

Bioinformatics II:

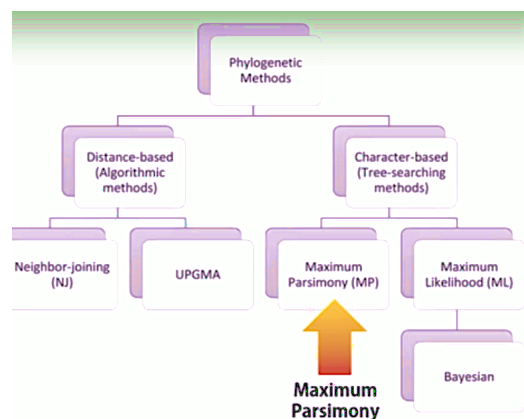
Building a phylogenetic tree using Parsimony methods

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1

What is Parsimony methods

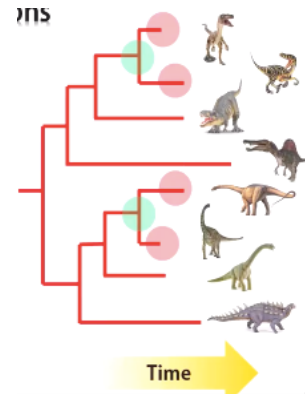
- It is a method taxa (for classification) in ways that minimize the number of evolutionary changes.
- What is the Goal of the method?
- Find the tree that allows evolution of the sequences with the fewest changes.
- This is called a *most parsimonious* (MP) tree
- **NOTE: Taxonomists : scientists who do classification through evaluations.**



2

What is the idea of the Parsimony method?











- It is based on, all other species being equal.
- For e.g: 4 nucleotide changes, is more likely to be true than a complex one. (sub-grouping).
- The method assumes that change in characteristic occurs in lineage over time.
- But, the rate of mutation is NOT constant over time.
- So, leaves (descendent) can have different distances from the root.



3

Example? Construct a tree that represent minimum evolutionary changes

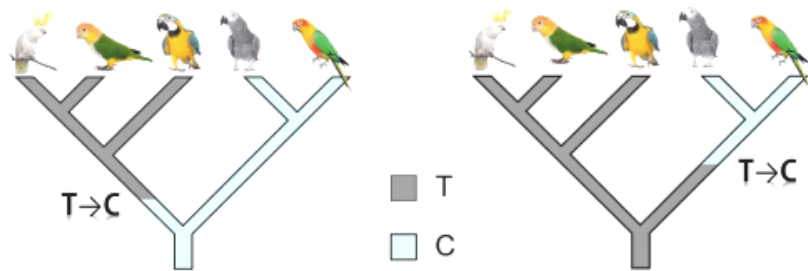
- For site 1, the tree that represents minimum changes groups all the (parrots) - a type of birds - show "T" in one group and all those showing "C" in another group.

	Sites				Sites		
Species	1	2	3	Species	1	2	3
	T	A	G		T	A	G
	C	A	A		C	A	A
	T	C	G		T	C	G
	T	C	G		T	C	G
	C	A	A		C	A	A

4

The question: How these taxa divergence started from an ancestor?

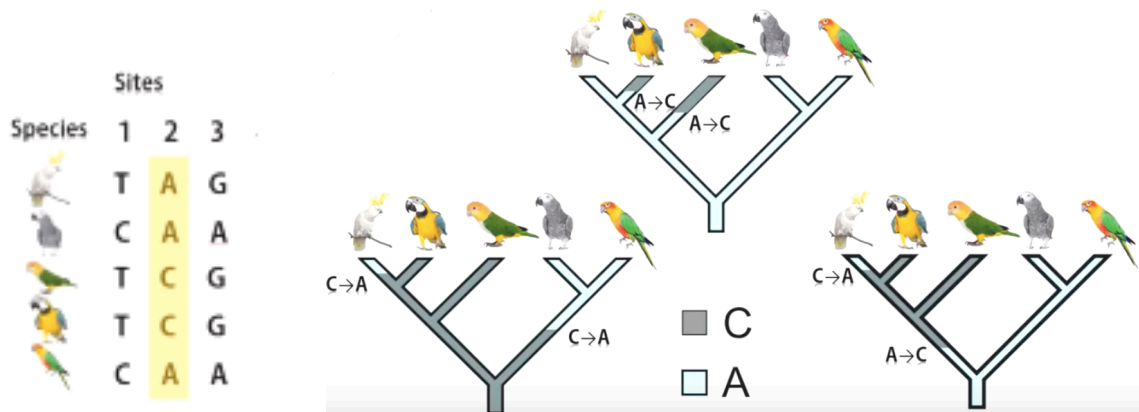
- The two trees are topologically identical, but they assume different ancestral states



5

2

- For site 2, there are three possible parsimonious trees.



6






2

- All these trees agree on:
- How to cluster parrots in different groups.
- The minimum number of substitution.
- But they disagree on:
- How this evolutionary divergence has occurred in the course of evolution.
- Again, tree are topologically identical, but they assume different ancestral state

7

3

- For site 3, there are 2 possible parsimonious tree.

	Sites		
Species	1	2	3
	T	A	G
	C	A	A
	T	C	G
	T	C	G
	C	A	A



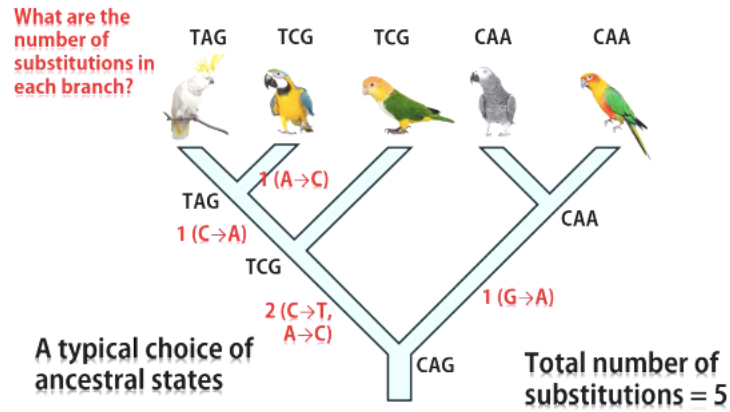
■ A
□ G



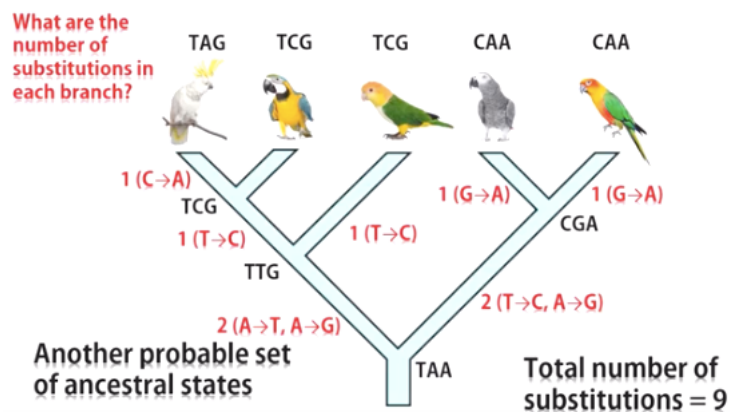
8

Calculate the number of substitutions steps on each branch?

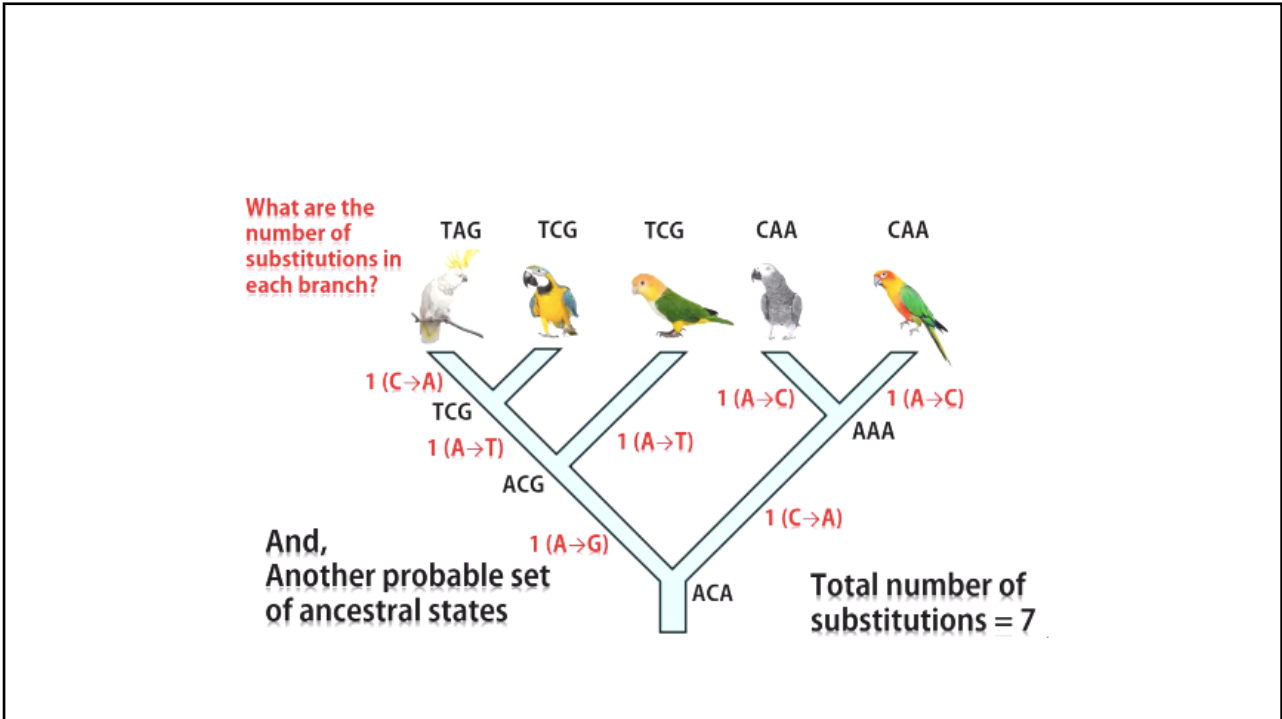
- So, this depends on the ancestral states.



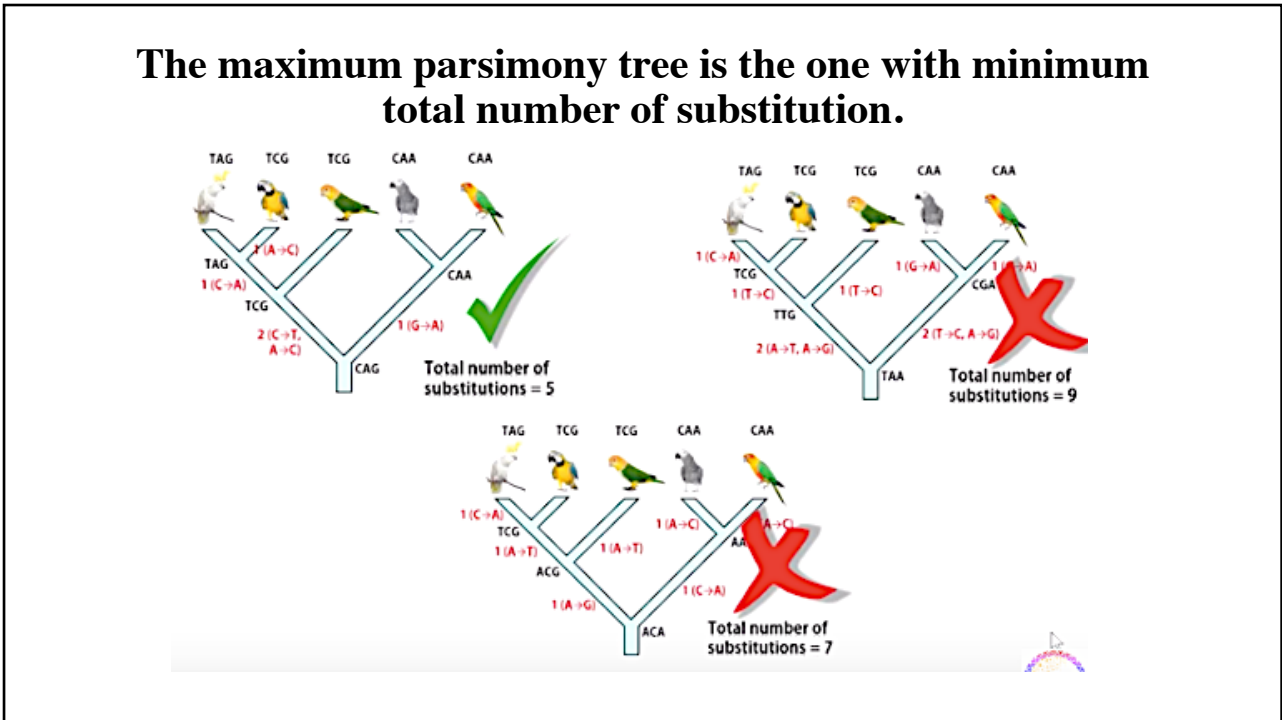
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10



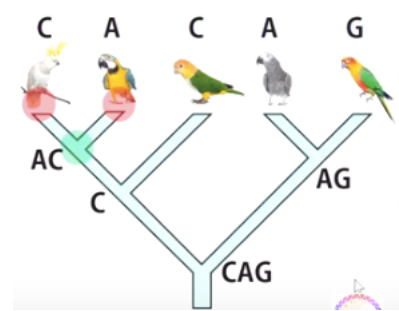
11



12

Fitch's algorithm

- To count the number of steps of a tree requires at given site:
- Construct a set of nucleotides that are observed there.
- Go down the tree.
- For each ancestral node (say A).
- Consider its two immediate descendent sets (say D1 and D2).
- Nucleotide set in ancestor A
- $A = D1 \cup D2$.
- if D1 are dis-joint
- Else, $A = D1 \cap D2$



13

Tutorial

- Make a Phylogenetic tree using NCBI?
- <https://www.youtube.com/watch?v=iIE-SkJCFOc>

14