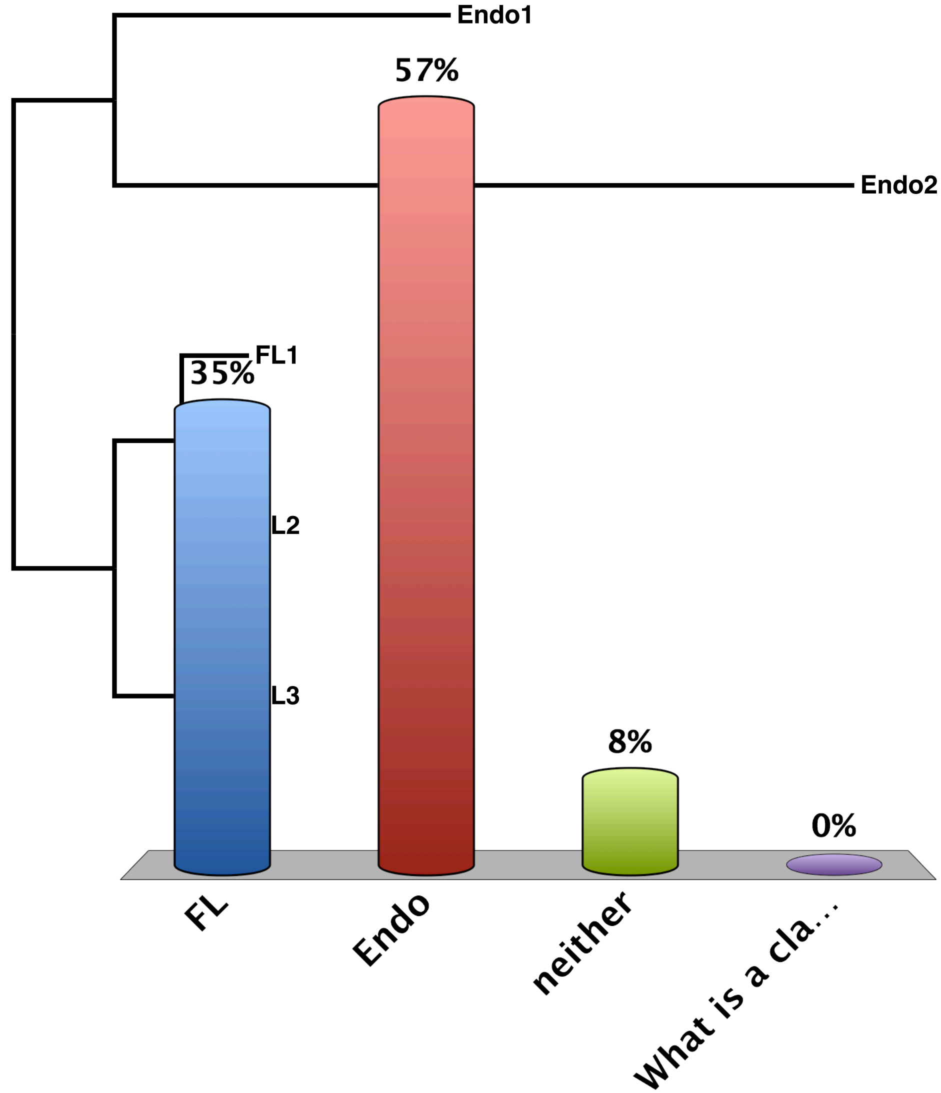
-dating methods used to calibrate phylogenetic trees

-used to infer actual divergence times



In which clade are members the most different from one another?

A. FL
B. Endo
C. neither
D. What is a clade?



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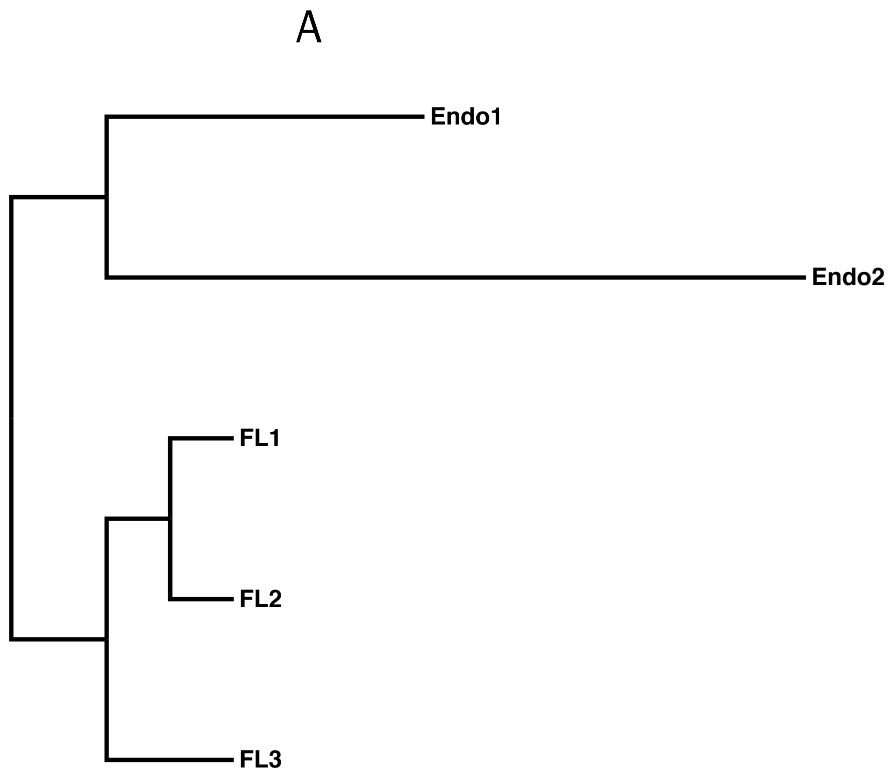


Short-lived organisms = faster mutation rates (more heritable changes)

Generations per year (GPY): Herbaceous plants > shrubs/trees

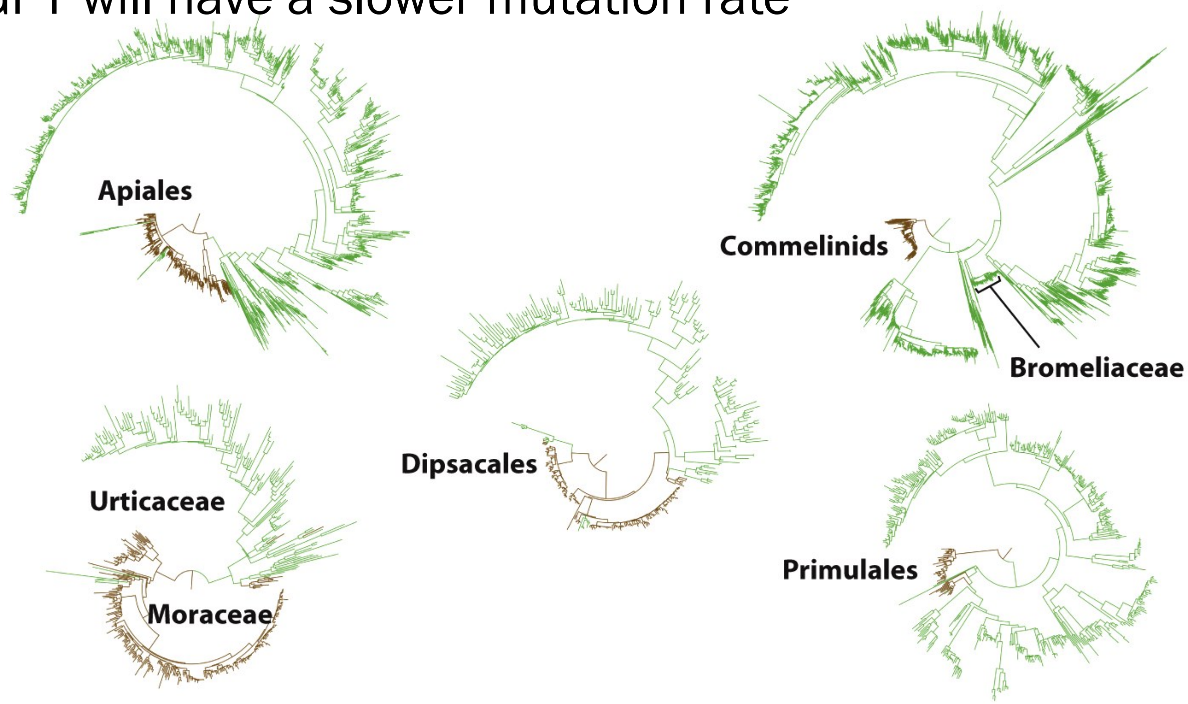
Hyp.: Plants with fewer GPY will have a slower mutation rate

Green: herbs

Brown: shrubs/trees

Phylograms using DNA sequences

Branch lengths indicate amount of change



Evolution, 1/e Figure 4.17

Short-lived organisms = faster mutation rates (more heritable changes)

Generations per year (GPY): Herbaceous plants > shrubs/trees

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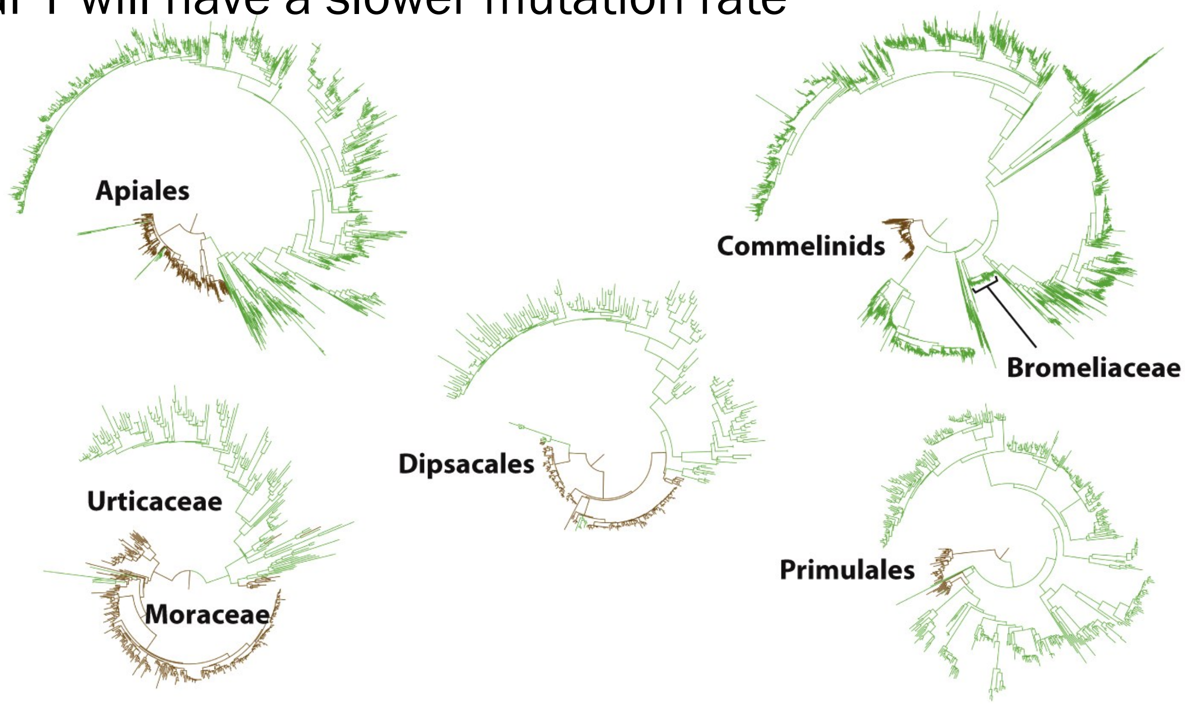
Green: herbs

Brown: shrubs/trees

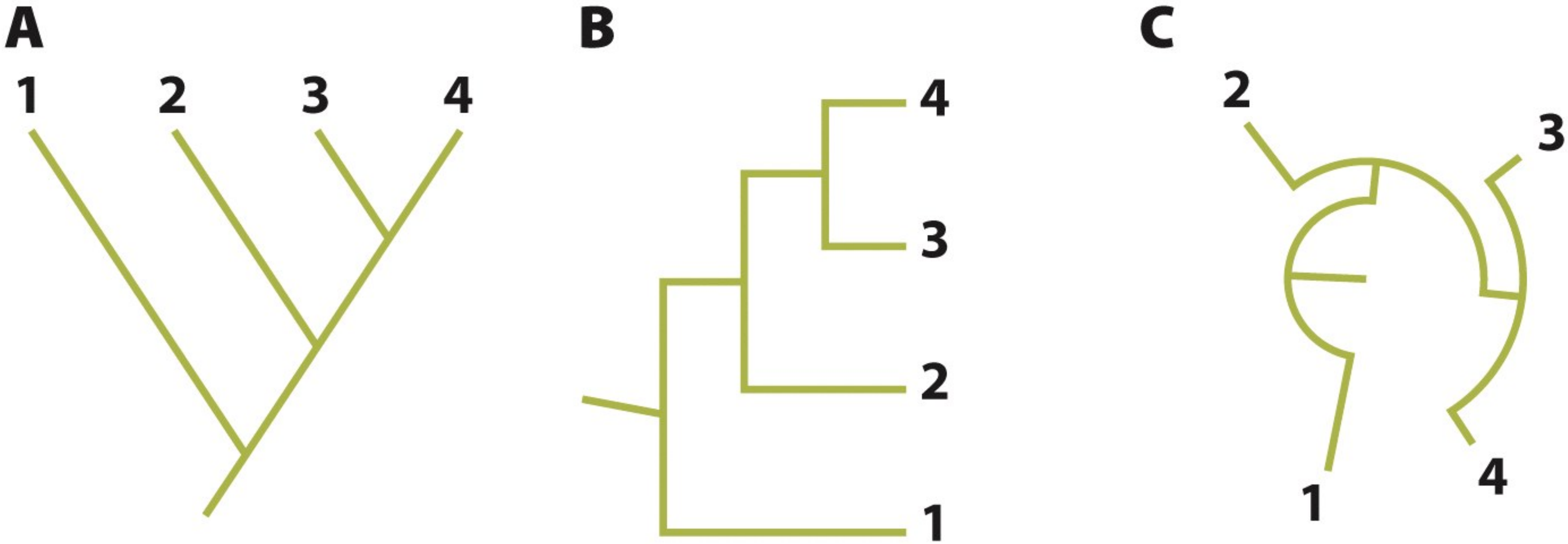
Phylograms using DNA sequences

Branch lengths indicate amount of change



Evolution, 1/e Figure 4.17

Conclusion: Shrubs and trees evolved more slowly than herbaceous plants



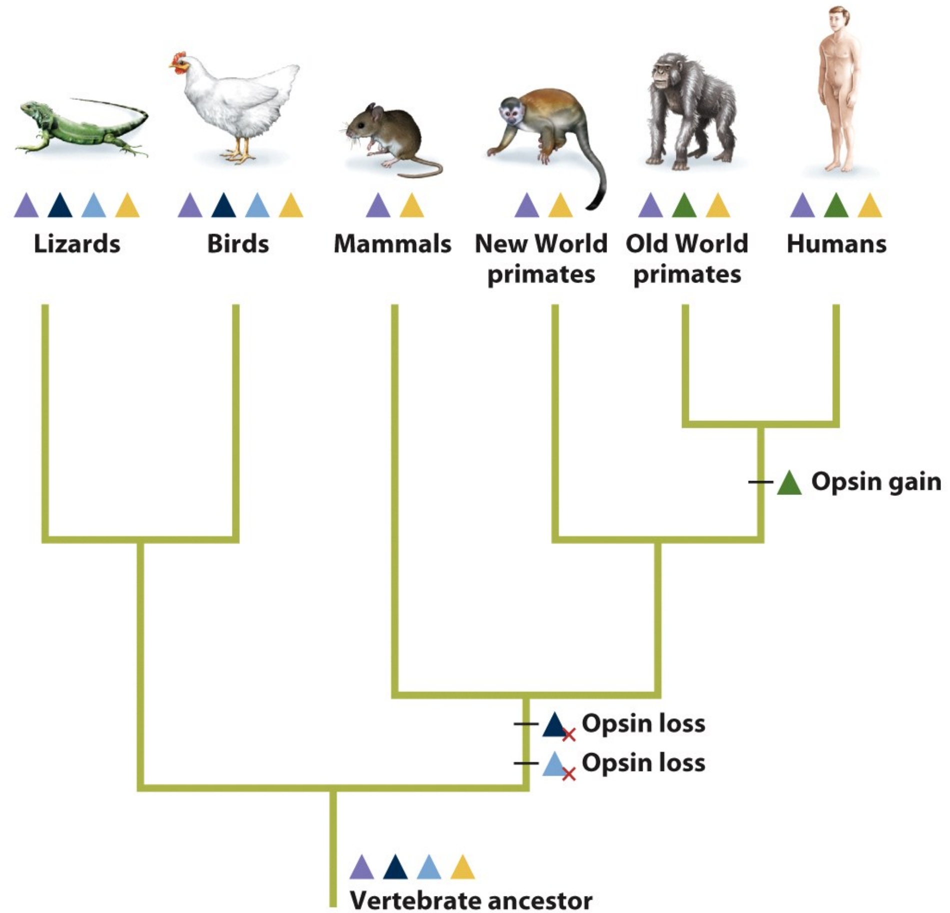
Evolution, 1/e Figure 4.18

Each tree depicts the same relationships

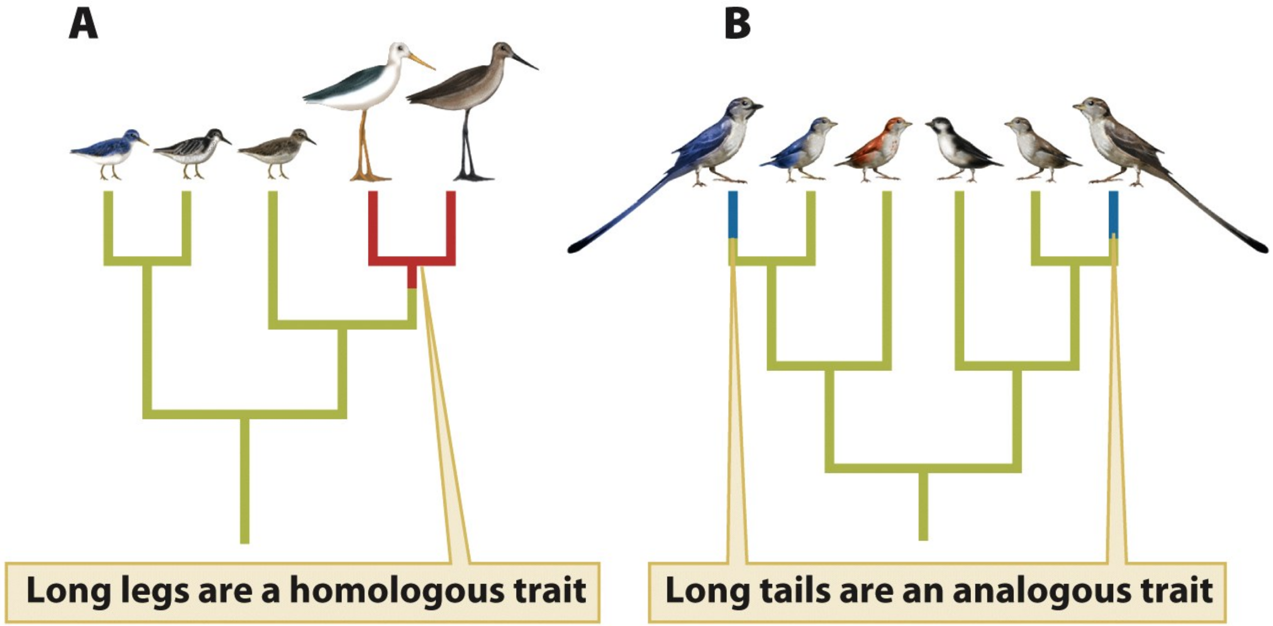
“Painting” traits onto trees

Known evolutionary relationships are used to develop a hypothesis about trait loss and gain

Ancestral traits are recreated from extant examples



Evolution, 1/e Figure 4.20



Evolution, 1/e Figure 4.21

Many, but not all, similarities are due to shared ancestry

Homologous traits due to ancestral inheritance

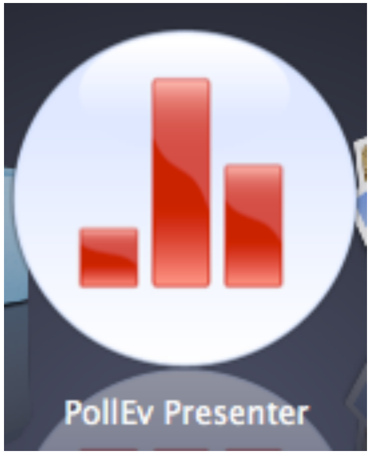
Analogous traits are similar but not of ancestral origin

-often analogous traits are the result of natural selection for a similar solution for a similar problem

Homoplasy is when two species share traits that are not derived from a common ancestor

THINK-PAIR-SHARE (90 sec)

What are some examples of homoplasic traits?



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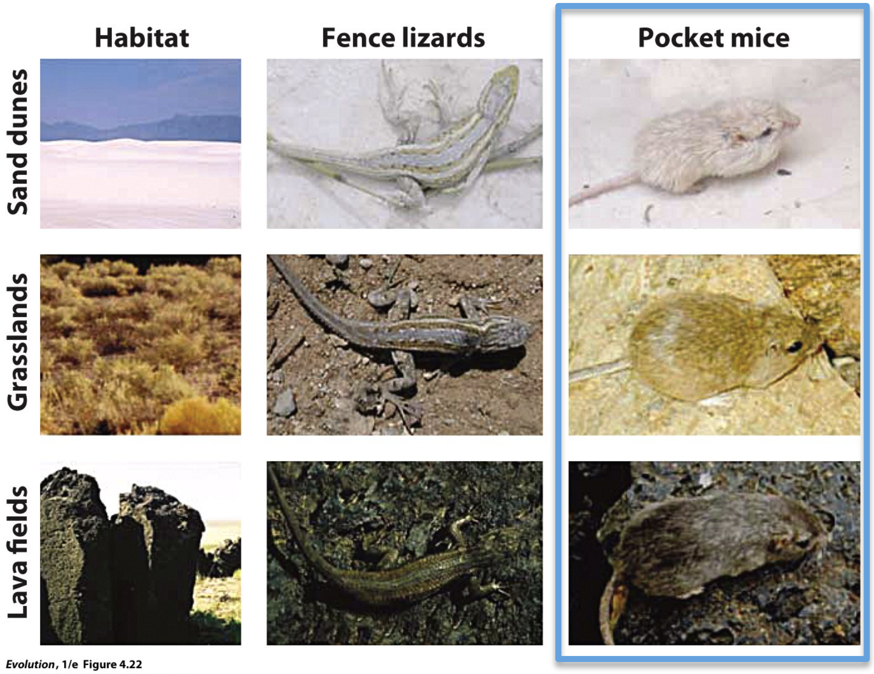
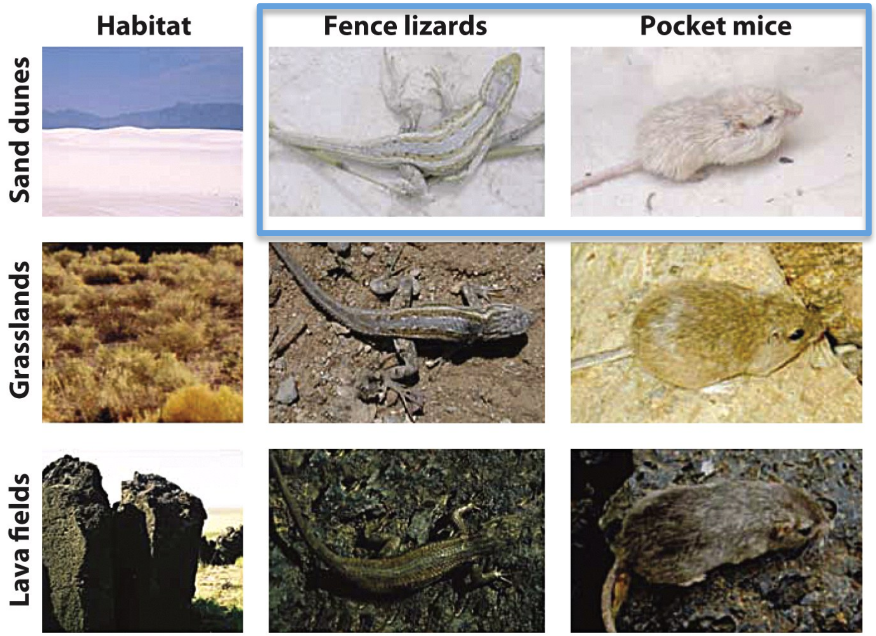


Evolution, 1/e Figure 4.22

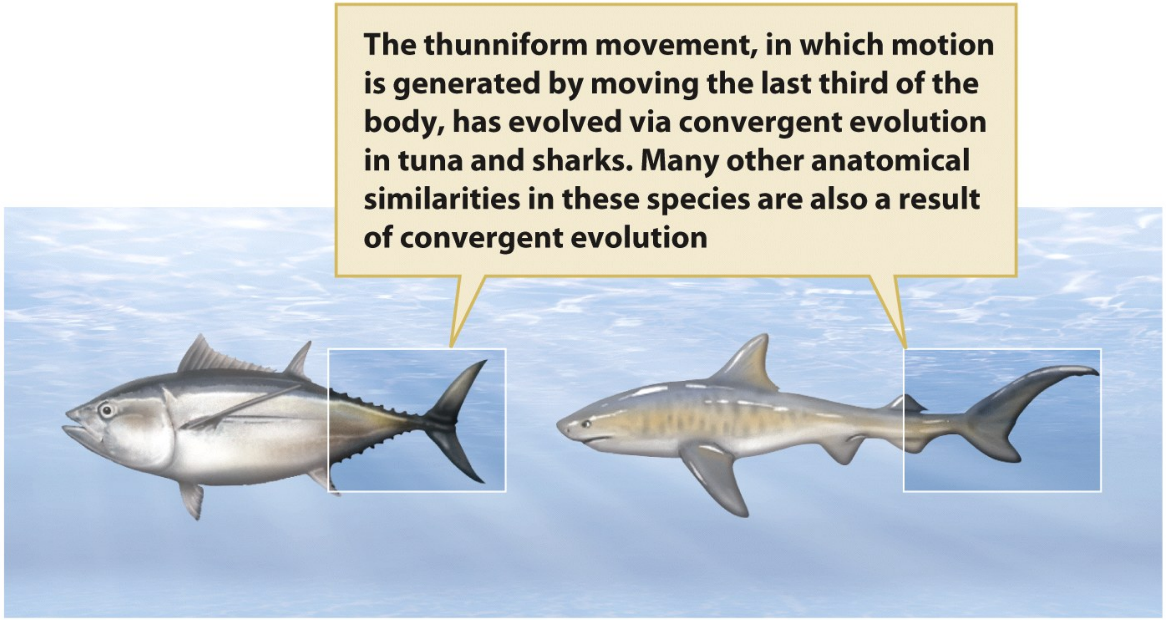
Divergent evolution is when closely related organisms diverge



Evolution, 1/e Figure 4.22

Divergent evolution is when closely related organisms diverge

Convergent evolution is when similar traits arise in non-related organisms



Evolution, 1/e Figure 4.23

Convergence can be misleading when constructing phylogenies

Sharks and bony fishes diverged over 400Mya

Similar mobility mechanisms

Including multiple traits in building trees improves accurate reconstruction of evolutionary histories

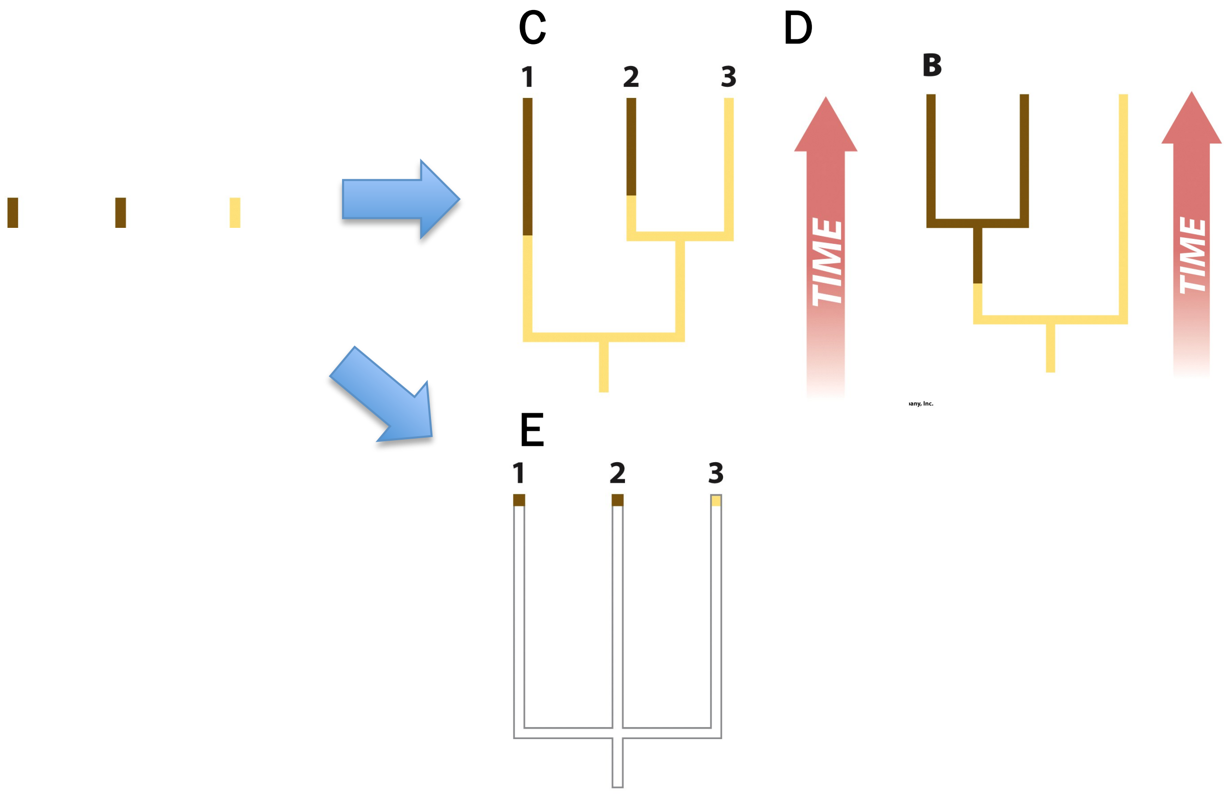
Reconstructing evolutionary history

(A1) represents two traits, yellow and brown

(A2) are three species each exhibiting one of the two traits

(B) assumes that brown is a shared **derived** state, or **synapomorphy**, and yellow is an **ancestral** state

Reconstructing evolutionary history



Tree building often uses current info about populations, which means that neither (C) or (D) can be excluded. Uncertainty can be depicted as a **polytomy** (E)

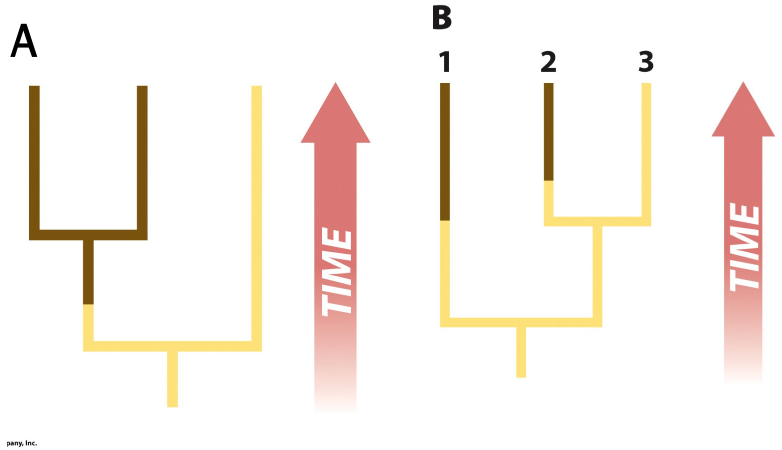
The brown traits are _____ in (A) and _____ in (B).

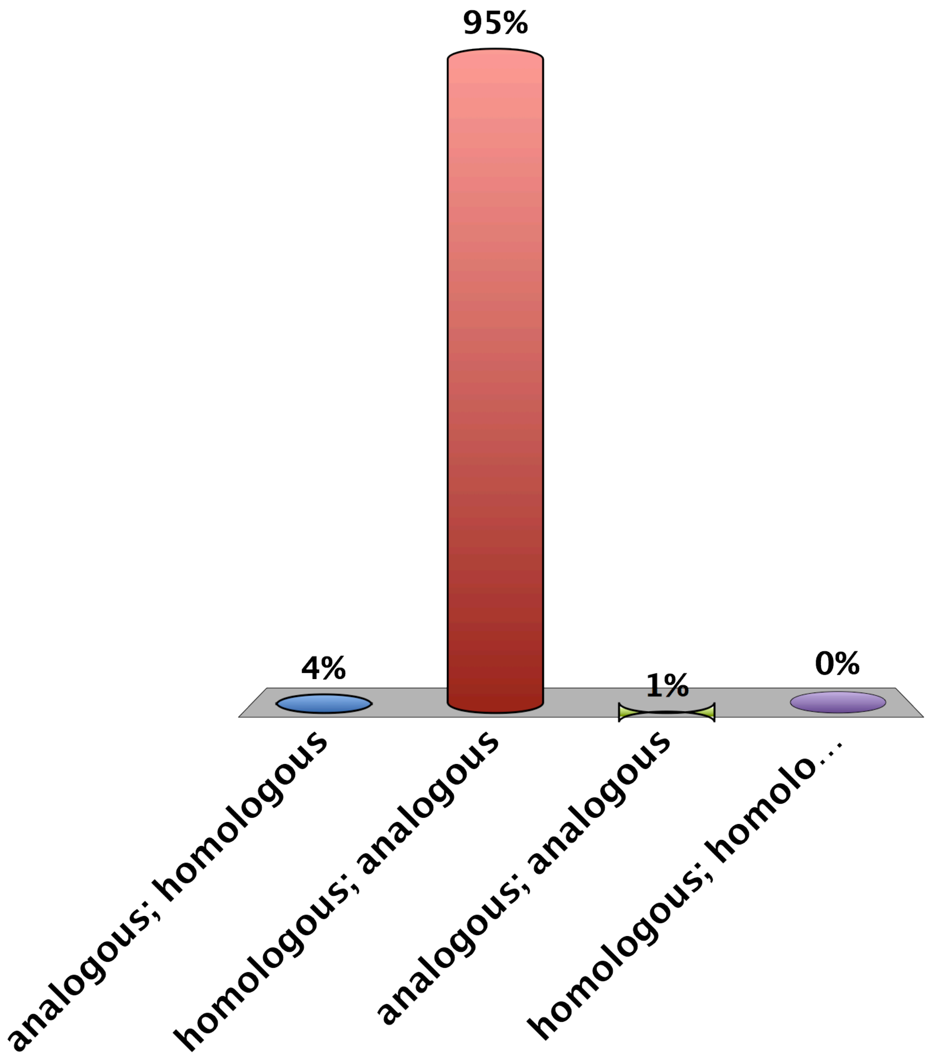
A. analogous; homologous

B. homologous; analogous

C. analogous; analogous

D. homologous; homologous





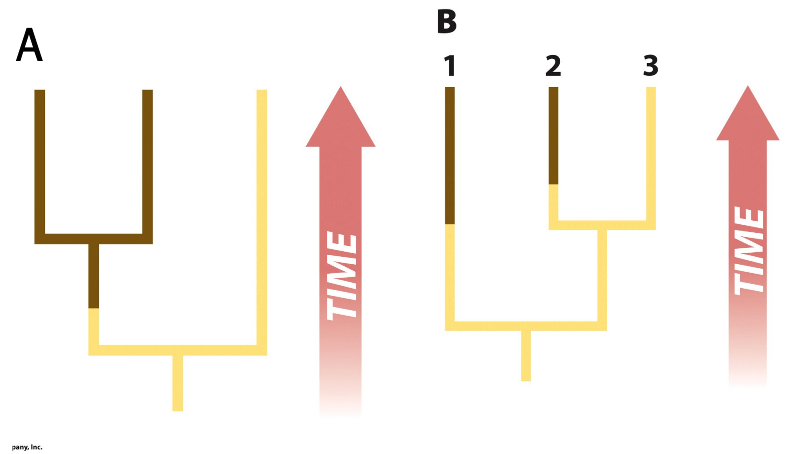
The brown traits are _____ in (A) and _____ in (B).

1) analogous; homologous

2) homologous; analogous

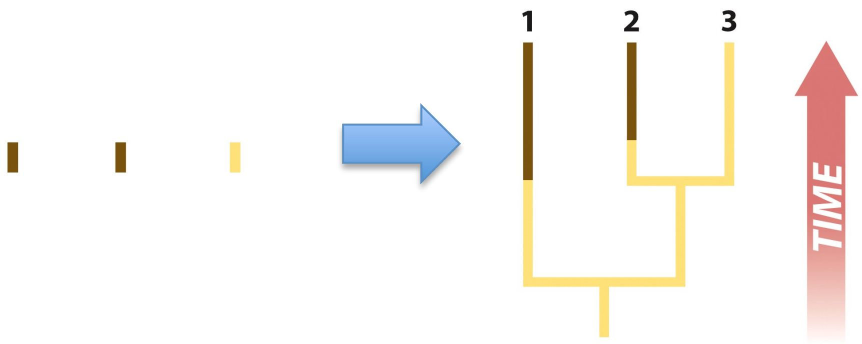
3) analogous; analogous

4) homologous; homologous



Shared, but nonancestrally-acquired, traits would be analogous and **homoplasic**

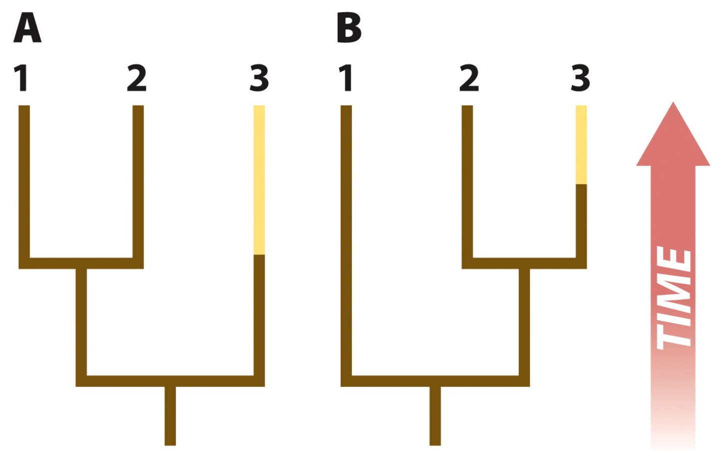
Reconstructing evolutionary history



Shared, but nonancestrally-acquired, traits would be analogous and **homoplasic**

Without any other info, one might conclude that the brown trait is synapomorphic and that (1) and (2) are more closely related than (2) and (3)

Reconstructing evolutionary history



Evolution, 1/e Figure 4.26

Alternatively, brown could be ancestral and yellow derived

Neither (A) or (B) can be excluded

(B) can occur if the derived state has recently arisen and is rare-occurring

-**symplesiomorphy** is when an ancestral state is not shared by closely related species

Tips for building good trees

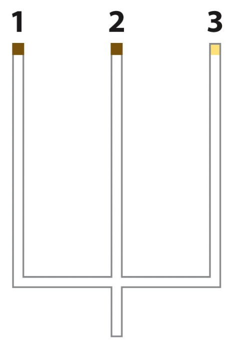
GOAL: overcome homoplasies and symplesiomorphies to draw accurate inferences about evolutionary history

1) Use synapomorphic traits (i.e. slowly evolving)

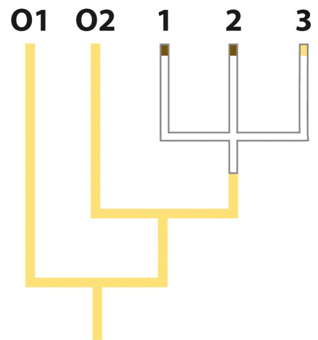
-vestigial (low-or-no cost nonfunctioning) traits can provide linkages between species

2) Use many traits (e.g. many phenotypes, genes or proteins)

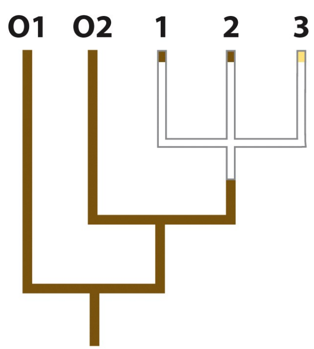
3) Use outgroups with a known evolutionary relationship with the taxon of interest to better estimate the appearance of traits (polarity) of interest in time

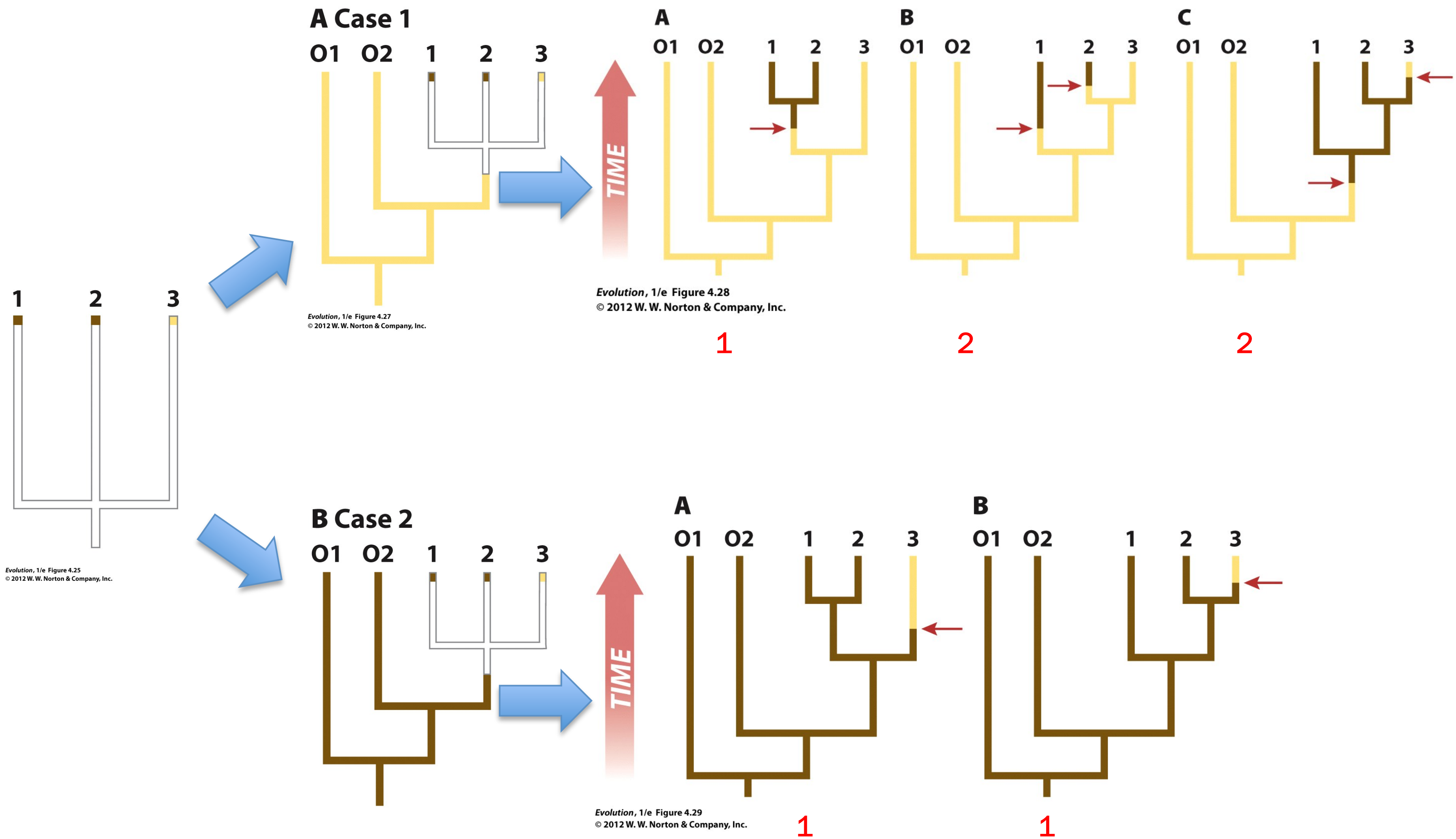


A Case 1



B Case 2





Outgroups help reconstruct evolutionary events

Parsimony uses the fewest evolutionary changes to explain observed traits

Under parsimony, Case 1A is most agreeable