

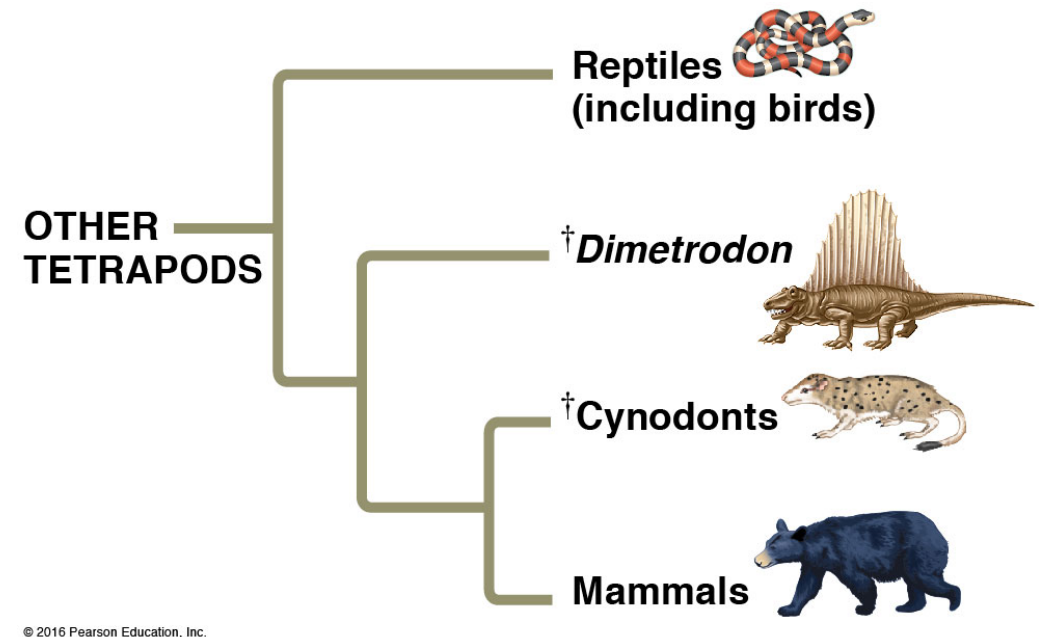
Phylogenetic trees and cladograms are graphical representations (models) of evolutionary history that can be tested.

PHYLOGENY

Cladograms

Diagrams that group items together based on the number of common characteristics.

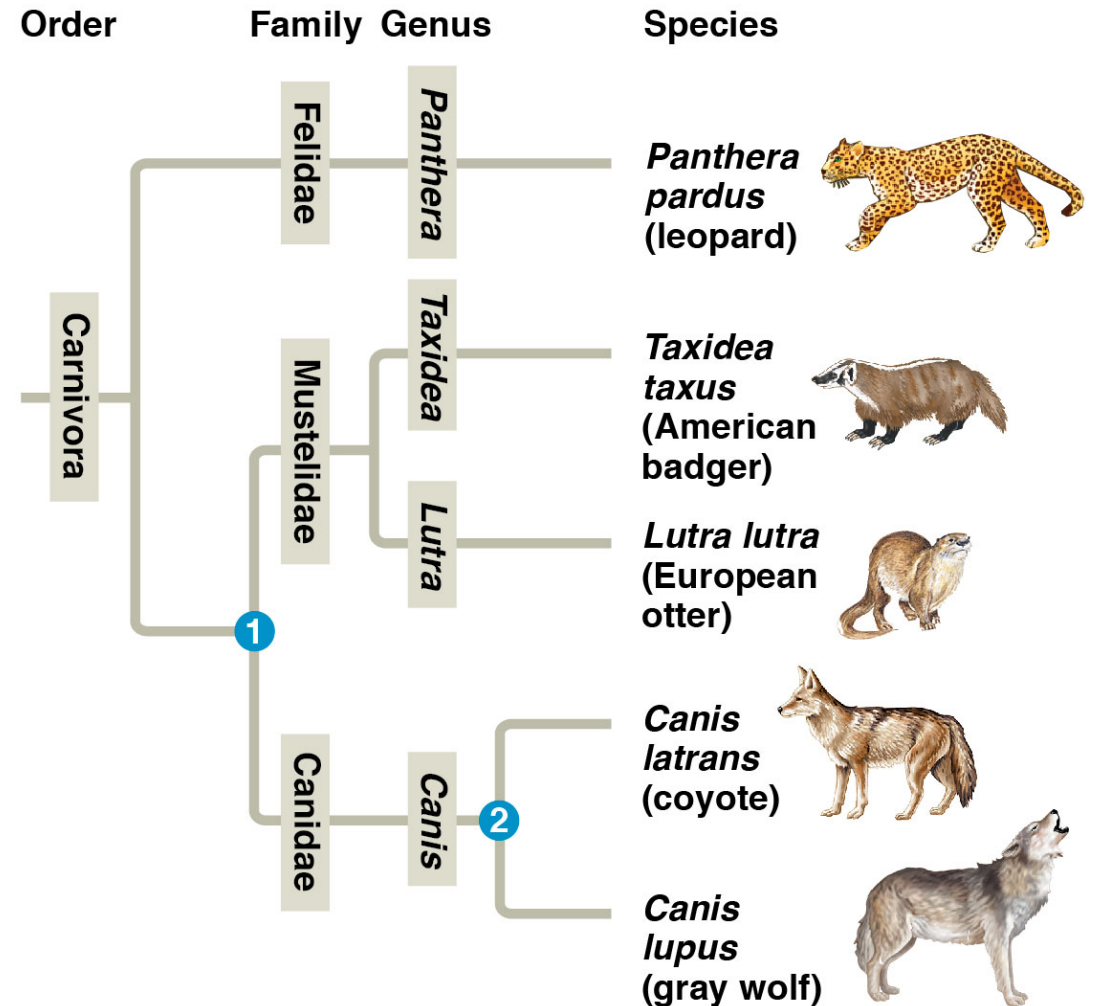
1. Determine number of shared characteristics.
2. Arrange items as a tree showing most commonality possible



Phylogenetic Tree

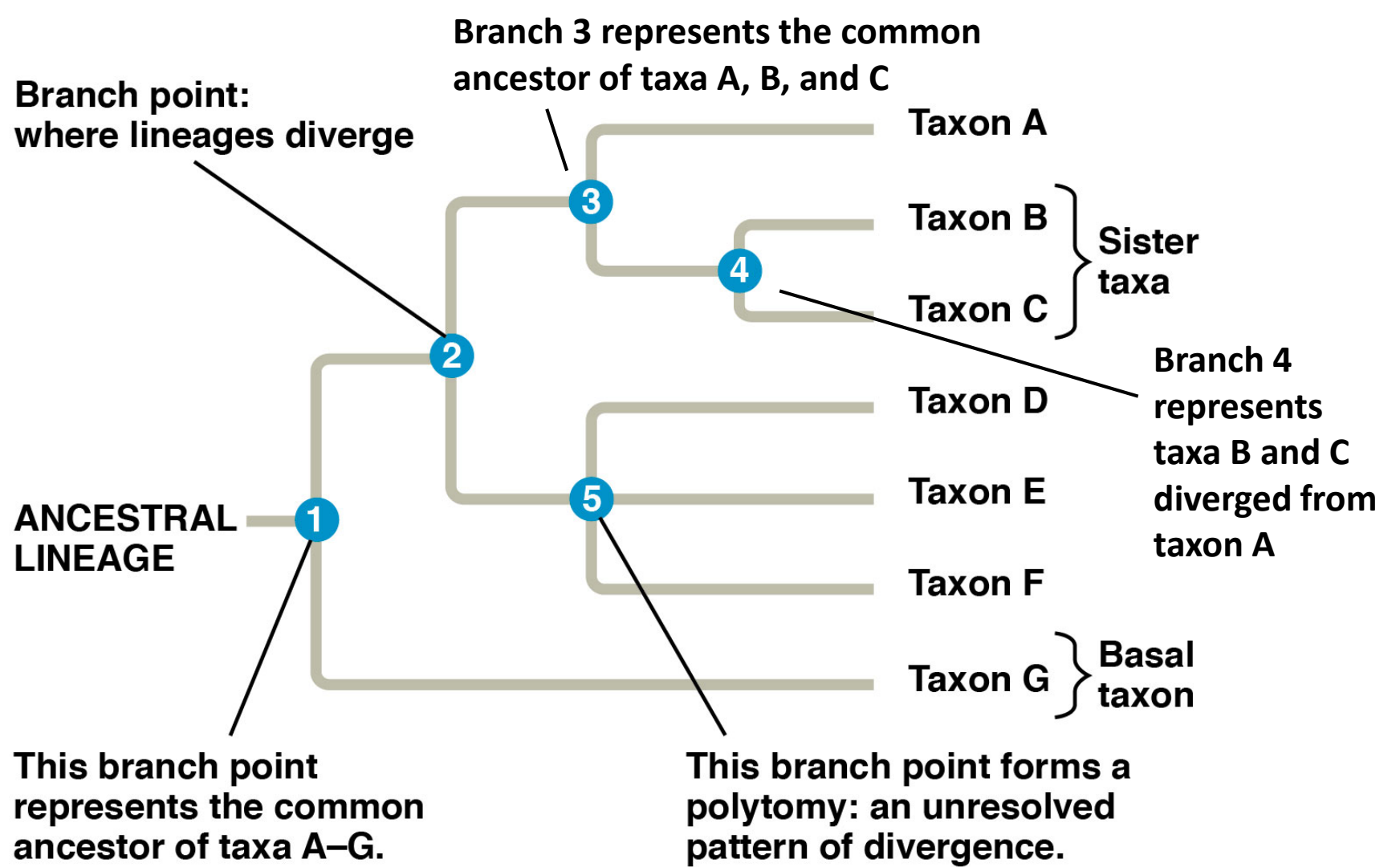
A cladogram that represents evolutionary relationships. Use two types of data:

- 1. Shared Derived Characters:** Physical traits that represent evolutionary history (homologous structures).
- 2. DNA/Protein sequence Data:** Differences in sequences accumulate as species evolve away from each other.



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How to Read a Phylogenetic Tree



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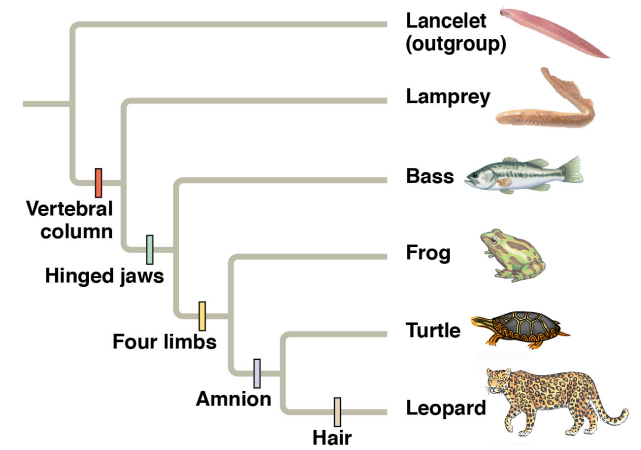
Phylogenetic Tree Construction

1. Determine similarities among organisms (character table works well).
2. Arrange organisms in a tree diagram showing simplest possible evolution.

Maximum parsimony: All else being equal, a trait is assumed to evolve once and be present in all descendants

CHARACTERS	TAXA					
	Lancelet (outgroup)	Lamprey	Bass	Frog	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four limbs	0	0	0	1	1	1
Amnion	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table



(b) Phylogenetic tree

SKILL: Create a tree- Selected Vertebrates

Character Table:

Animal	Opposable Thumb	4-chamber heart	Amniotic egg	lungs	Spinal column
Chimpanzee	1	1	1	1	1
Mouse	0	1	1	1	1
Turtle	0	0	1	1	1
Frog	0	0	0	1	1
Fish	0	0	0	0	1
Lamprey	0	0	0	0	0

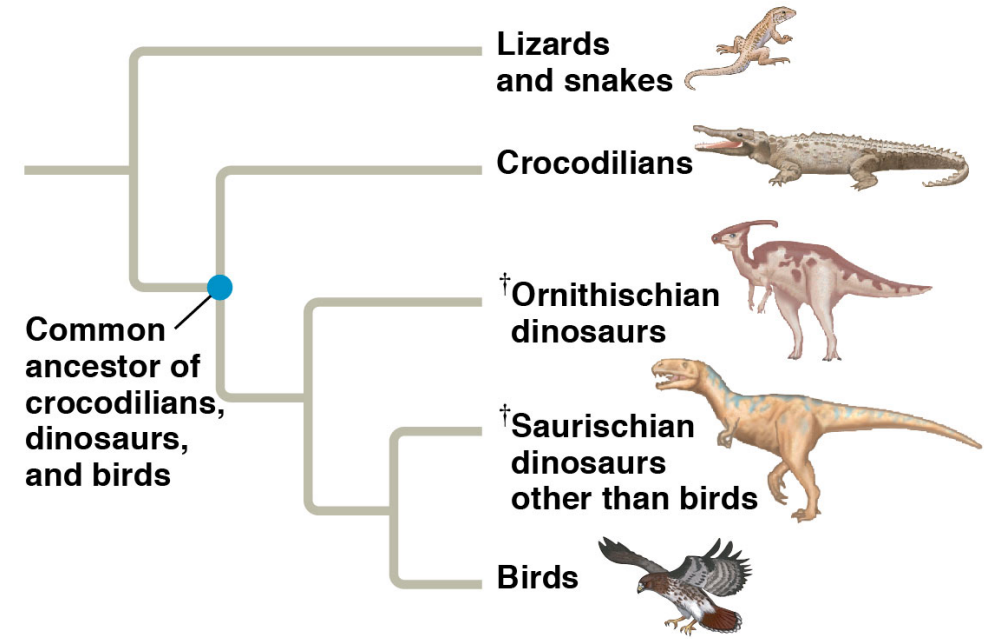
Trees are Hypotheses

Continual revision:

As more data is gathered, the phylogenetic relationships among organisms are continually revised.

Role of computers:

Computer analysis is needed to determine the similarities in large amounts of DNA/protein sequence information.



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