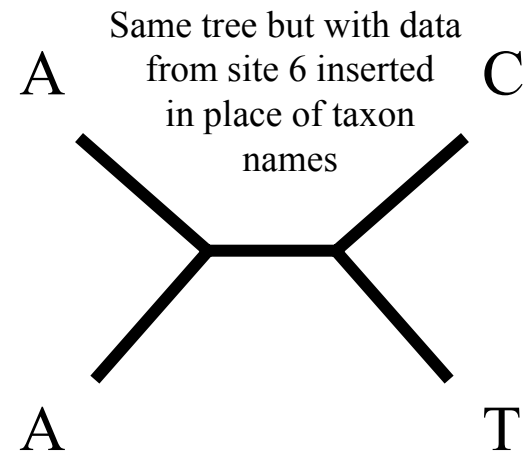
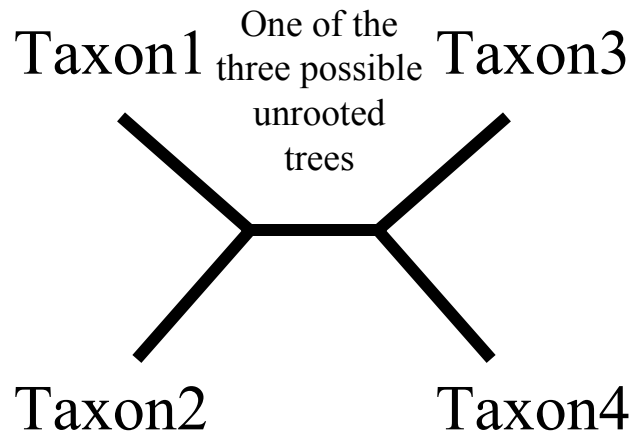
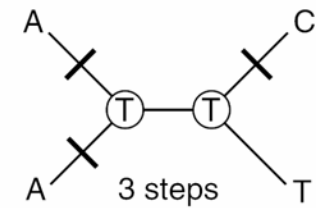
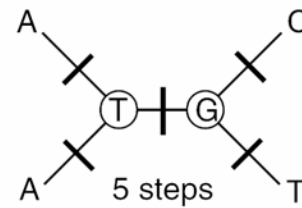
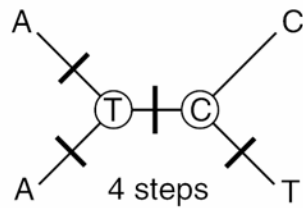
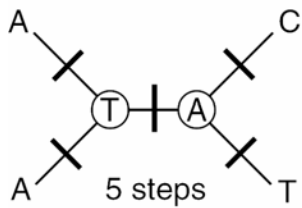
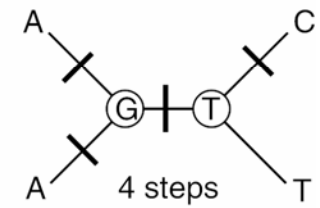
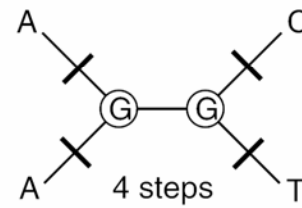
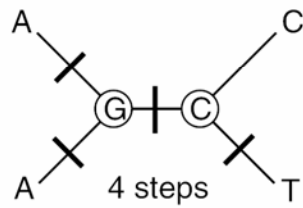
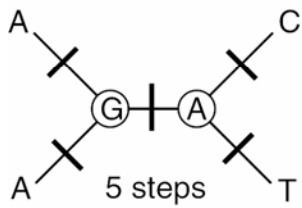
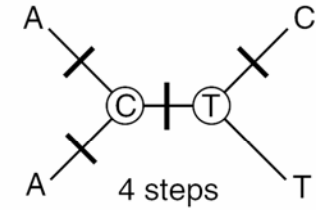
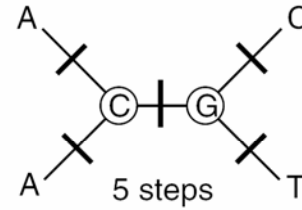
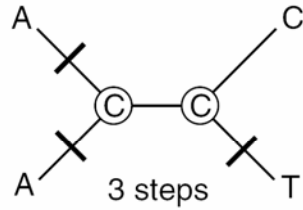
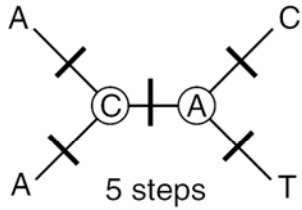
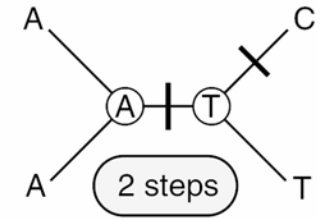
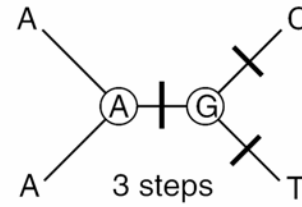
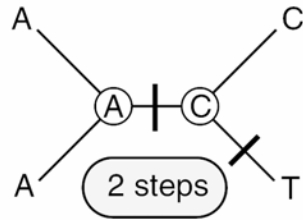
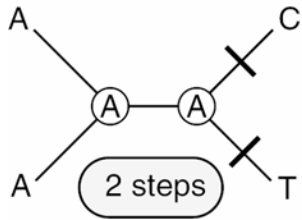


Parsimony

	123456789...
Taxon1	CGACC A GGT...
Taxon2	CGACC A GGT...
Taxon3	CGGT C GGT...
Taxon4	CGGC T GGT...



"Standard" Parsimony



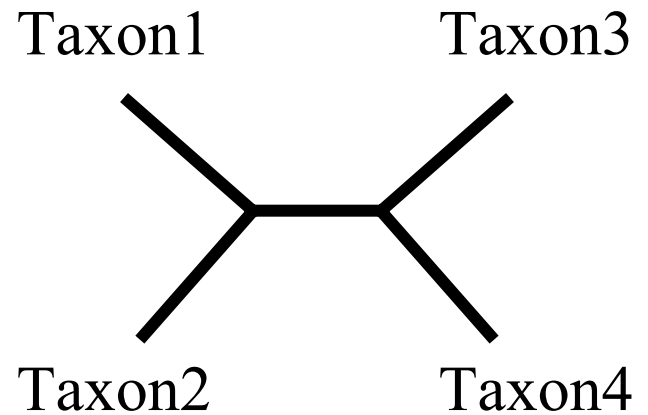
Important things to note about that last slide:

- *Two (2) steps was the minimum*
 - no way to explain the observed data with just 1 evolutionary change
- *More than one way to assign ancestral character states to get 2 steps*
 - one interior node must have A but the other interior node can have anything except G
- *Enumerating all possible combinations of ancestral states is not the most efficient way to determine the number of steps*
 - more on this later

Parsimony Steps

	1	2	3	4	5	6	7	8	9	...
Taxon1	C	G	A	C	C	A	G	G	T	...
Taxon2	C	G	A	C	C	A	G	G	T	...
Taxon3	C	G	G	T	C	C	G	G	T	...
Taxon4	C	G	G	C	C	T	G	G	T	...
Steps	0	0	1	1	0	2	0	0	0	...

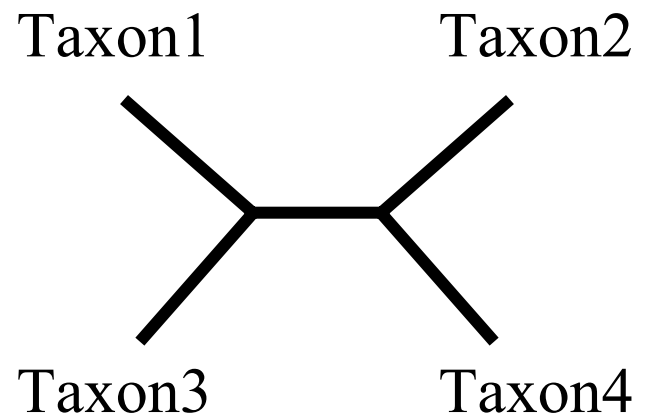
Tree 1's length for first 9 sites = 4



Let's call this tree 1:
(1,2,(3,4))

Parsimony Steps

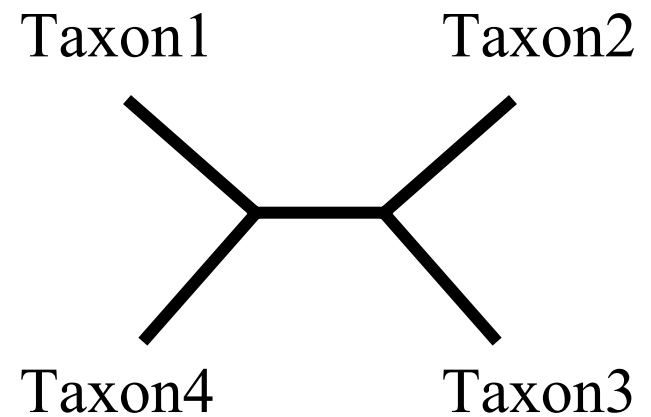
	1	2	3	4	5	6	7	8	9	...
Taxon1	C	G	A	C	C	A	G	G	T	...
Taxon2	C	G	A	C	C	A	G	G	T	...
Taxon3	C	G	G	T	C	C	G	G	T	...
Taxon4	C	G	G	C	C	T	G	G	T	...
Steps	0	0	2	1	0	2	0	0	0	...



Tree 2's length for first 9 sites = 5

Parsimony Steps

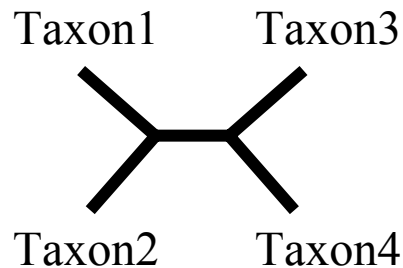
	1	2	3	4	5	6	7	8	9	...
Taxon1	C	G	A	C	C	A	G	G	T	...
Taxon2	C	G	A	C	C	A	G	G	T	...
Taxon3	C	G	T	C	C	G	G	T	...	
Taxon4	C	G	C	C	T	G	G	T	...	
Steps	0	0	2	1	0	2	0	0	0	...



Tree 3: (1,4,(2,3))

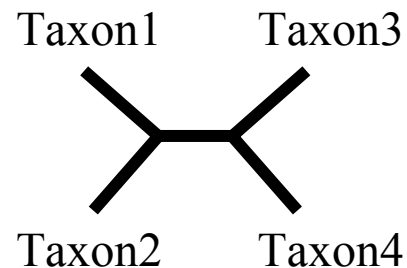
Tree 3's length for first 9 sites = 5

Parsimony (using only 9 sites)

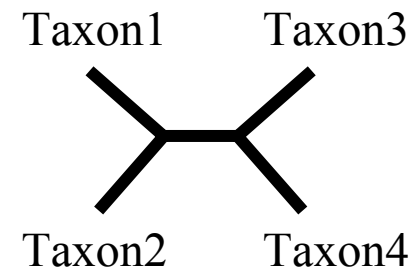


4 steps

most
parsimonious



5 steps



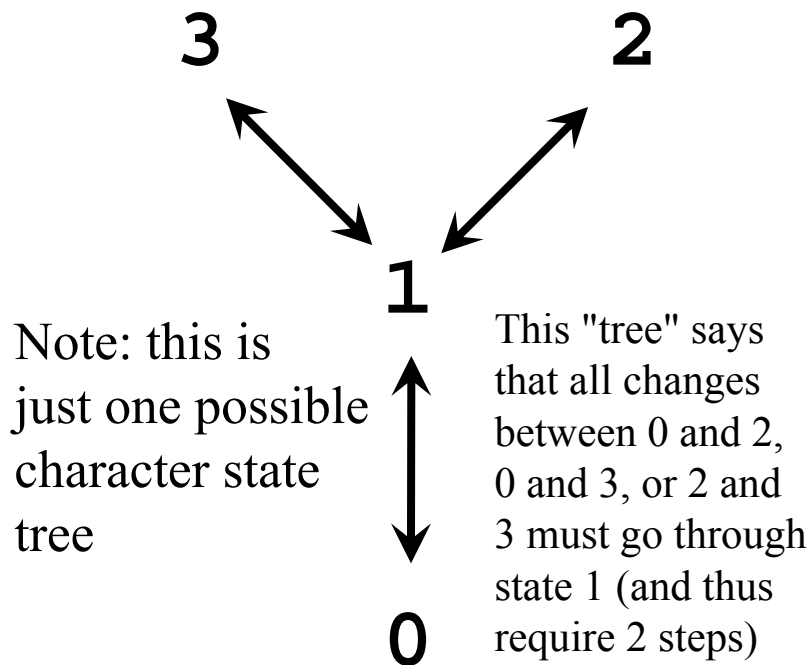
5 steps

This is the simplest explanation of the data for the first 9 sites according to the parsimony criterion.

Choosing one of the other two trees requires additional (ad hoc) justification.

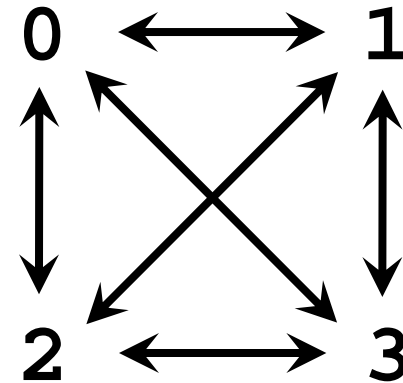
Wagner vs. Fitch Parsimony

(distinction exists only in case of multistate characters)



Wagner

(ordered characters)



In Fitch Parsimony, a change between any two states is possible, and all changes count just 1 step

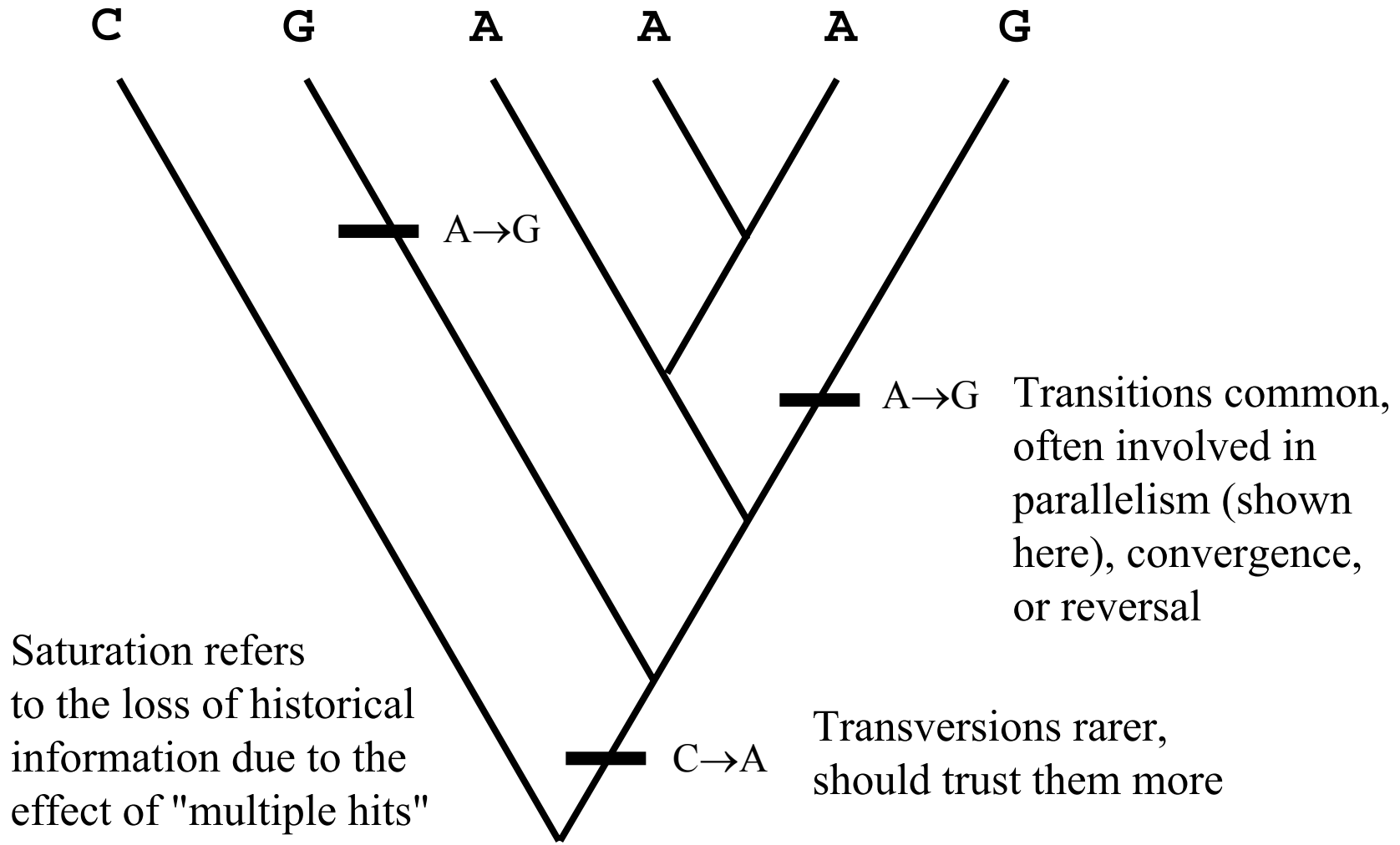
Fitch

(unordered characters)

Transversion Parsimony

- Transitions ($A \leftrightarrow G$, $C \leftrightarrow T$) more common than transversions (all other changes)
- Transitions *saturate* faster than transversions, thus transversions are sometimes more reliable for reconstructing history
- Transversion parsimony is extreme, ignoring all transitions, counts 1 step for each transversion

Saturation



Implementing Transversion Parsimony

- *Ambiguity codes:*
 - R means purine (A or G)
 - Y means pyrimidine (C or T)
- *Replace nucleotides with either R or Y*
 - only transversions will be detectable
- *Note: Nexus data file format allows you to do this substitution virtually*
 - no need to actually modify your data

Step Matrices

		To			
		A	C	G	T
From	A	0	1	1	1
	C	1	0	1	1
	G	1	1	0	1
	T	1	1	1	0

Step matrix for Fitch parsimony

Step Matrices

		To				
		A	C	G	T	
From	A	0	⑤	1	⑤	It counts 5 for each transversion
	C	⑤	0	⑤	1	
	G	1	⑤	0	⑤	
	T	⑤	1	⑤	0	

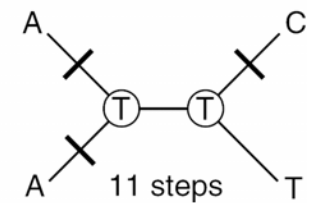
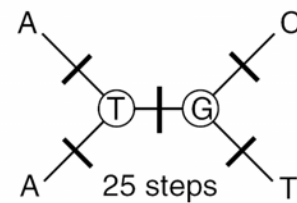
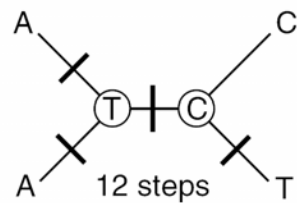
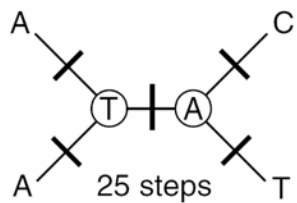
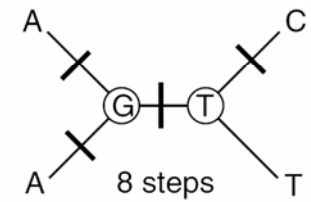
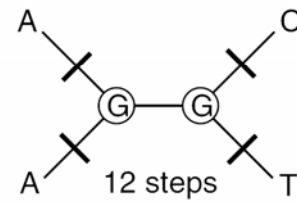
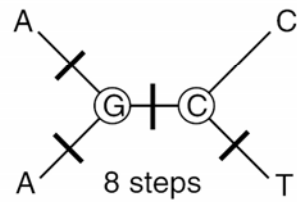
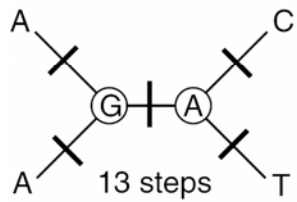
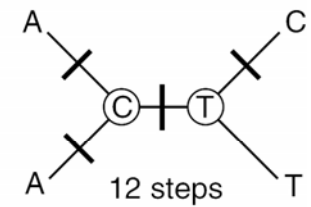
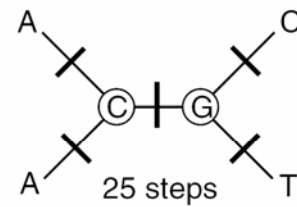
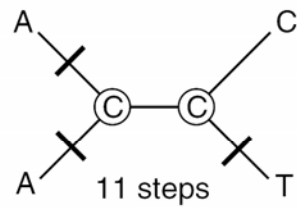
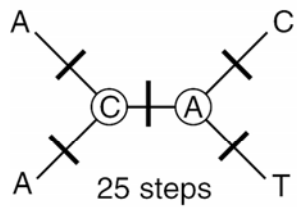
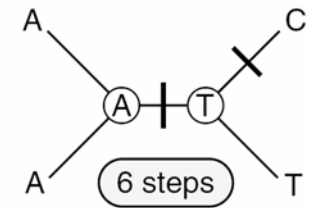
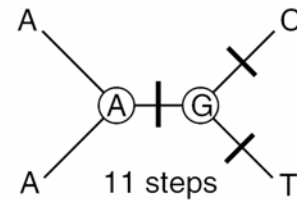
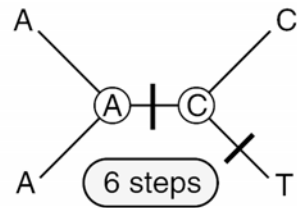
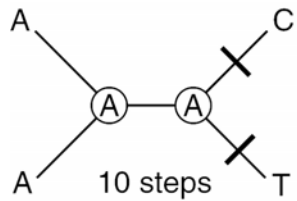
This step matrix implements something like transversion parsimony, but less severe

Step Matrices

		To				
		A	C	G	T	
From	A	0	5	①	5	And counts 1 step for each transition
	C	5	0	5	①	
	G	①	5	0	5	
	T	5	①	5	0	

This step matrix implements something like transversion parsimony, but less severe

Generalized Parsimony



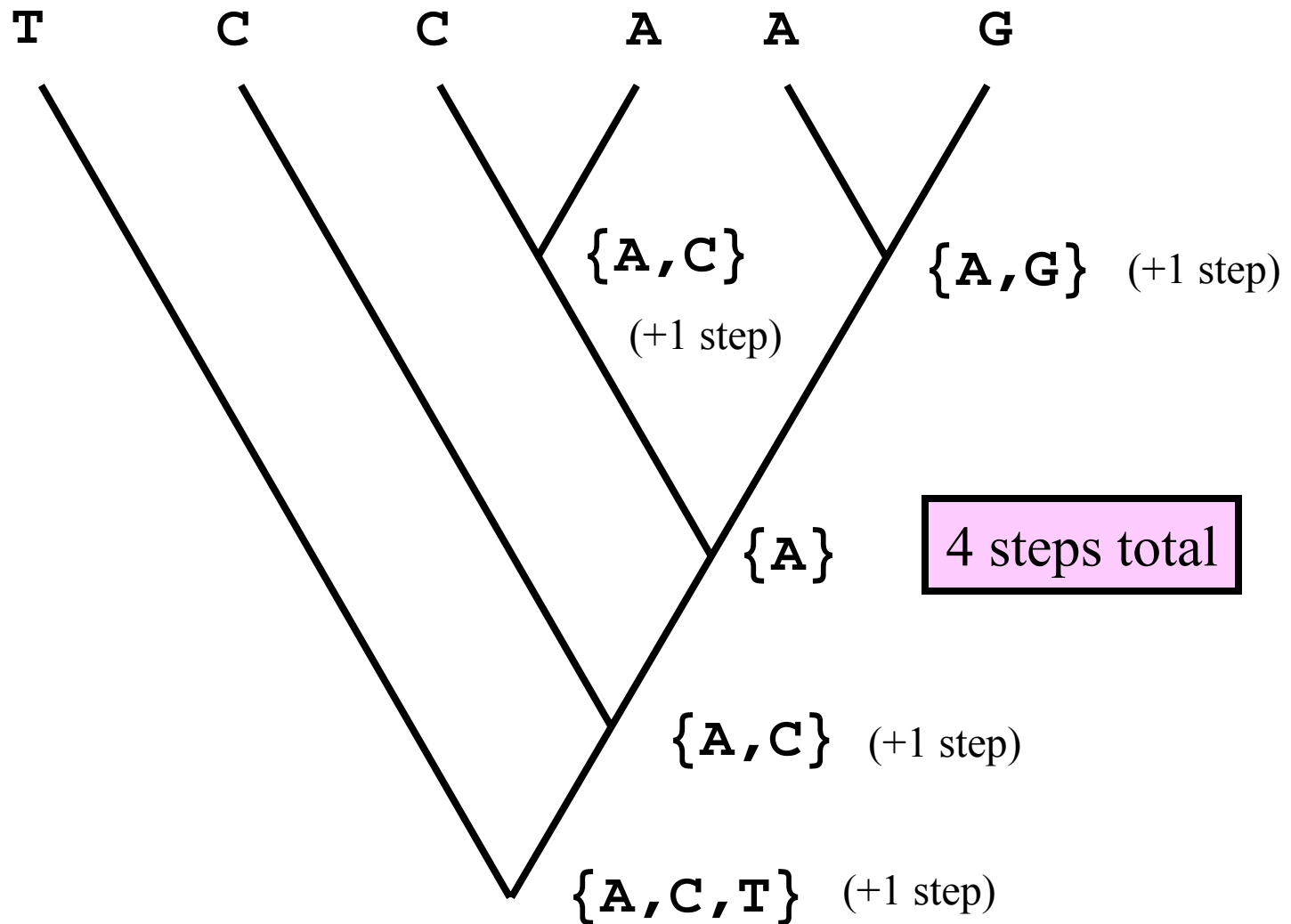
Important points

- *Do not compare scores across parsimony variants*
 - A tree with a transversion parsimony score of 25 is not necessarily better than a tree with a Fitch parsimony score of 31
- *Parsimony does not provide any guidance for selecting weights for step matrices*
 - parsimony cannot tell us that the transition:transversion weight ratio 1:5 is better than 1:1

Other variants

- *Camin-Sokal parsimony*
 - characters are assumed irreversible
 - ancestral state assumed known
 - forces use of rooted trees
- *Dollo parsimony*
 - derived state can arise only once, but as many reversals as needed are allowed
 - popular for modeling restriction sites (which are lost more easily than they are gained)
- *Unweighted parsimony, equal-weighted parsimony*
 - usually means Fitch parsimony (what I call standard parsimony)

Counting steps with a minimum of effort



What is "weighted" parsimony?

When someone says they are using weighted parsimony, this can mean more than one thing:

- *Some changes weighted more than others*
 - i.e. generalized parsimony
- *Some sites weighted more than other sites*
 - weighting may be determined *a priori*
 - weighting may be dynamic (i.e. a function of the number of changes reconstructed)