Cladistics

AP

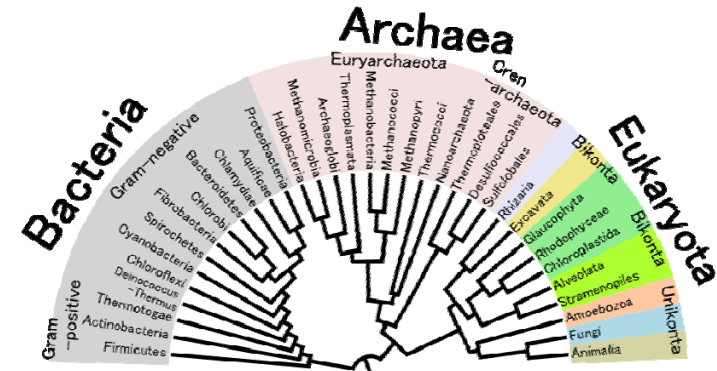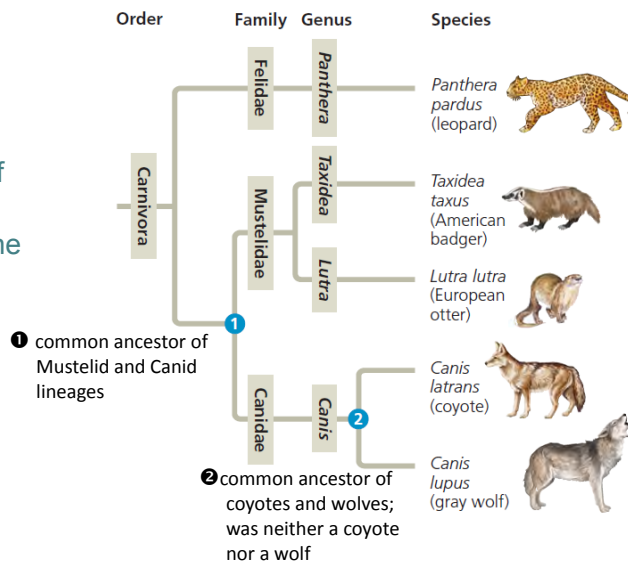**Phylogenetic trees** reflect proposed evolutionary relationships between organisms.


Phylogenetic trees:

- show **patterns** of descent
- do not necessarily indicate the ages of species
- do not imply that one species evolved "from" another

❶ common ancestor of Mustelid and Canid lineages

❷ common ancestor of coyotes and wolves; was neither a coyote nor a wolf

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Cladistics is an approach to developing phylogenies, that groups organisms according to **shared, derived characteristics.**
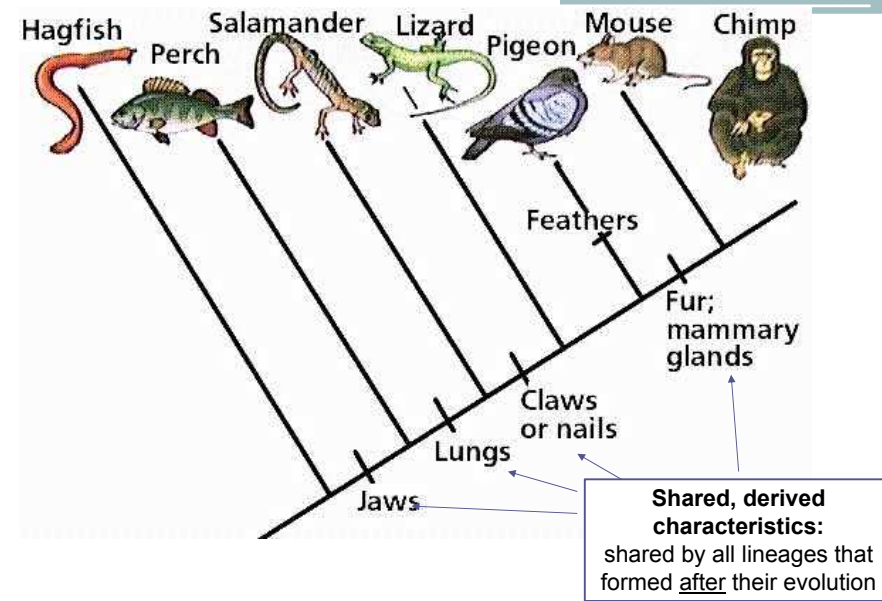
characteristics that are <u>new</u> to a lineage

can be: structural, physiological, **molecular**

Slide 1

TRAIT: BACKBONE

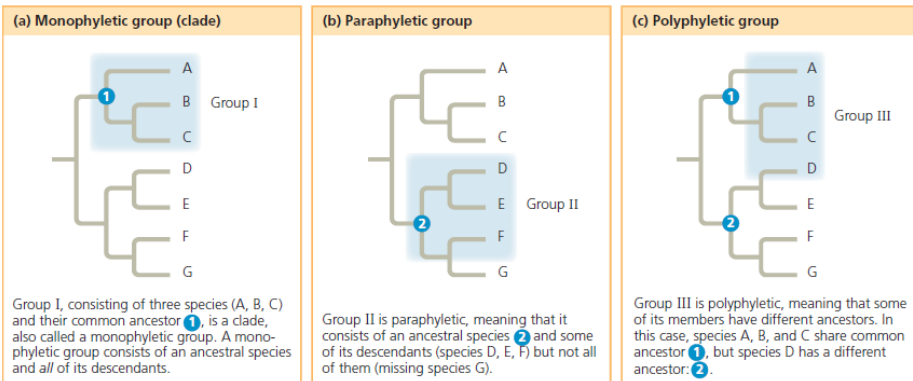fish, amphibians, reptiles, birds, mammals

TRAIT: HAIR
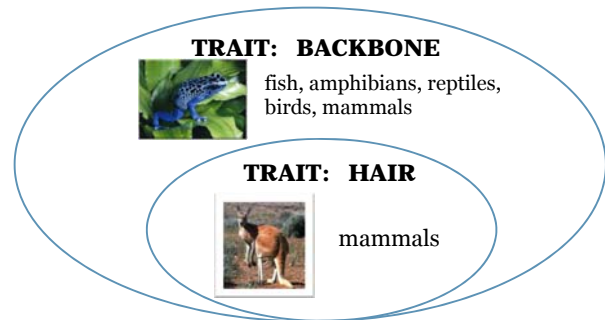
mammals

Example: Identifying mammals
- A **backbone** cannot distinguish mammals from other vertebrates.
  - It is an **ancestral** characteristic shared by mammals and other types of animals.

- Mammals are the only type of vertebrate with **hair**.
- Hair can distinguish mammals from other vertebrates.
  - It is a **derived** characteristic shared only by mammals.

Slide 2

Hagfish Perch Salamander Lizard Pigeon Mouse Chimp

Feathers

Fur; mammary glands

Claws or nails

Lungs

Jaws

Shared, derived characteristics: shared by all lineages that formed _after_ their evolution

Slide 3

Goal of cladistics: to place species into **clades**.
- also called **monophyletic** groups
- consist of an ancestral species and <u>all</u> of its descendants

(a) Monophyletic group (clade)

A
B Group I
C
D
E
F
G

Group I, consisting of three species (A, B, C) and their common ancestor ❶, is a clade, also called a monophyletic group. A monophyletic group consists of an ancestral species and *all* of its descendants.

(b) Paraphyletic group

A
B
C
D
E Group II
F
G

Group II is paraphyletic, meaning that it consists of an ancestral species ❷ and some of its descendants (species D, E, F) but not all of them (missing species G).

(c) Polyphyletic group

A
B
C Group III
D
E
F
G

Group III is polyphyletic, meaning that some of its members have different ancestors. In this case, species A, B, and C share common ancestor ❶, but species D has a different ancestor: ❷.

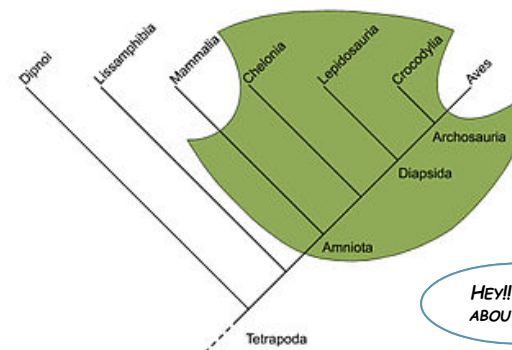An ancestral species, and all of its descendants

An ancestral species, and <u>some</u> of its descendants

Organisms do not share a common ancestor

Slide 4

The traditional class **Reptilia** is **paraphyletic**.

It excludes Aves (birds), though recent evidence indicates they have a common ancestor.

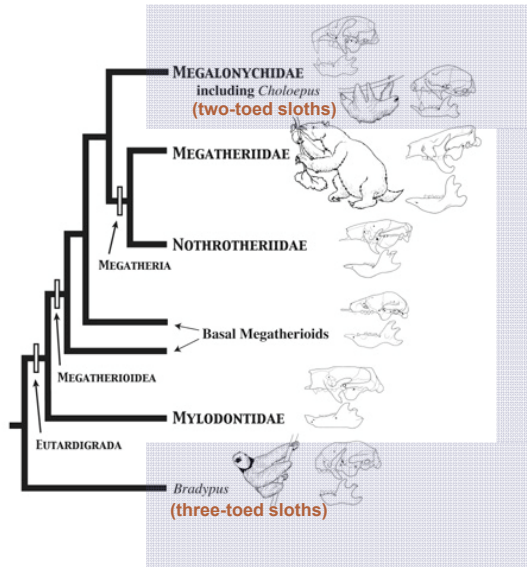Dipnoi Lissamphibia Mammalia Chelonia Lepidosauria Crocodylia Aves

Archosauria

Diapsida

Amniota

Tetrapoda

HEY!! WHAT ABOUT ME??

Slide 1

The group of **"sloths"** is **polyphyletic**.

It includes *Choleopus* and *Bradypus*, which do not share a recent common ancestor.

MEGALONYCHIDAE including *Choloepus* (two-toed sloths)

MEGATHERIIDAE

NOTHROTHERIIDAE

MEGATHERIA

Basal Megatherioids

MEGATHERIOIDEA

MYLODONTIDAE

EUTARDIGRADA

Bradypus (three-toed sloths)

Slide 2

Constructing a cladogram:

1. Select an **outgroup**:
   A lineage <u>known</u> to have diverged a long time ago. This represents the most ancestral form.

2. Select the traits to examine.
3. ID whether the organisms' characters are **ancestral** (same as outgroup) or **derived** (not present in outgroup).

Traits: Organism	Jaws	Lungs	Amniotic membrane	Hair	No tail	Bipedal
Lamprey	0	0	0	0	0	0
Shark	1	0	0	0	0	0
Salamander	1	1	0	0	0	0
Lizard	1	1	1	0	0	0
Tiger	1	1	1	1	0	0
Gorilla	1	1	1	1	1	0
Human	1	1	1	1	1	1

0 = organism does not have trait
1 = organism has trait

Outgroup:
• lamprey

Ingroup:
• gorilla
• human
• lizard
• salamander
• shark
• tiger

Slide 3

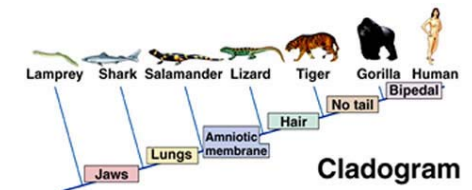| Traits: Organism	Jaws	Lungs	Amniotic membrane	Hair	No tail	Bipedal
Lamprey	0	0	0	0	0	0
Shark	1	0	0	0	0	0
Salamander	1	1	0	0	0	0
Lizard	1	1	1	0	0	0
Tiger	1	1	1	1	0	0
Gorilla	1	1	1	1	1	0
Human	1	1	1	1	1	1

0 = organism does not have trait
1 = organism has trait

1. Which organism is the most closely related to the lamprey?
2. Which trait is the most recently derived?

Slide 4

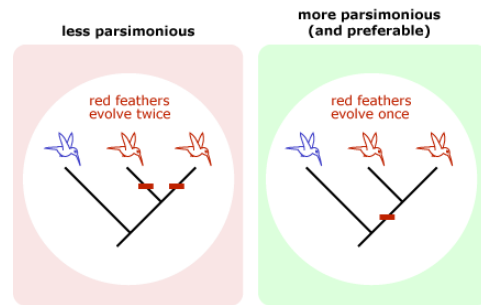4. Group the organisms based on shared, derived characteristics.
   ▫ a Venn diagram may be helpful

bipedal: human
no tail: gorilla
hair: tiger
amniotic membrane: lizard
lungs: salamander
jaws: shark
lamprey
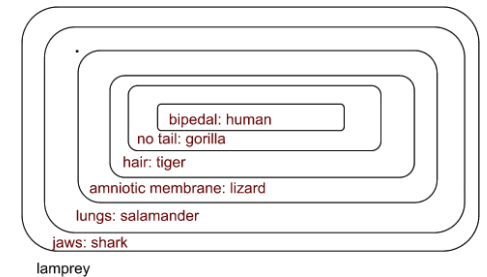
5. Construct your cladogram!

Lamprey Shark Salamander Lizard Tiger Gorilla Human
Bipedal
No tail
Hair
Amniotic membrane
Lungs
Jaws

Cladogram

Slide 1

The principle of **maximum parsimony** guides the construction of phylogenetic trees:

The simplest explanation is usually the correct one.

less parsimonious — red feathers evolve twice

more parsimonious (and preferable) — red feathers evolve once

Slide 2

Example:

A man is found dead on a pile of garbage bags, with a knife in his chest. He is in an area known for high drug activity.

Which scenario is more likely to account for this?

Scenario A
- The man was walking when he slipped on a banana peel and fell.
- He landed on a pile of garbage bags.
- One of the garbage bags contained a knife, which pierced his chest.
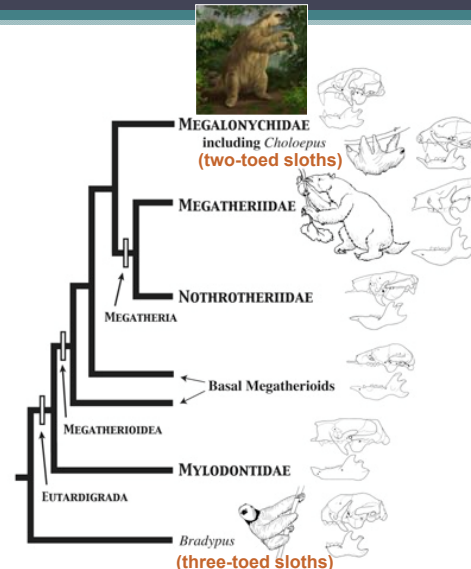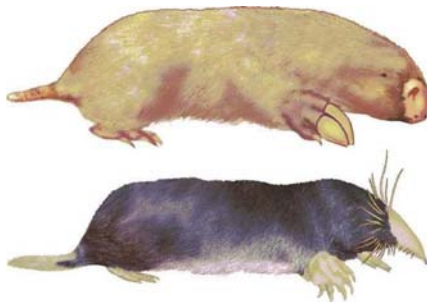- A raccoon removed the banana peel before authorities arrived.

Scenario B
- The man was involved in a drug deal.
- The drug deal went wrong, and the man was stabbed.

*The simpler scenario is more **parsimonious**.*

Slide 3

Convergent evolution makes it difficult to reliably classify organisms based on morphology.
- **Molecular homologies** are more reliable.

- **DNA**: Nucleotide sequences
- **Proteins**: Amino acid sequences

Slide 4

MEGALONYCHIDAE including *Choloepus* (two-toed sloths)

MEGATHERIIDAE

NOTHROTHERIIDAE

MEGATHERIA

Basal Megatherioids

MEGATHERIOIDEA

MYLODONTIDAE

EUTARDIGRADA

Bradypus (three-toed sloths)

"**Sloths**" represent two **distantly-related** groups that share many similarities due to convergent evolution.

- What defining features do these sloths share?
- Why might these have evolved independently?

# Phylogeny Using Molecular Homologies

- Higher degree of **similarity** implies **relatedness**
  - □ Two organisms share a recent common ancestor

Example: The DNA sequence of the American badger is more similar to the DNA of the European otter than of the coyote.
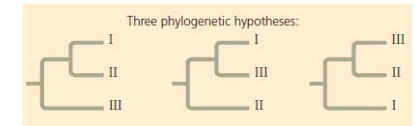
Taxidea taxus (American badger)

Lutra lutra (European otter)

Canis latrans (coyote)

Canis lupus (gray wolf)
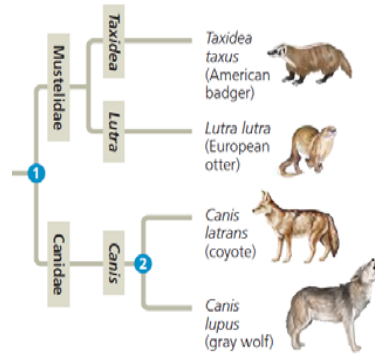
Applying parsimony to phylogeny:

- DNA mutations are relatively rare.
- Scenarios with the **least amount of mutations** are preferred.
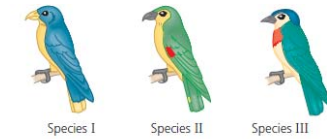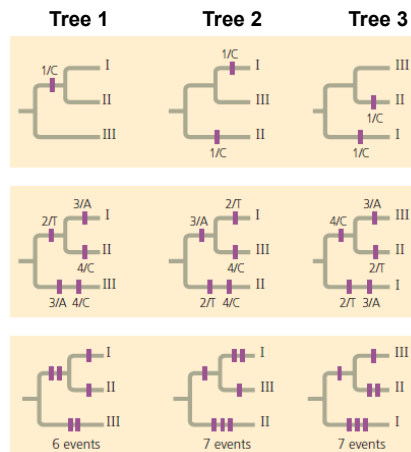
Three related bird species

Species I   Species II   Species III

Three possible phylogenetic trees

Three phylogenetic hypotheses:

Species I   Species II   Species III

Each notch represents a change to the ancestral sequence.

DNA sequences

	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 (outgroup)	A	G	T	T

The first tree requires the least mutations. It is the most parsimonious.

Tree 1   **Tree 2**   **Tree 3**

6 events   7 events   7 events

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① These homologous DNA sequences are identical as species 1 and species 2 begin to diverge from their common ancestor.

1 CCATCAGAGTCC
2 CCATCAGAGTCC

② Deletion and insertion mutations shift what had been matching sequences in the two species.

1 CCATCAGAGTCC Deletion
2 CCATCAGAGTCC (G T A) Insertion

③ Of the regions of the species 2 sequence that match the species 1 sequence, those shaded orange no longer align because of these mutations.

1 CCATCAAGTCC
2 CCATGTACAGAGTCC

④ The matching regions realign after a computer program adds gaps in sequence 1.

1 CCAT___CA_AGTCC
2 CCATGTACAGAGTCC

Bioinformatics is a branch of biology that involves using technology to manage biological information.

In cladistics: Gene sequences are **aligned**, and differences are used to evaluate relatedness.

Some phylogenetic trees indicate the relative **amount of change**.

- all organisms have been evolving for **same amount of time!**
  - **branch length ≠ time**
- longer branch length = more change has occurred
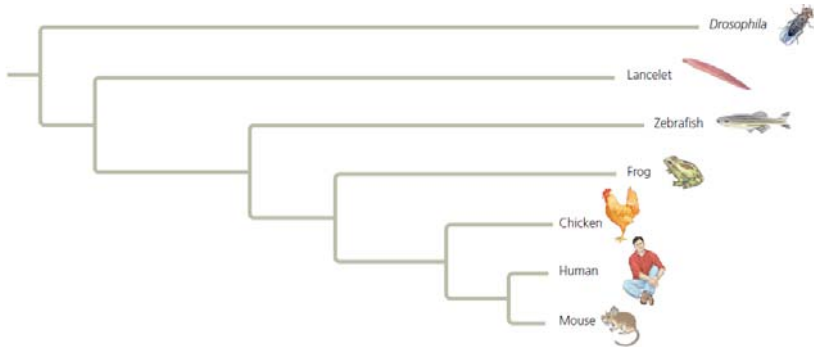
On the subject of parsimony...

How do <u>you</u> turn the pages of your book?

http://www.youtube.com/watch?v=GOMIBdM6N7Q

Summary

- Phylogenetic trees represent proposed evolutionary relationships between organisms.
  - They show lines of descent.
  - The length of branches <u>may</u> indicate the degree of divergence from the common ancestor.

- Cladistics seeks to classify organisms into monophyletic groups that reflect common descent.
  - Utilizes the presence of shared, derived characteristics.

- DNA sequences are more reliable than morphological similarities for determining common descent.
  - Analysis can be aided by use of computer programs.

- When more than one phylogeny is possible, the most parsimonious option is chosen.
  - The principle of maximum parsimony reflects the likelihood of events occurring naturally.