Cladistics Module

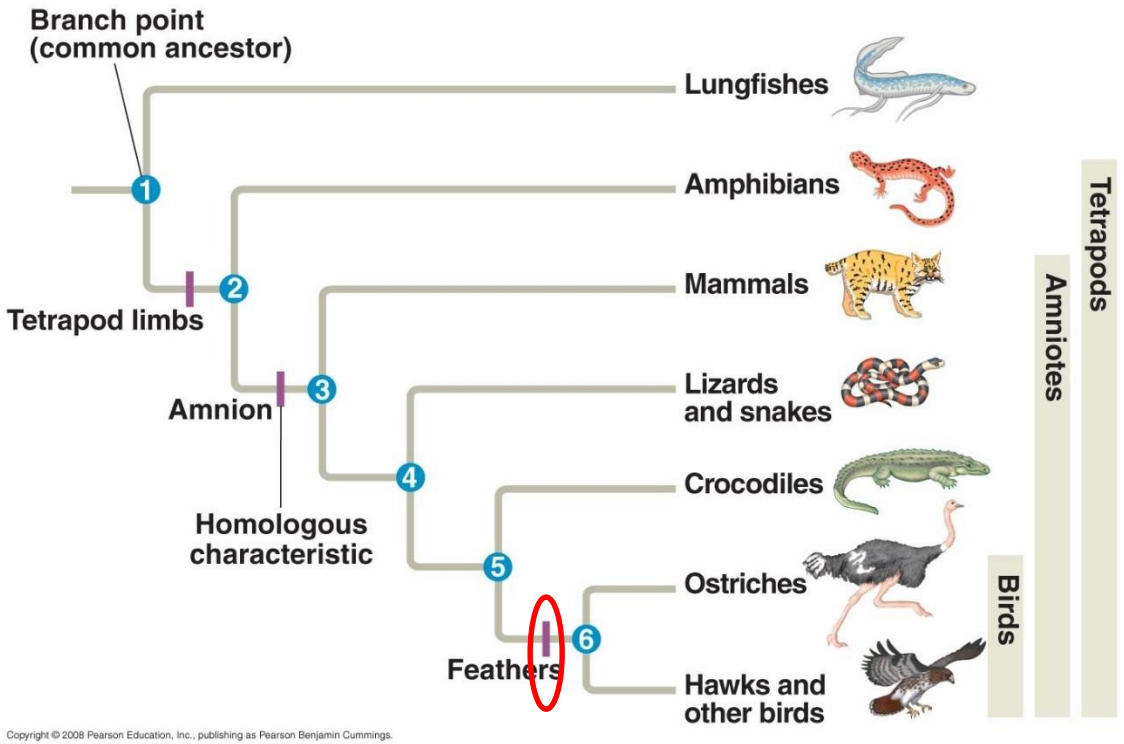
Using Inherited Characteristics

To

Compile a Cladogram Showing Phylogeny

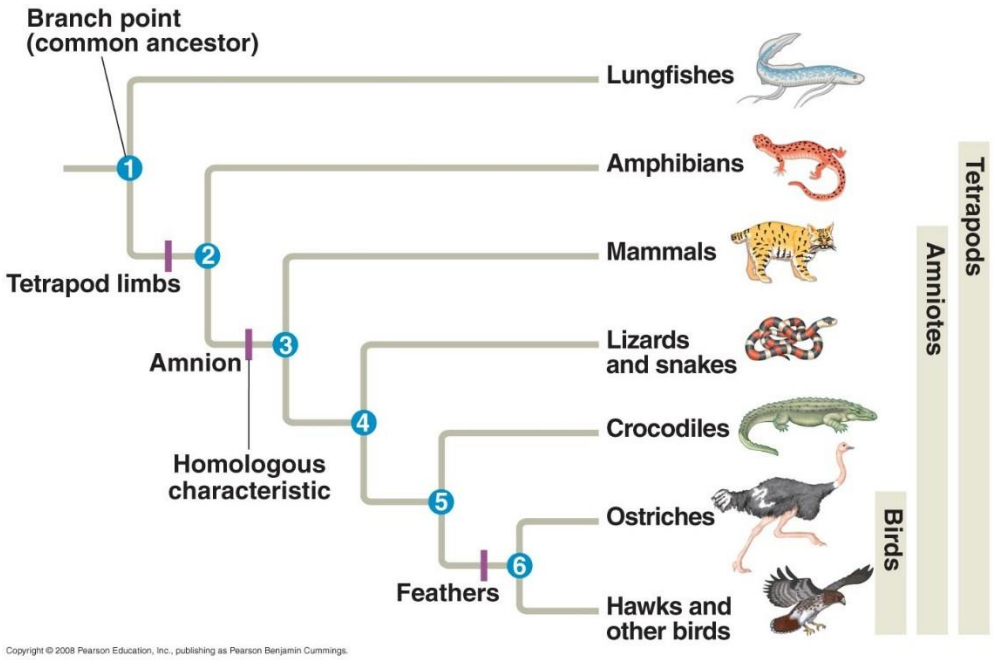
BIOL1407

Characters



- Cladograms often show new traits that arise (acquisition of characters) with lines drawn across the branches.
- In this cladogram, the acquisition of feathers is shown on the branch leading to birds, as indicated by the red oval.

Characters

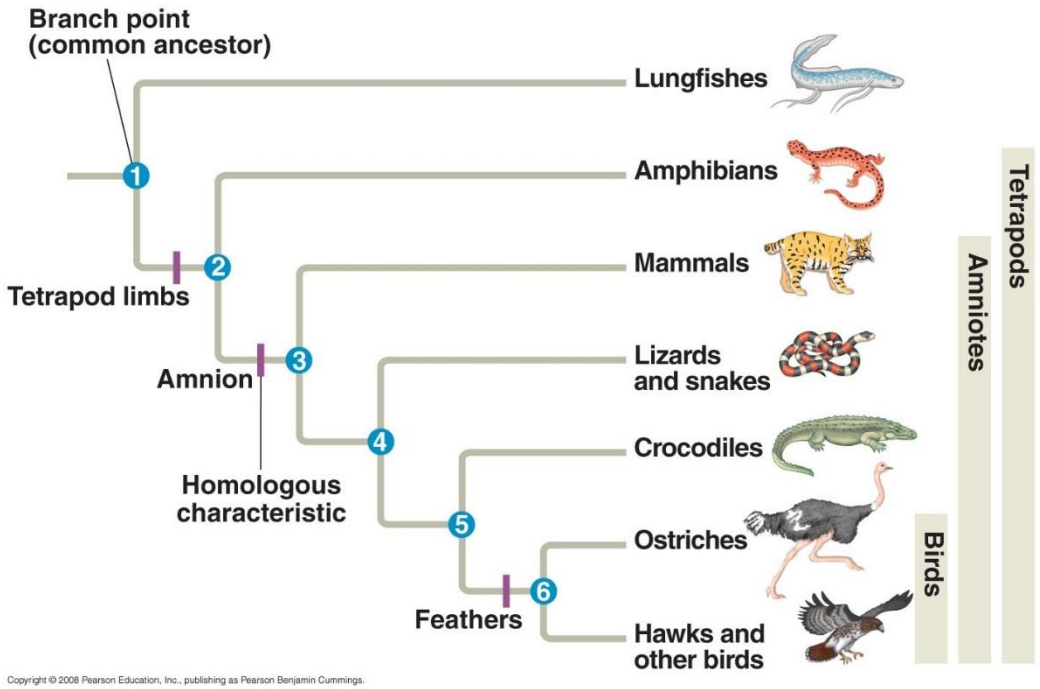


- Characters can also be lost.
- The loss of a trait is a character that is different from the gain of a trait.
- For example, snakes have no legs. However, they are still tetrapods because they descended from an ancestor with legs.

Types of Characters

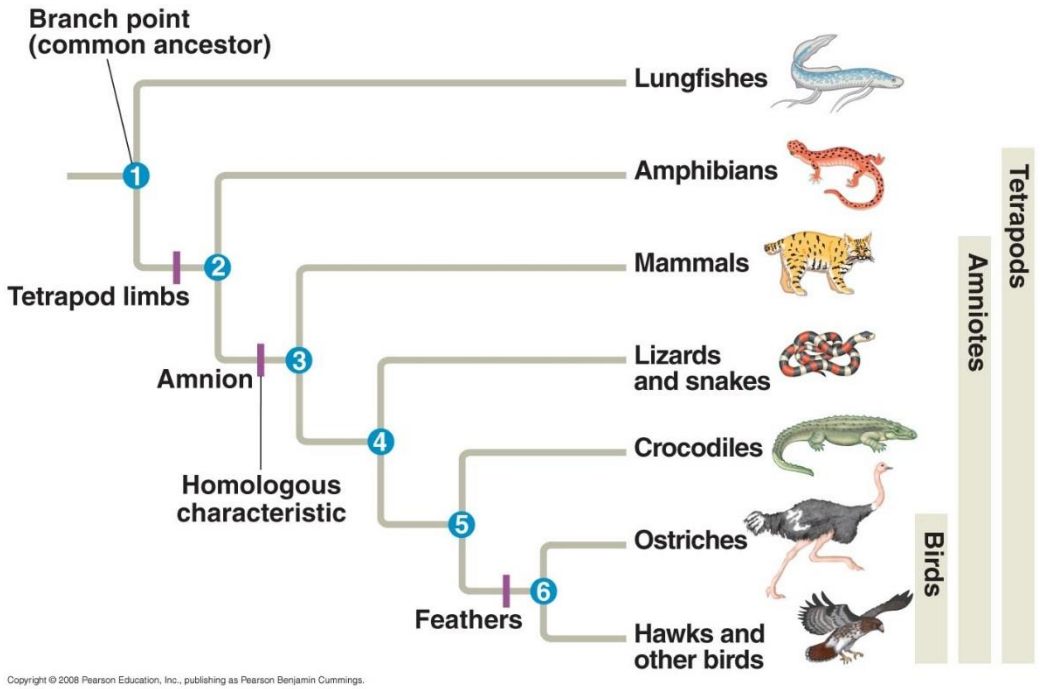
- From the perspective of a cladogram, there are three types of characters:
  - Shared primitive characters
  - Shared derived characters
  - Unique derived characters

Types of Characters



- **Shared primitive character** – a character that is common to all of the taxa under consideration because their common ancestor had it.
- For the tetrapods in this cladogram, the trait “tetrapod limbs” is a shared primitive character

Types of Characters

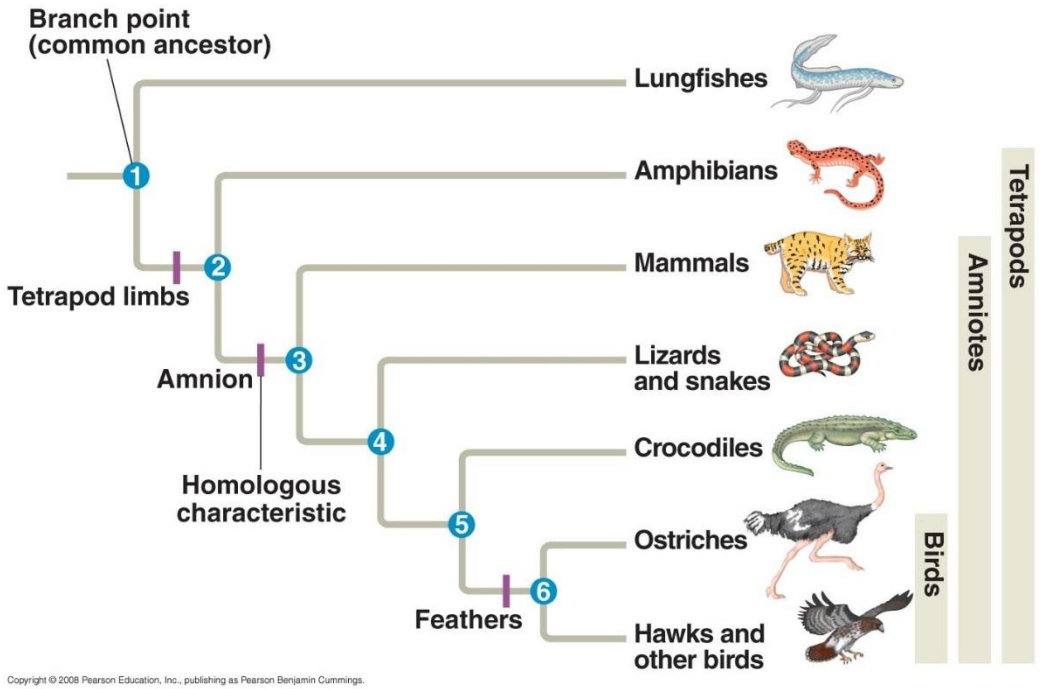


- **Shared derived character** – a character that is present in more than one taxon but is not found in all of the taxa under consideration.
- The trait “amnion” is a shared derived character because some of the tetrapods have it but not all.

Perspectives

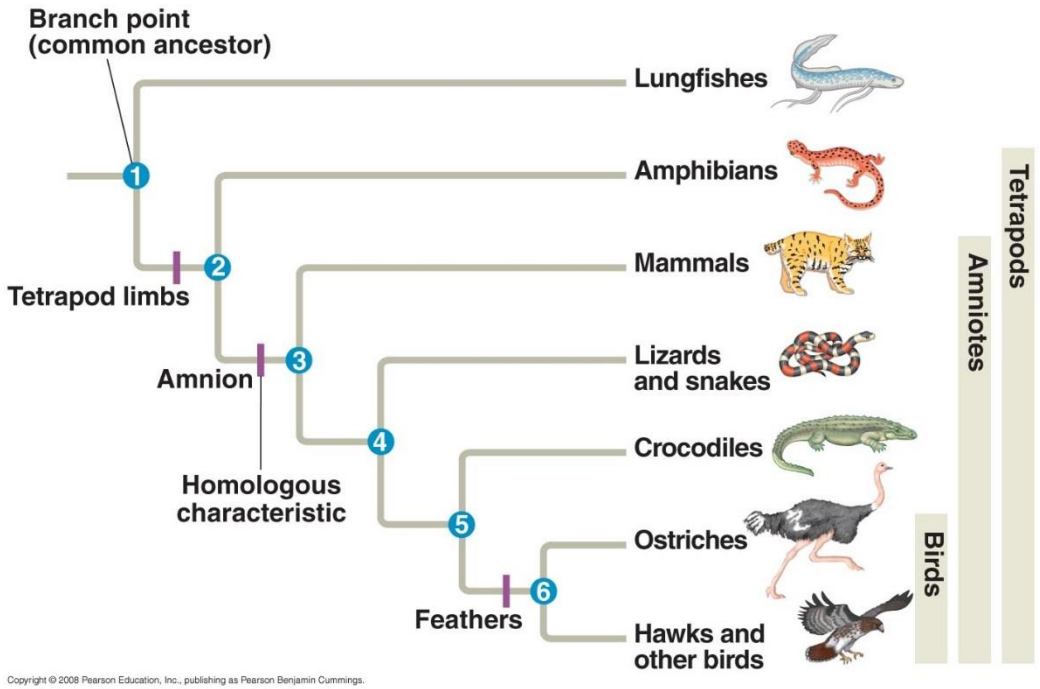
- Whether a character is “shared primitive” or “shared derived” depends on which group you are considering.
- It is a matter of perspective.

Perspectives: An Example



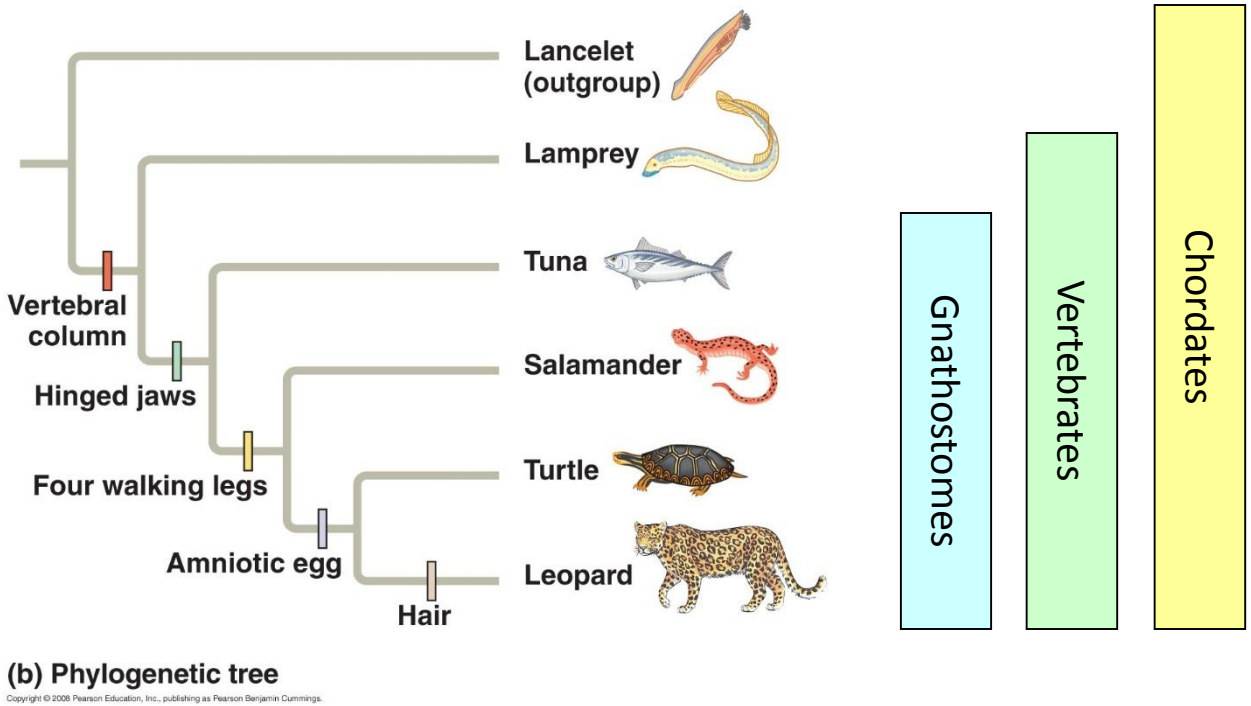
- **Reconsider the character “tetrapod limbs”.**
- **From the perspective of tetrapods only, it is a shared primitive character.**
- **From the perspective of all taxa on the tree (including lungfishes), it is a shared derived character.**

Perspectives: Another Example



- **Consider the character “feathers”.**
- **From the perspective of birds only, it is a shared primitive character.**
- **From the perspective of amniotes, it is a shared derived character.**

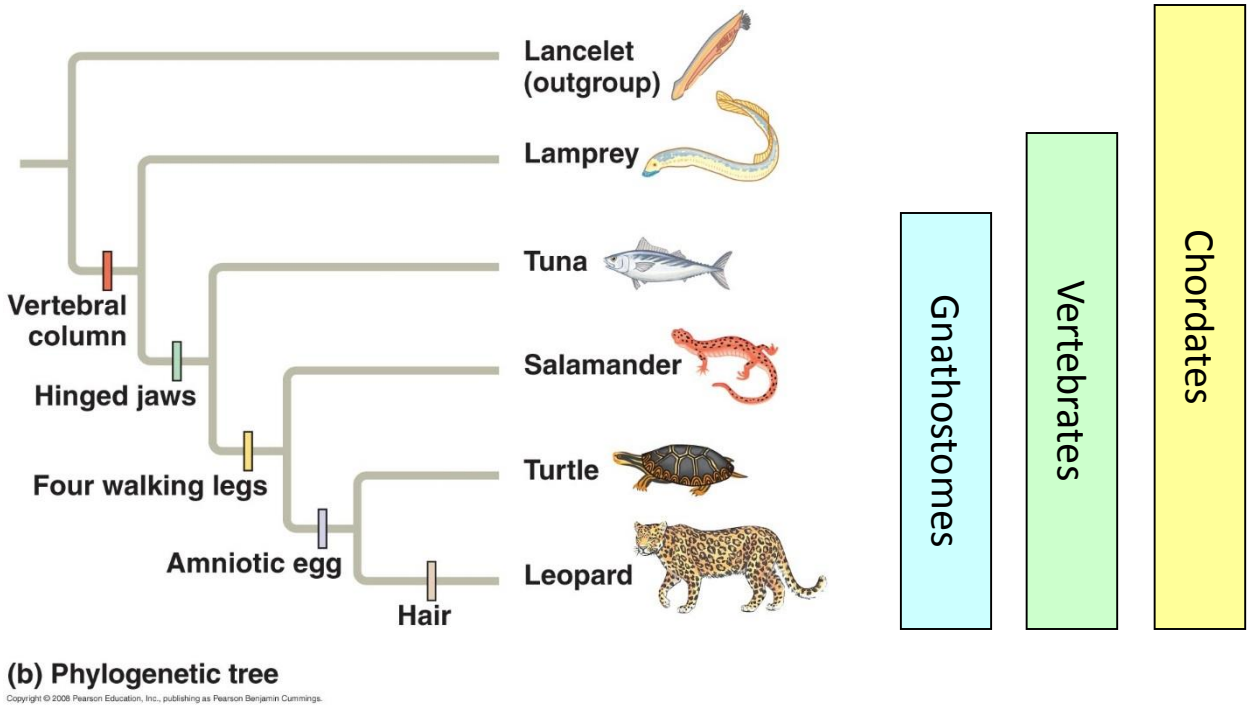
Question



(b) Phylogenetic tree

- **Consider the character “hinged jaws”.**
- **Hinged jaws would be a shared primitive character for what group?**
- **Hinged jaws would be a shared derived character for what group?**

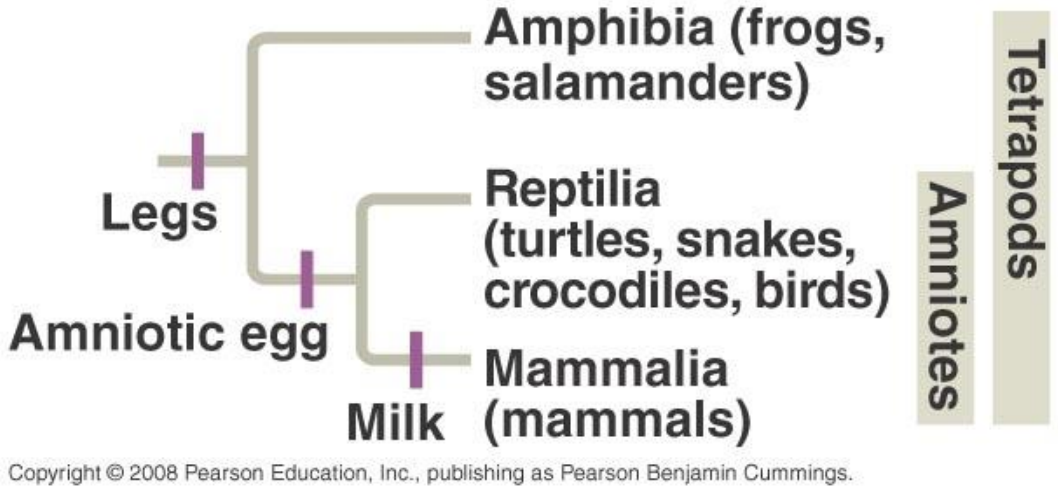
Types of Characters



(b) Phylogenetic tree

- **Unique derived character** – a character found only in one taxon under consideration.
- In this cladogram, hair is a unique derived character found only in the leopard.

Question



- Which character on the cladogram is an unique derived character?
- Which character on the cladogram is a shared primitive character for tetrapods?
- Which character on the cladogram is a shared derived character for tetrapods?
- Which character on the cladogram is a shared primitive character for amniotes?

Technique of Cladistics

- First, you pick the taxa under consideration.
- Then, you pick characters that are:
  - Heritable
  - Independent of one another
  - Unambiguous
  - Homologous, if possible

Technique of Cladistics

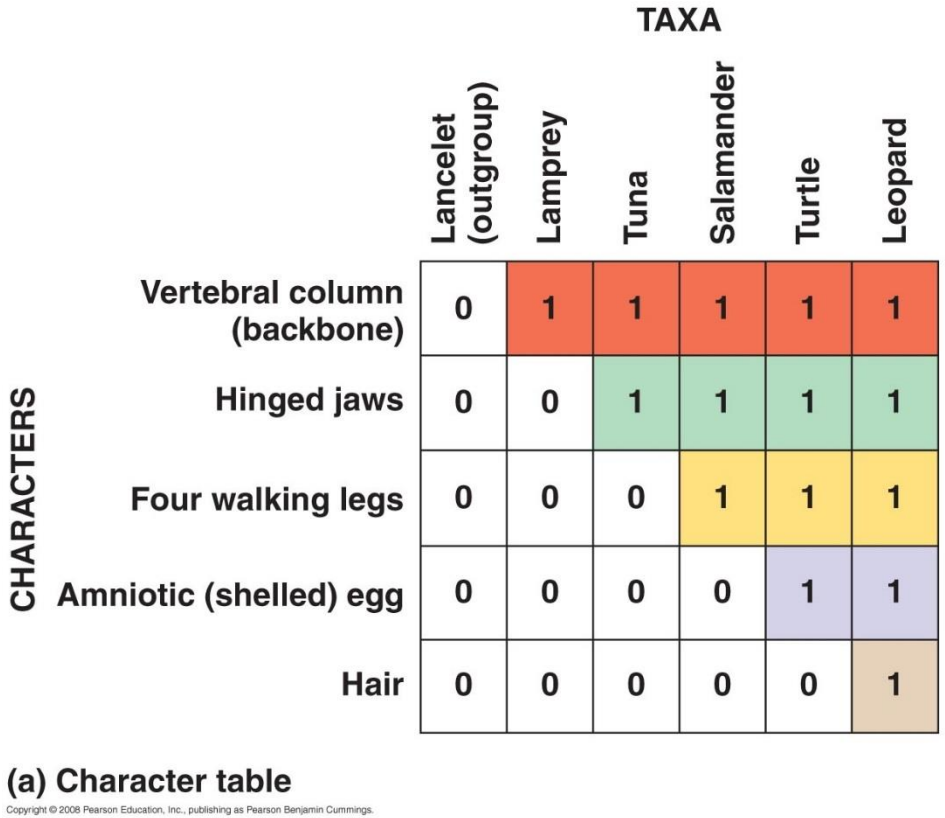
- Next, you choose an **outgroup**.
- The outgroup is a taxon you think is a close relative to the taxa under consideration and shows the most primitive traits of the group.
- What you are trying to do with the outgroup is choose a taxon that is as similar to the group's common ancestor as possible.

Technique of Cladistics

- The next step is to build a **data matrix** for each character.
- For each taxon, including the outgroup, you code whether each character is present or absent.

Data Matrix

- In this data matrix, “0” means a character is absent.
- “1” means a character is present.



CHARACTERS	TAXA: Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

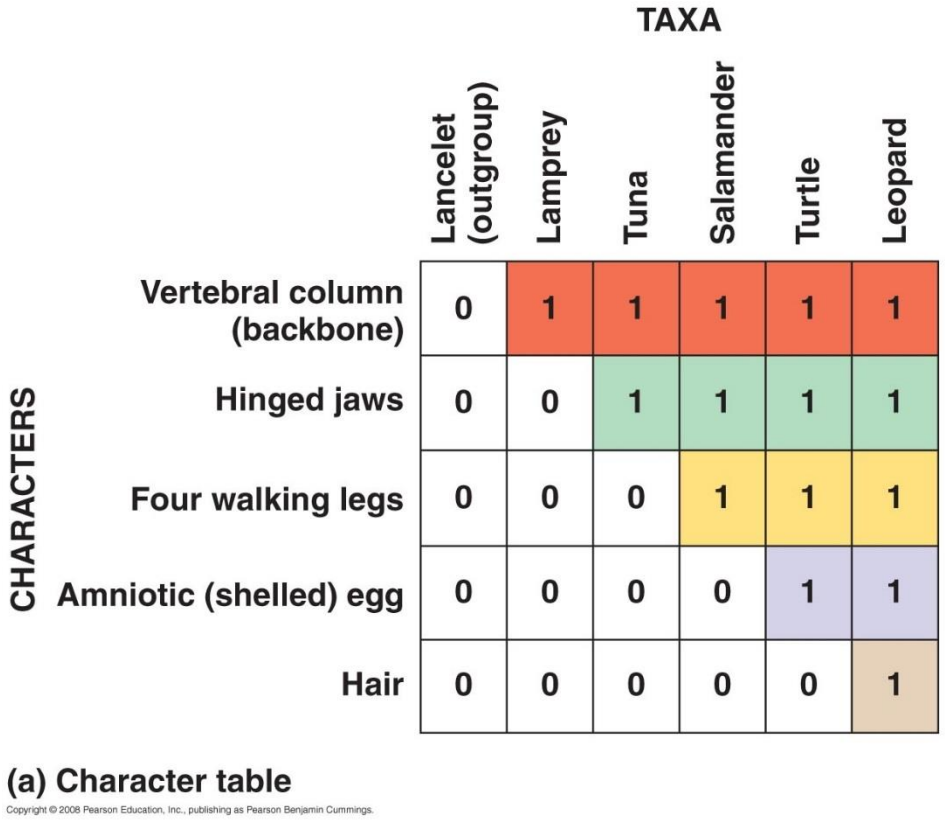
(a) Character table

Technique of Cladistics

- The last step is to use the data matrix to build your cladogram.
- The two taxa that share the most characters are grouped together first.
- Then, that pair is connected to the taxon that shares the most characters with them.
- You continue this process until all taxa are represented on the tree.

Building a Cladogram from a Data Matrix

- In this example, the turtle and the leopard share 4 characters.
- They are the first pair.

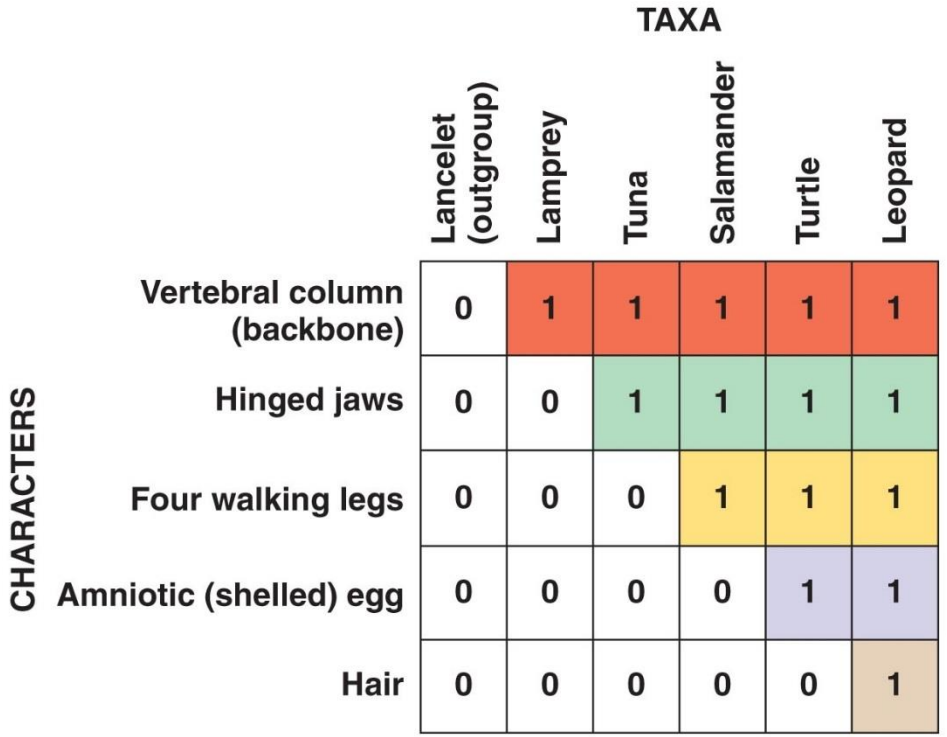


CHARACTERS	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
	TAXA					
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

Building a Cladogram from a Data Matrix

- The salamander shares 3 characters with the turtle-leopard pair.
- It is the next taxon added to the tree.



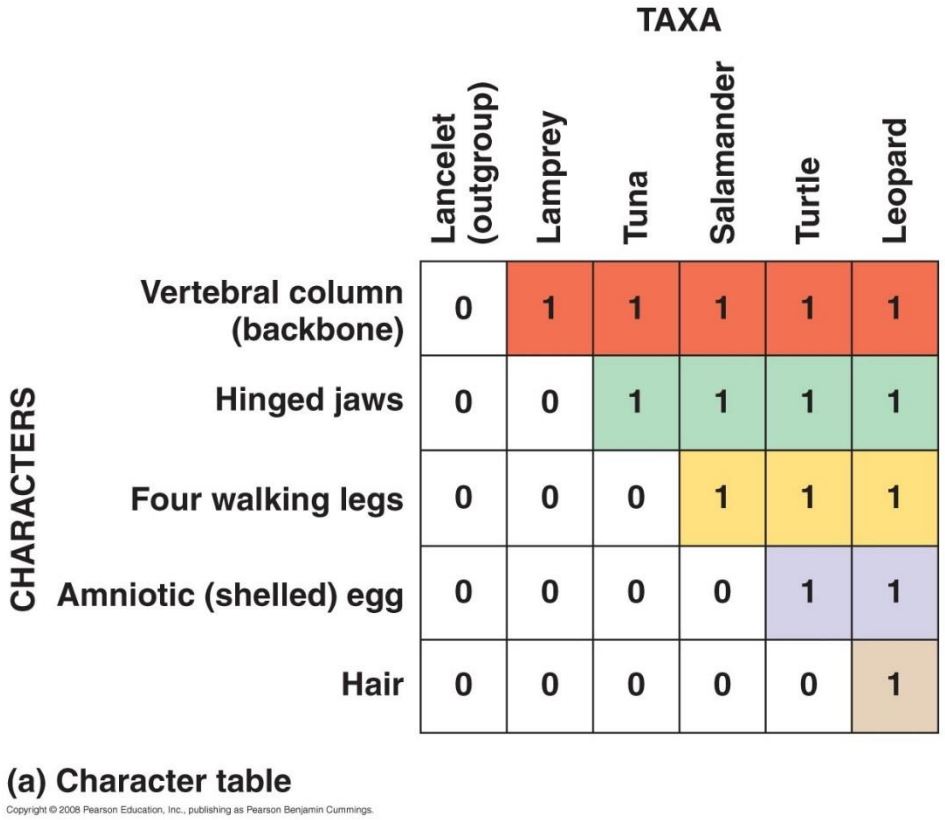
TAXA

CHARACTERS	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

Building a Cladogram from a Data Matrix

- The tuna shares 2 characters with the salamander-turtle-leopard group.
- It is the next taxon added to the tree.



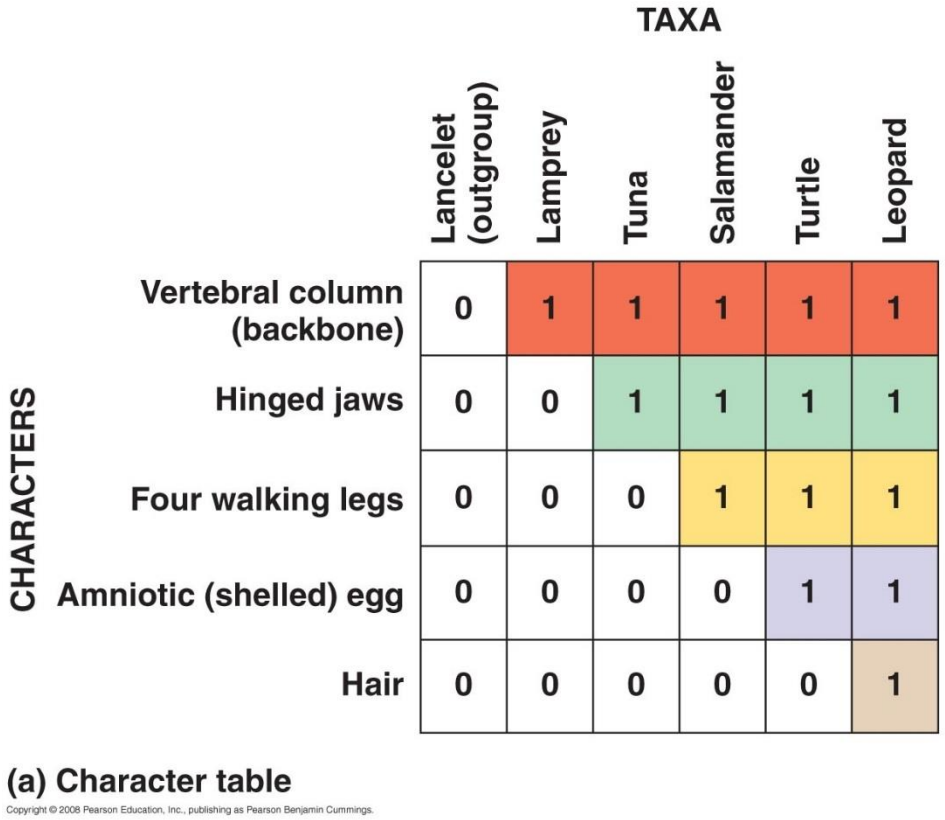
TAXA

CHARACTERS	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

Building a Cladogram from a Data Matrix

- The lamprey shares 1 character with the tuna-salamander-turtle-leopard group.
- It is the next taxon added to the tree.



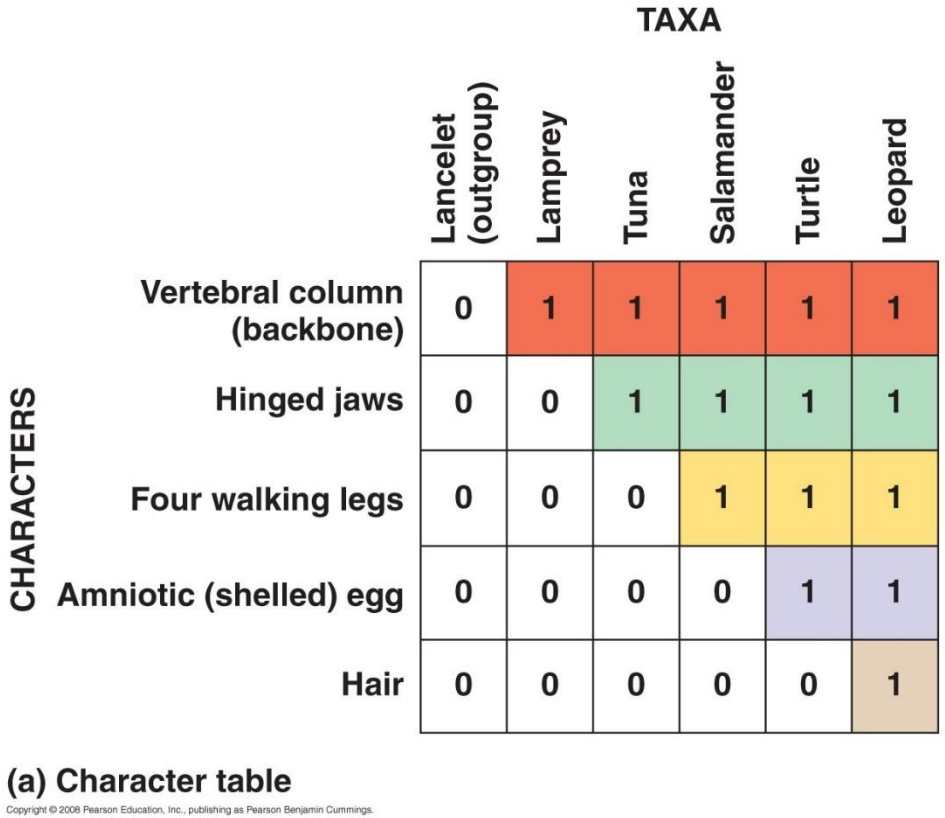
TAXA

CHARACTERS	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

Building a Cladogram from a Data Matrix

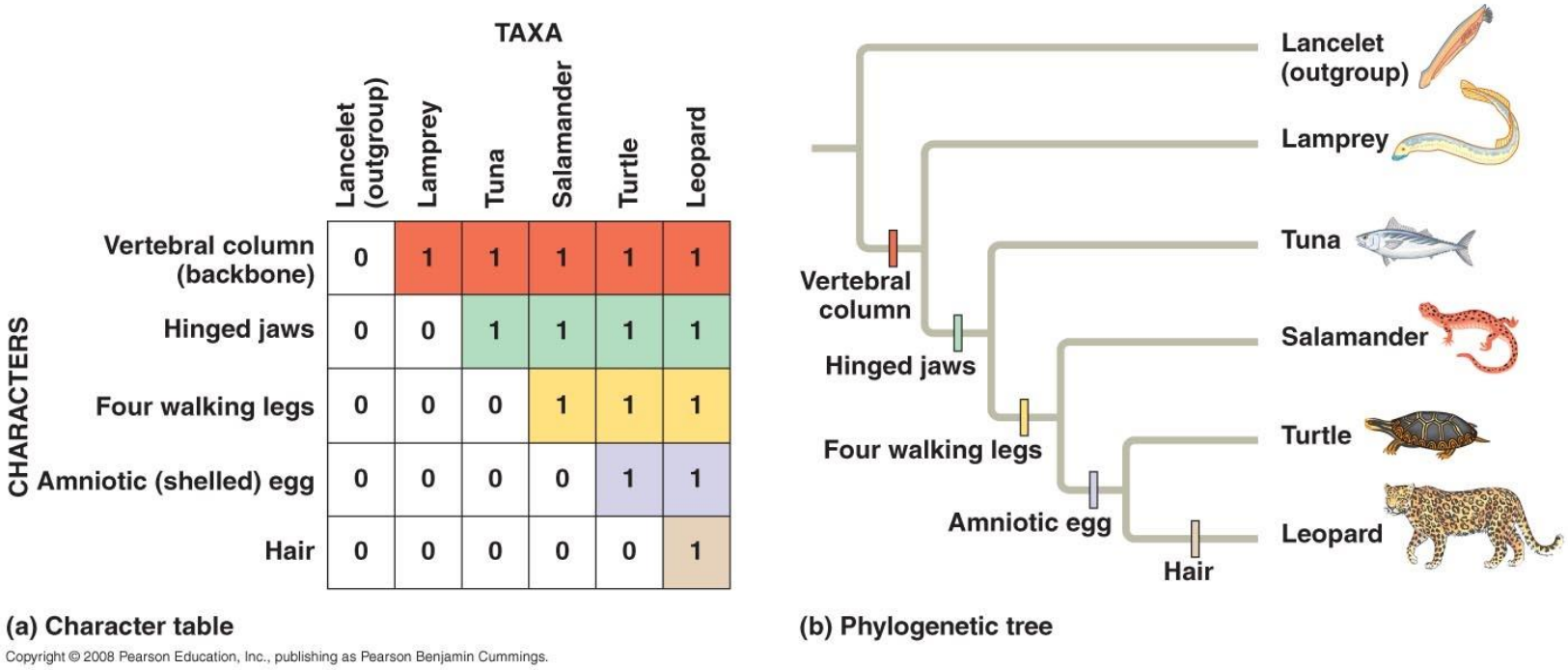
- Finally, the lancelet is added to the tree.
- Note that the lancelet is the outgroup.



CHARACTERS	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
	TAXA					
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

The Cladogram



Principle of Parsimony

- The example that we used was very straightforward.
- In reality, a cladogram can include many taxa and many characters.
- In fact, the more characters included, the better the analysis.
- This makes the data matrix complicated and building the tree becomes too difficult to do by hand.

Principle of Parsimony

- Modern cladistics uses computer programs to build cladograms from large data matrices.
- Sometimes an analysis produces more than one possible cladogram for a data matrix.
- When this occurs, you use the **Principle of Parsimony** to choose the most likely cladogram.

Principle of Parsimony

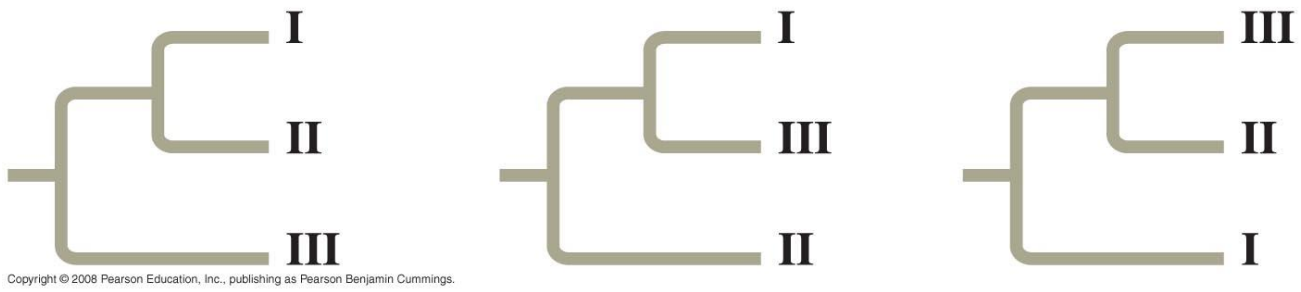
- The underlying assumption of the Principle of Parsimony is that the simplest cladogram is most likely to be true.
- The cladogram with the fewest steps is the simplest cladogram.
- A step involves the acquisition or loss of a character.

Principle of Parsimony

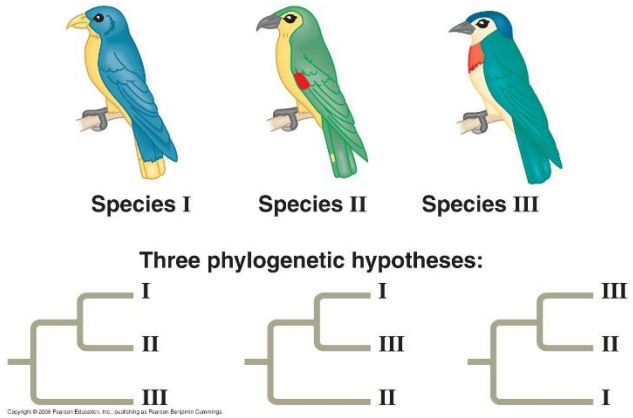
- Cladistics only uses shared derived characters to determine relationships.
- Shared primitive characters and unique derived characters are not counted.

An Example

Three phylogenetic hypotheses:



An Example



- For these three birds, there are three possible cladograms.
- Using DNA sequencing information, a data matrix was built.

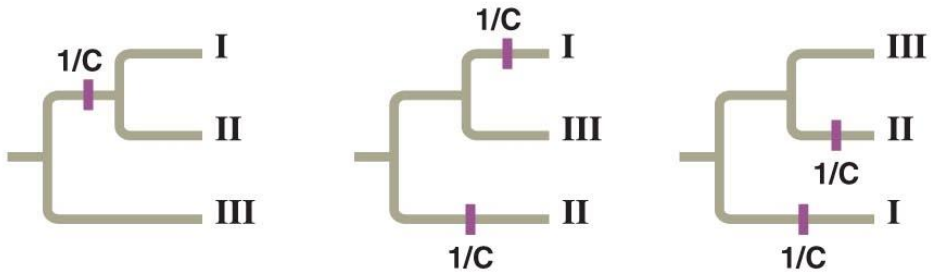
An Example

	Site 1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T

- The data matrix shows which nucleotide is found at four locations in the DNA sequence.

An Example

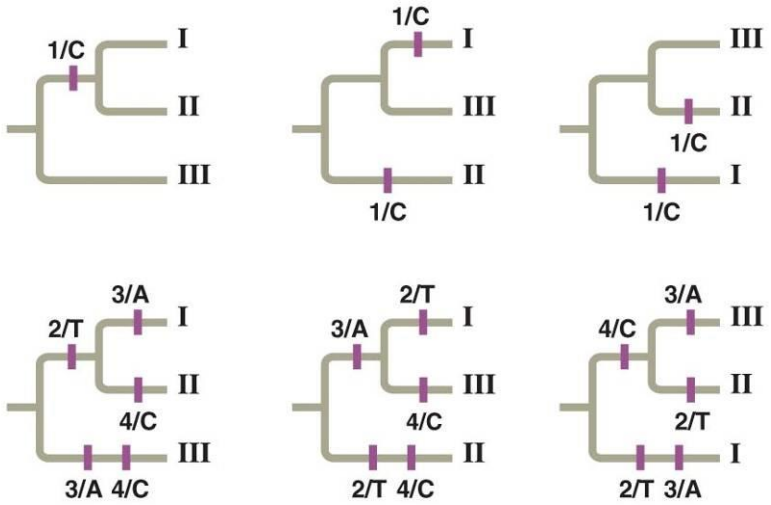
	Site 1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T



- These three cladograms map changes at Site 1 for the three possibilities.

An Example

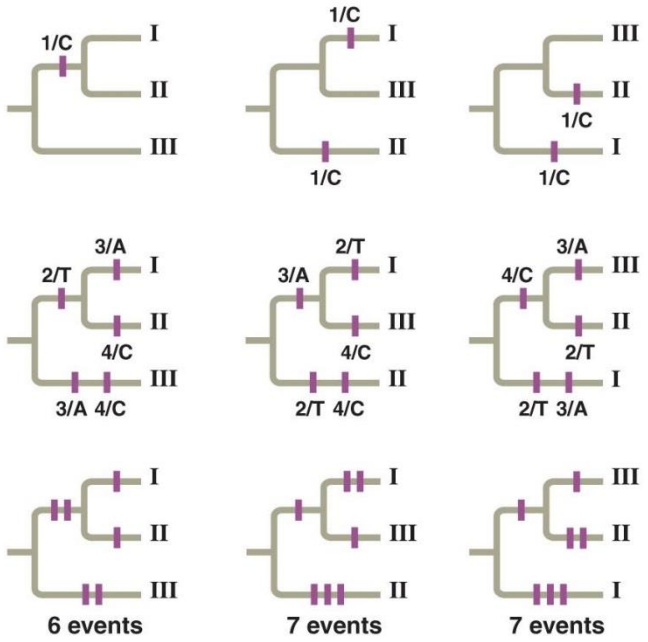
	Site 1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T



- The lower three cladograms map changes at Sites 2, 3 and 4 for the three possibilities.

An Example

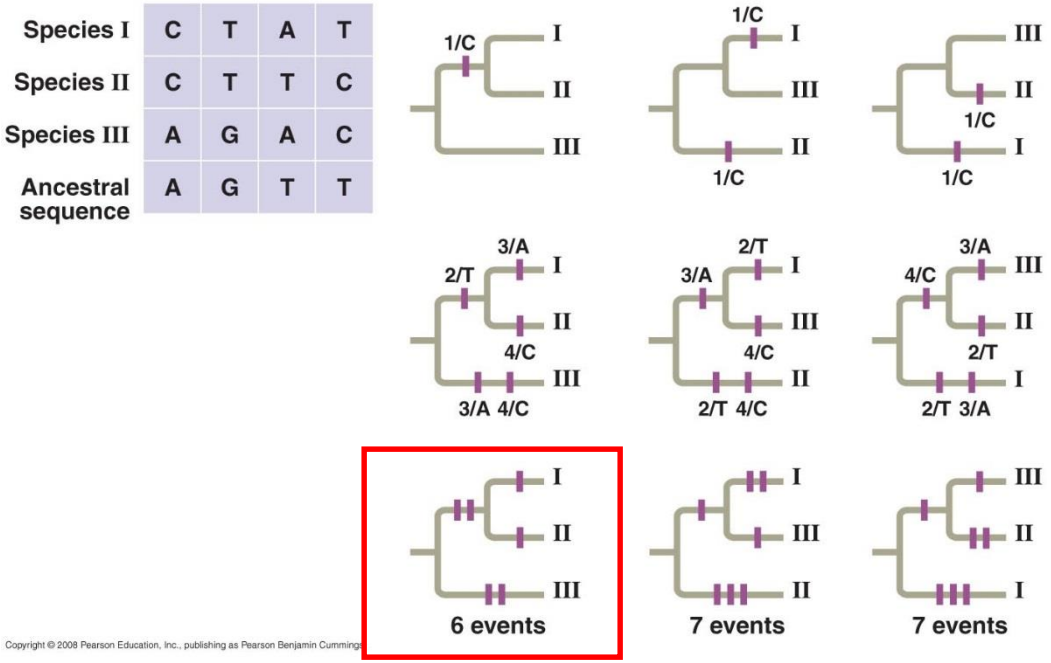
	Site 1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T



- The lowest three cladograms map changes at all four sites and count the number of steps for each possibility.

An Example

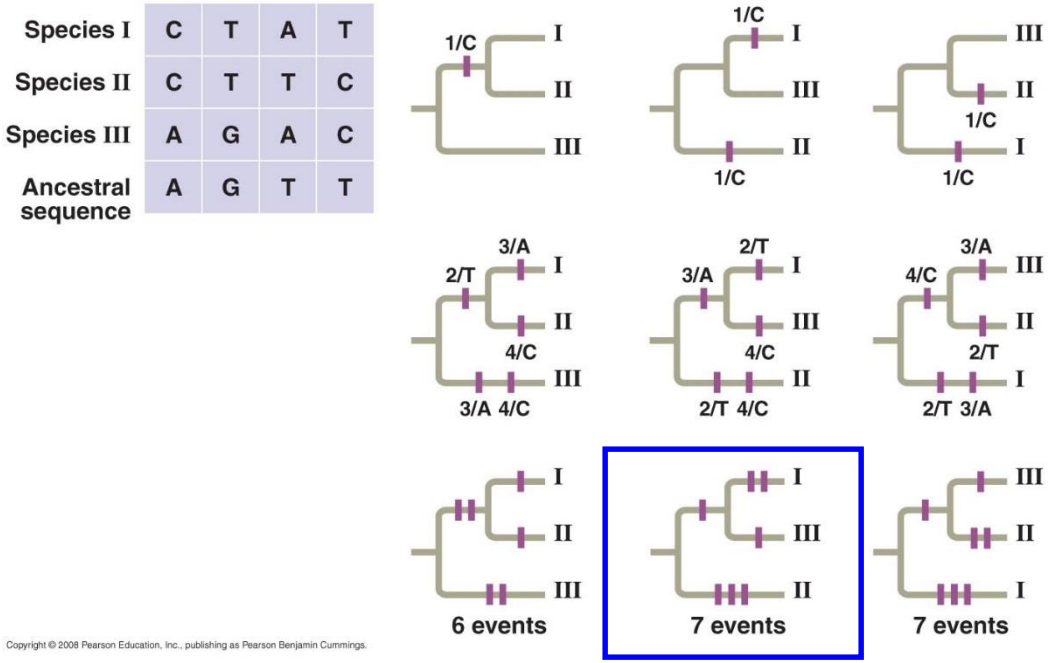
	Site 1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T



- The cladogram in the red box has 6 steps.

An Example

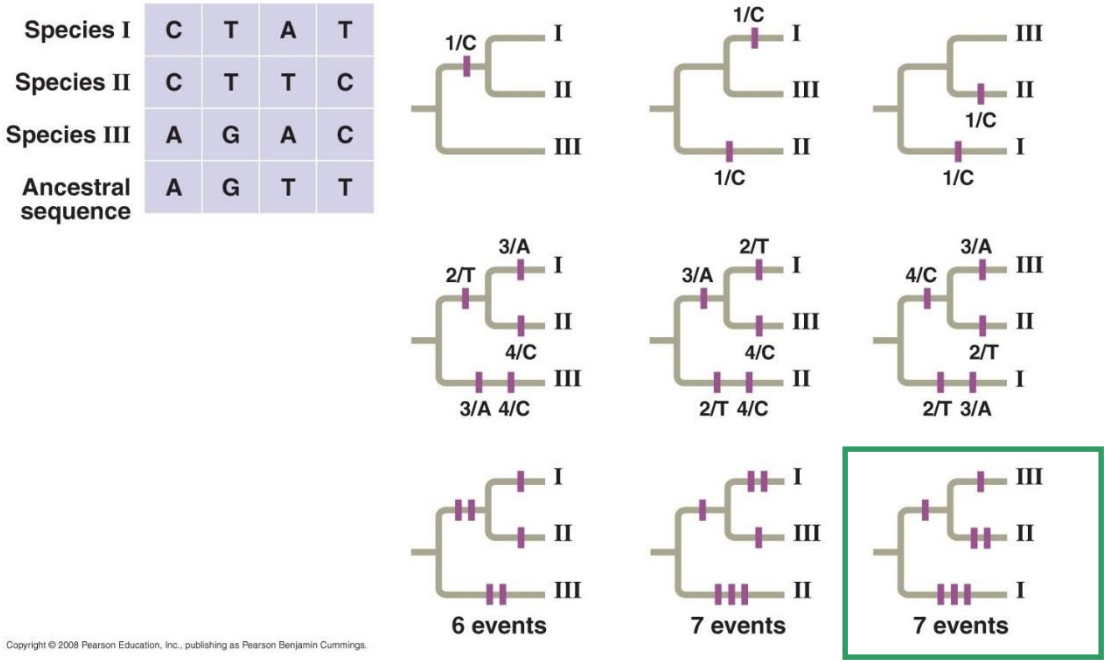
	Site 1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T



- The cladogram in the blue box has 7 steps.

An Example

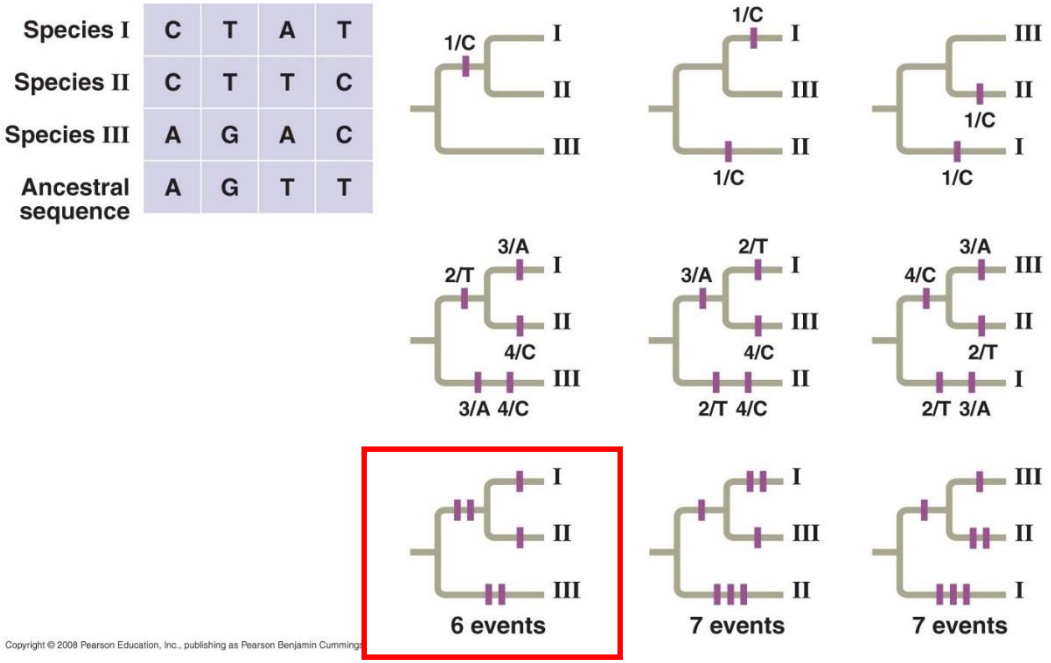
	Site 1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T



- The cladogram in the green box has 7 steps.

An Example

	Site 1	2	3	4
Species I	C	T	A	T
Species II	C	T	T	C
Species III	A	G	A	C
Ancestral sequence	A	G	T	T



- Applying the Principle of Parsimony, you would choose the cladogram with the fewest steps.

The End