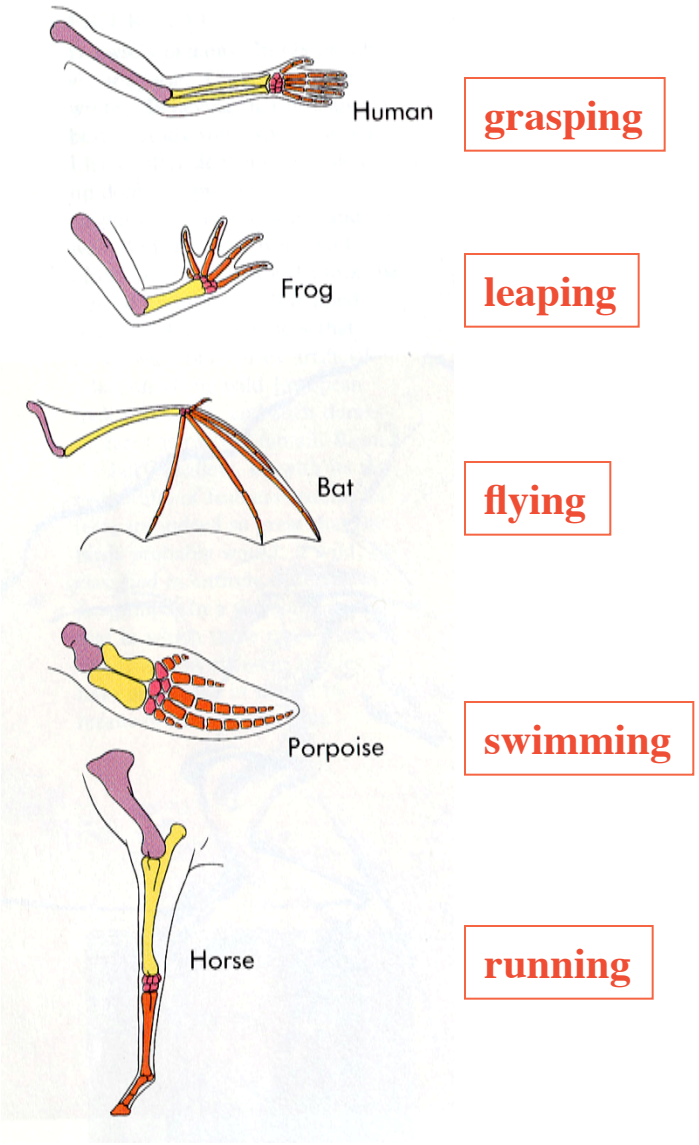
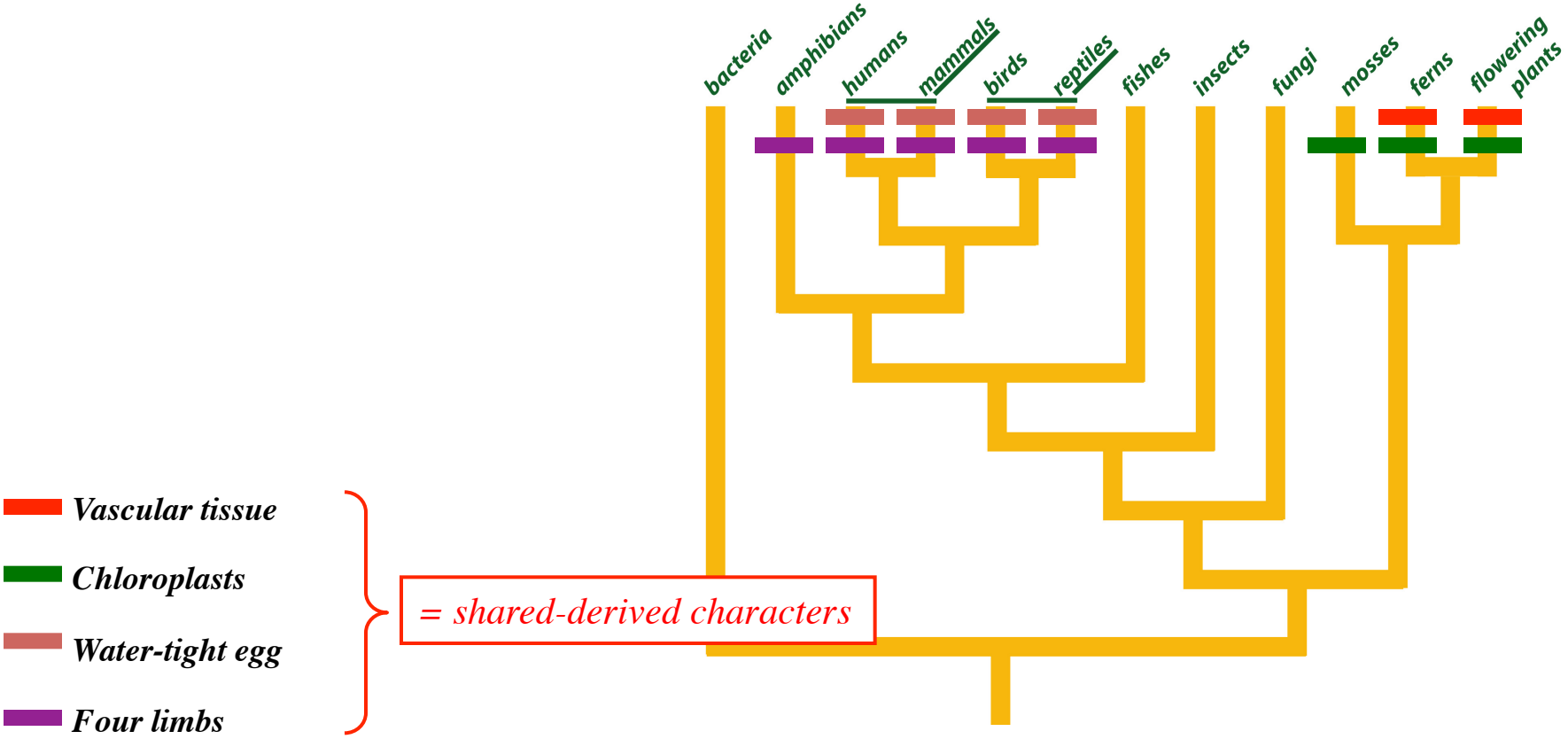
Homology

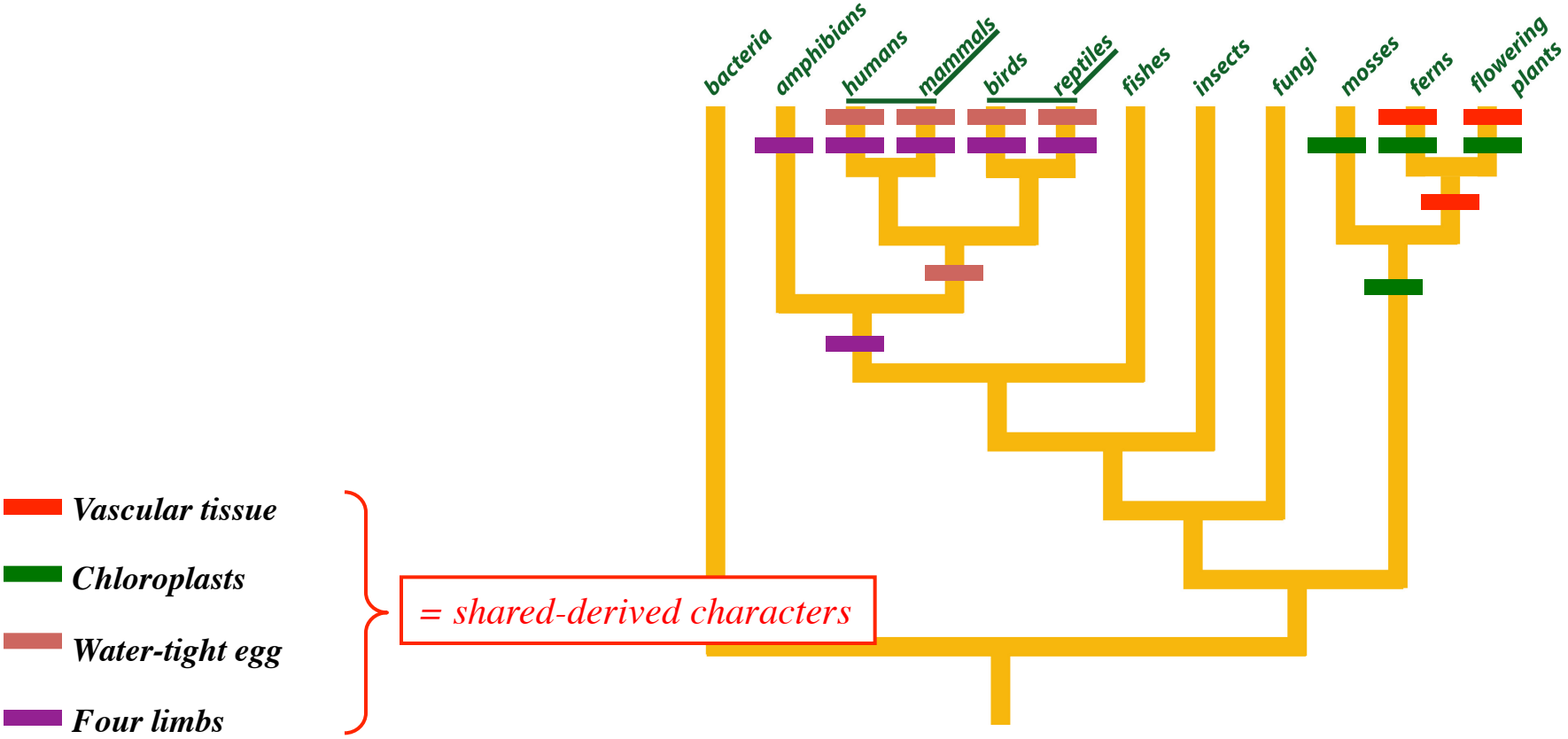
- Distantly related organisms share structural similarities
- Function varies
- Explicable by common ancestry



Nested hierarchical structure
"groups within groups"



Nested hierarchical structure
"groups within groups"

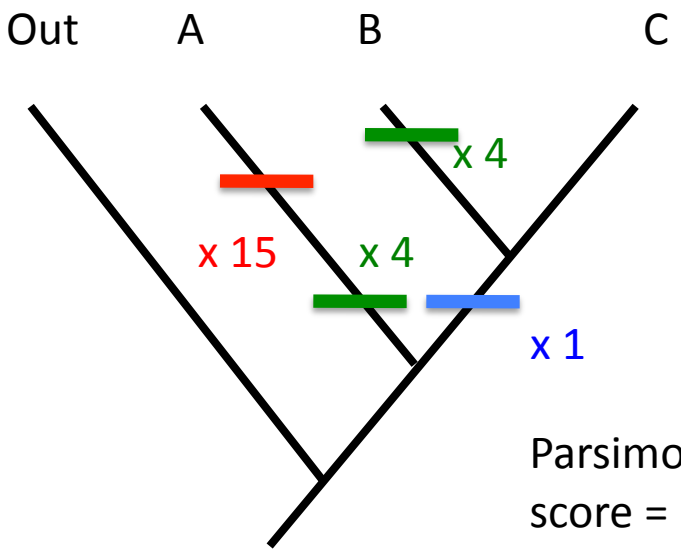


Parsimony – simple example

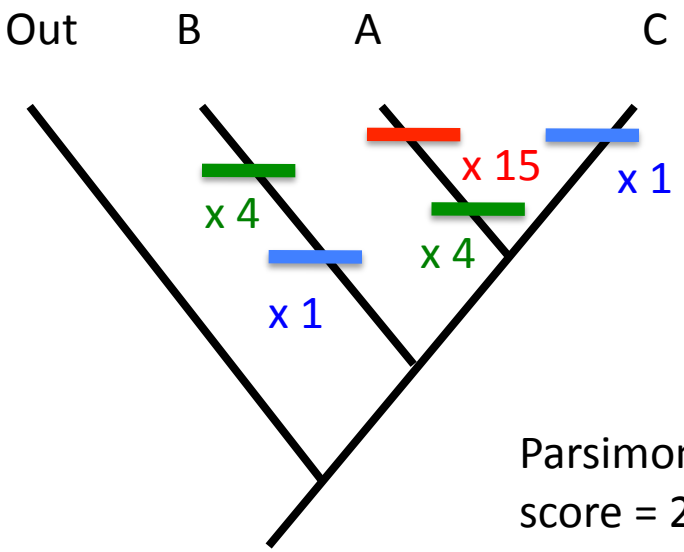
		A	B	C
Characters 1-15		1	0	0
Characters 16-19		1	1	0
Character 20		0	1	1
Outgroup		0	0	0

Taxa B + C are more similar in terms of shared character states --- (they agree on 16/20 characters)

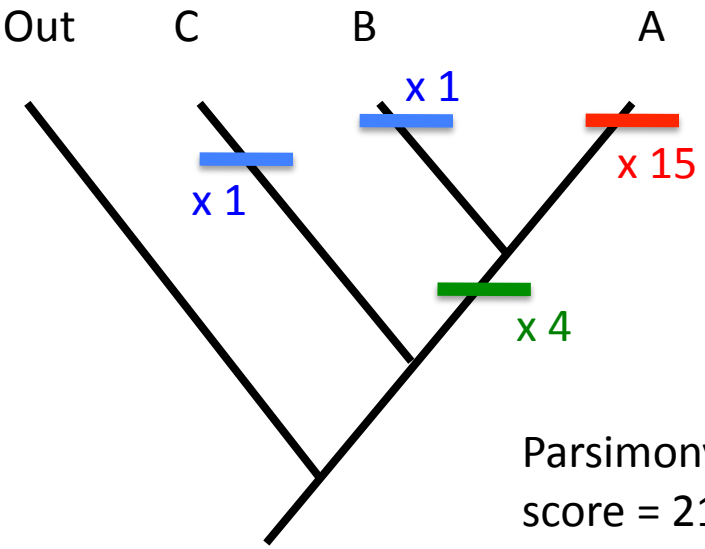
But which tree is the most parsimonious?



Parsimony score = 24



Parsimony score = 25

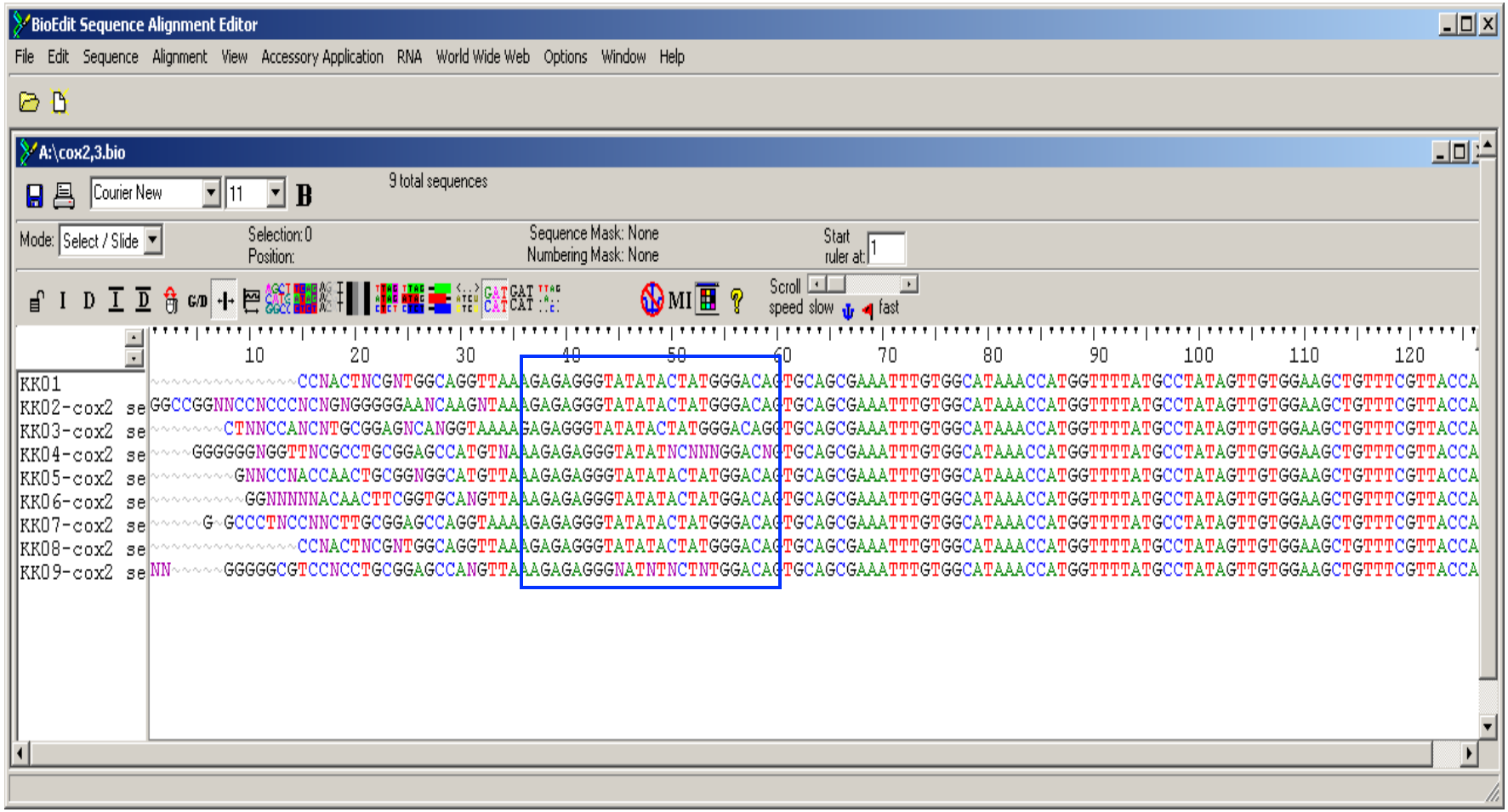


Parsimony score = 21

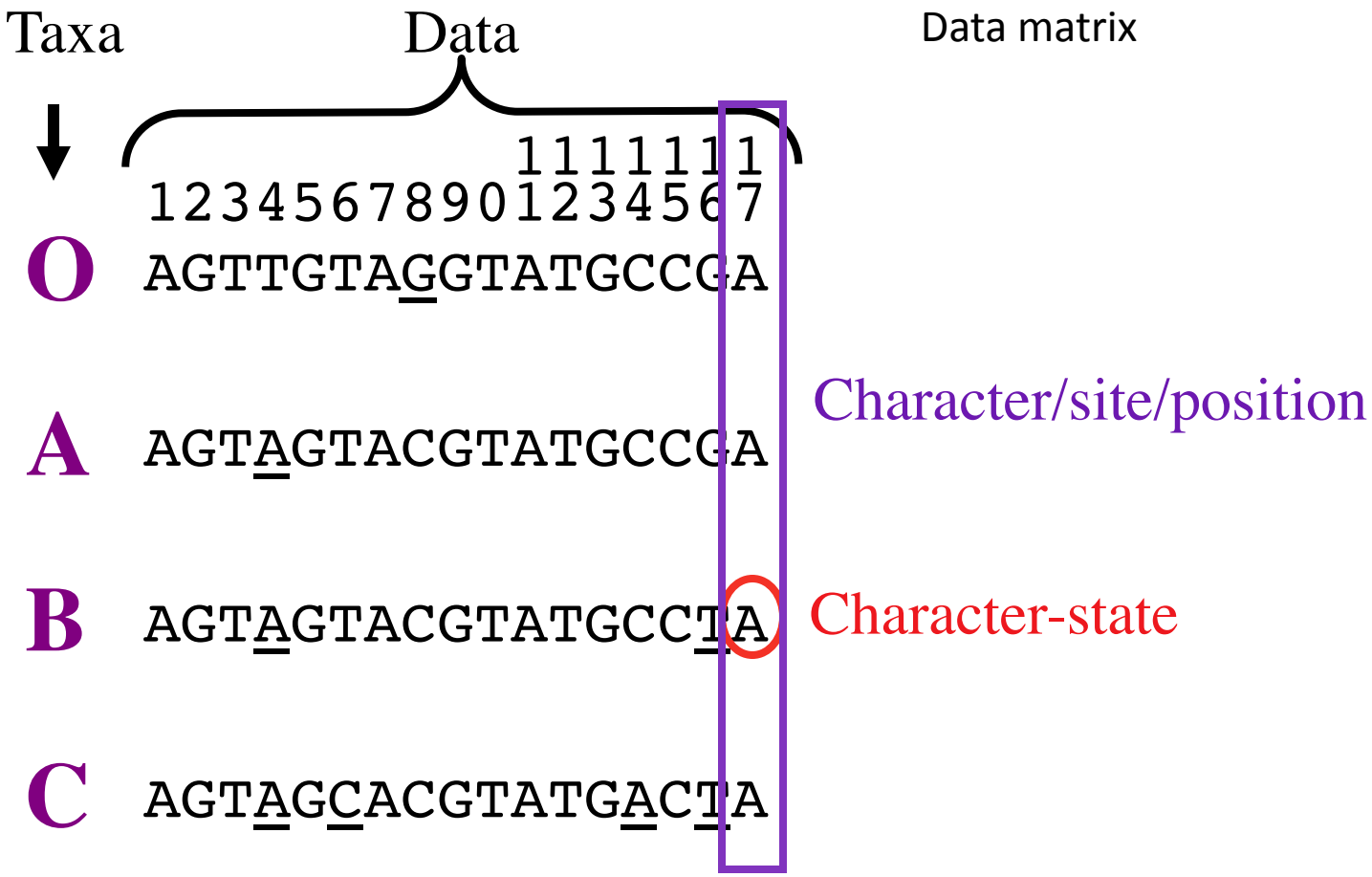
		A	B	C
Characters 1-15		1	0	0
Characters 16-19		1	1	0
Character 20		0	1	1
Outgroup		0	0	0

The Data – Genetic Sequences

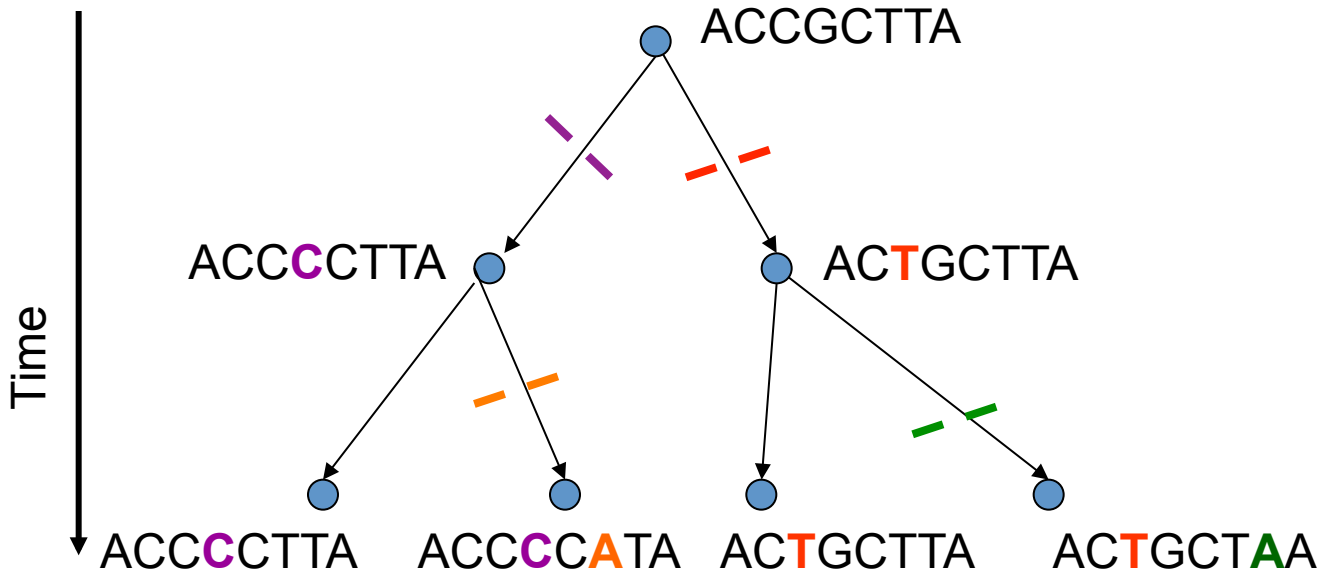
Sequence alignment issues



Specific procedure

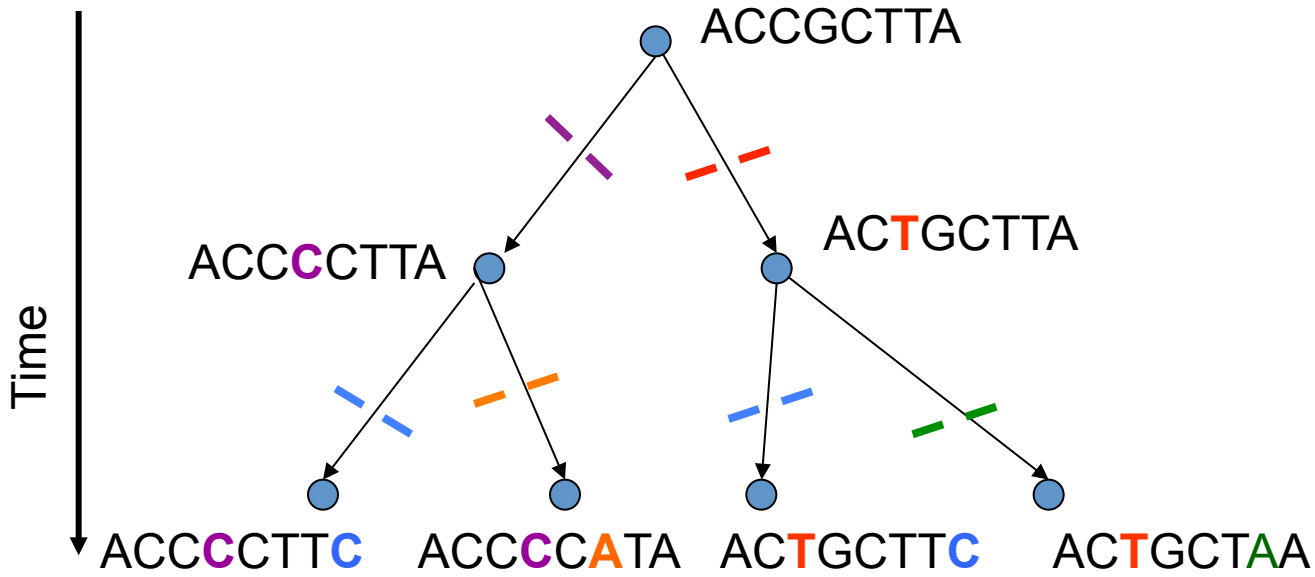


Parsimony - data agrees



ACCCCTTA
ACCCCATA
ACTGCTTA
ACTGCTAA

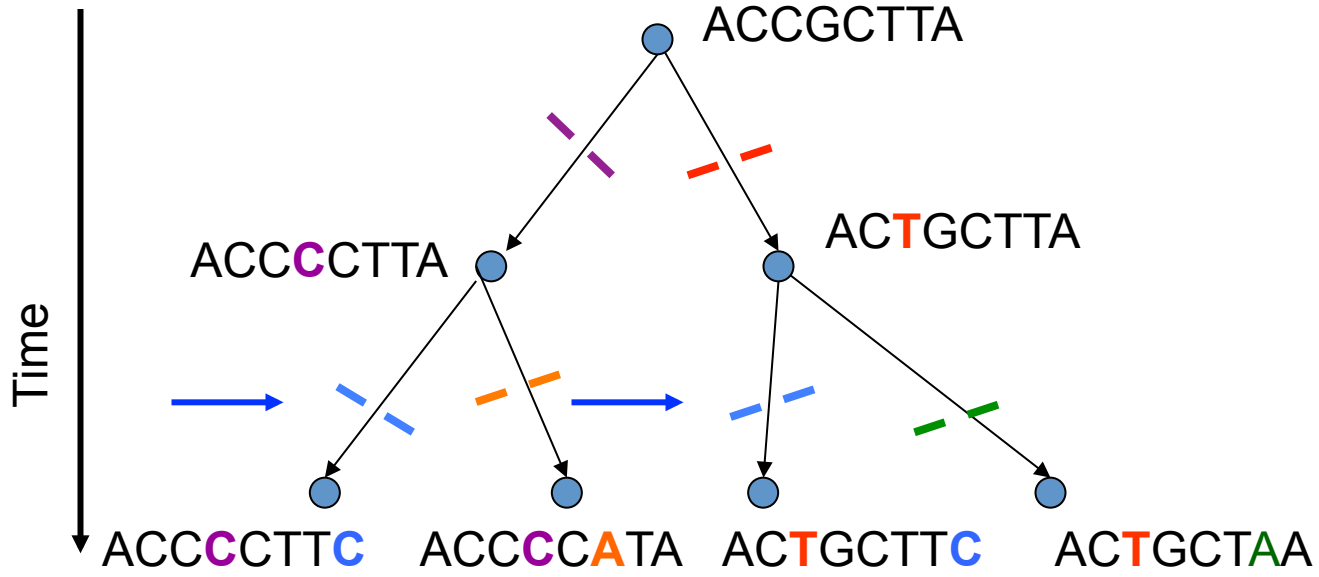
Parsimony - data disagrees



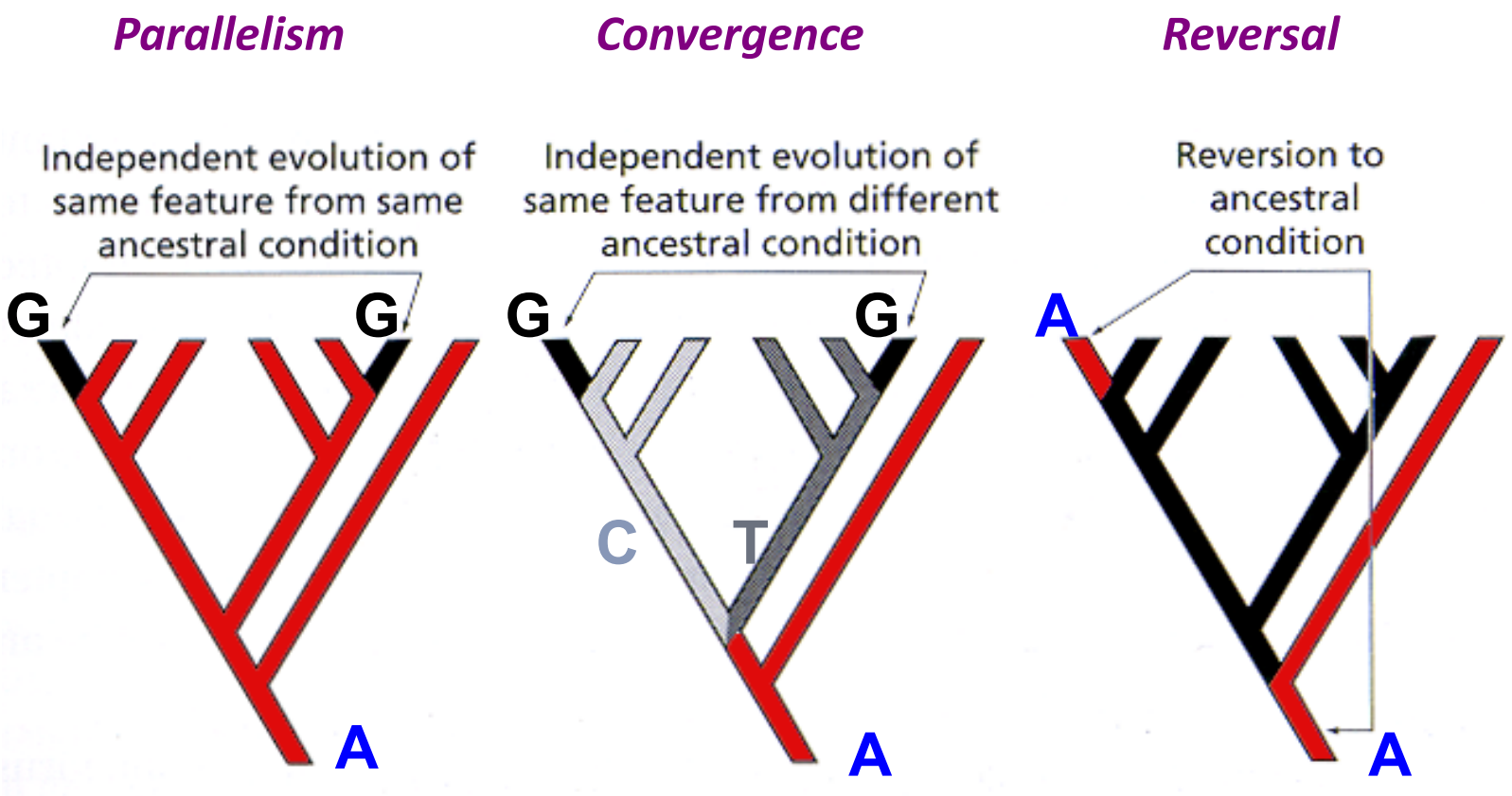
ACCCCTTC
ACCCCATA
ACTGCTTC
ACTGCTAA

Homoplasy

When two or more characters can't possibly fit on the same tree without requiring one character to undergo a parallel change or reversal



Parsimony - homoplasy



Three kinds of homoplasy

Parsimony can still work (According to some people)

- If characters are independent (a key assumption), homoplasy will be randomly distributed
- Homoplasies will tend to cancel each other out
- Non-homoplastic changes will tend to agree
- Therefore, with enough characters the shortest tree is a good estimate of the true tree

Real Example

- Any real instance of phylogenetic inference will follow the logic of what we were just talking about, but with sophisticated statistical modeling, it is not always obvious.
- For pretty clear cases, see the most recent issue of *Cladistics* such as:
- http:/dx.doi.org/10.1111/j.1096-0031.2009.00303.x/