

# Biological Classification

## Cladistics

- **Clade** ("branch") — replace traditional taxon
  - Groups of organisms presumed to be derived from a common ancestor are organized by **bifurcating** (two-way splitting) of a branch
  - Each bifurcation is based upon the acquisition of a new, unique character (**apomorphy**).
- **Maximum parsimony**: the branch pattern that can be created with the fewest required steps is most likely the most correct.

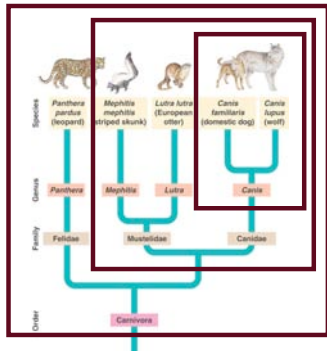
## Cladistics

More vocabulary:

- A true **clade** must be **monophyletic**
  - must include an ancestor and all of the known descendants of that ancestor.
  - A grouping that only includes an ancestor and some of its descendants is **paraphyletic**.
  - A grouping that includes organisms from different ancestries is **polyphyletic**.
- **Derived apomorphic** characters shared by members of a clade are **synapomorphic**.
- **Ancestral** characteristics inherited prior to the branching of a clade are **plesiomorphic**.

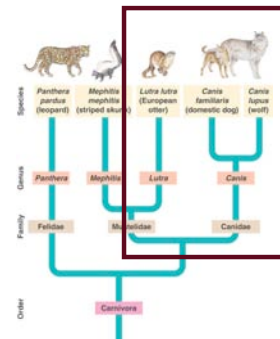
## Cladograms

Monophyletic clades



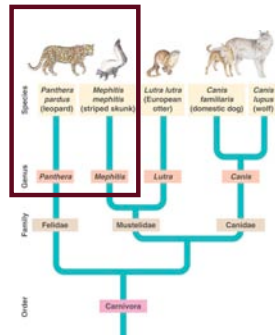
## Cladograms

Paraphyletic grouping



## Cladograms

Polyphyletic grouping



## Building Cladograms

Assemble a **table of character states**

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

# Biological Classification

## Building Cladograms

**Major assumptions:**

1. The group of organisms is monophyletic
2. The **outgroup** (used for comparison) is closely related to, but separate from your group
3. You can tell which character states are homologous or analogous.

	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
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Amniotic (shelled) egg	0	0	0	0	1	1
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## Building Cladograms

Each bifurcation of the branch is based upon the state (presence/absence) of an apomorphic character

## Cladograms

Cladograms are made by determining the sequence of evolution of shared derived characters

## Cladograms

**Rule of Parsimony:**  
The simplest explanation is the most likely explanation.

	Sites in DNA sequence						
	1	2	3	4	5	6	7
I	A	G	G	G	G	G	T
II	G	G	G	A	G	G	G
III	G	A	G	G	A	A	T
IV	G	G	A	G	A	A	G

## Cladograms

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## Cladograms

**Rule of Parsimony:**  
The simplest explanation is the most likely explanation.

**But not always!**