

Cladistic Analysis using Bats: An Introduction to Chiropteran Phylogeny & Morphology

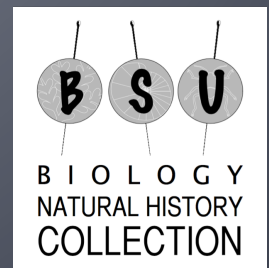


Activity: Morphological Cladistic Analysis & Character Mapping



Course: Biology Of Bats
(BIO 492)

Maria Armour, M.S.





Diversity of Bats



- Mammalian Order: Chiroptera
- Extraordinary adaptations with Niches exploited
- Wider variety of food than any other mammal
- All bat species perform true powered flight
- Most echolocate
- 2 Suborders
- 20 Extant Families
- 1,400+ Species



All photos: Merlin Tuttle

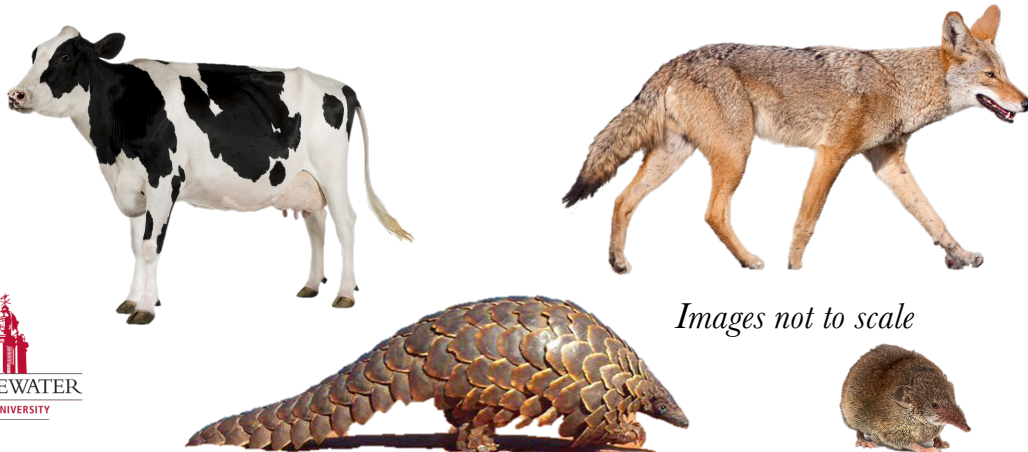
Merlintuttle.org

Bats within Class Mammalia

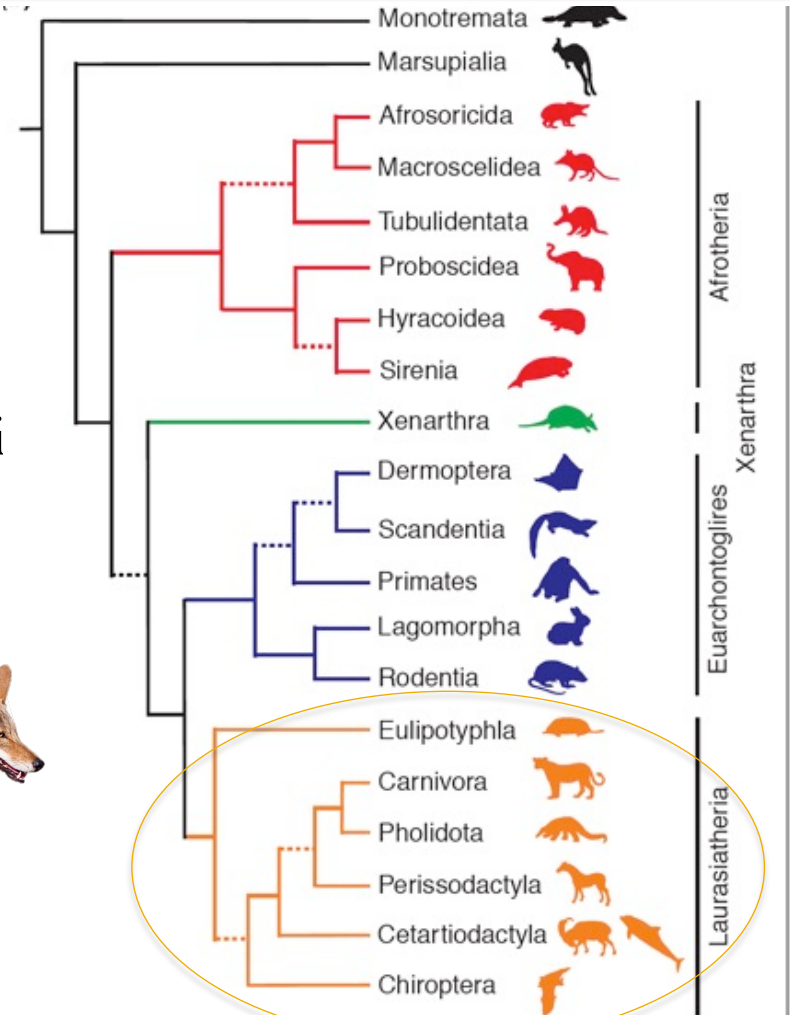


- Only mammal to evolve ability to fly
- Closest living lineages:
 - Shrews, ungulates, carnivores, and Pangoli

= Superorder LAURASIATHERIA



Images not to scale



Evolution of the Flying Mammal

- Bats are not well represented in fossil record
 - Mostly jaws, insectivorous
 - Missing intermediate forms
- Date back to the Eocene (60+ MYA)
- Evidence suggests bats evolved from small nocturnal and arboreal mammals
- Natural selection
 - Often response to changing environment

Over 60 million years, bats evolved diverse **morphological** structures from other mammals and from one another

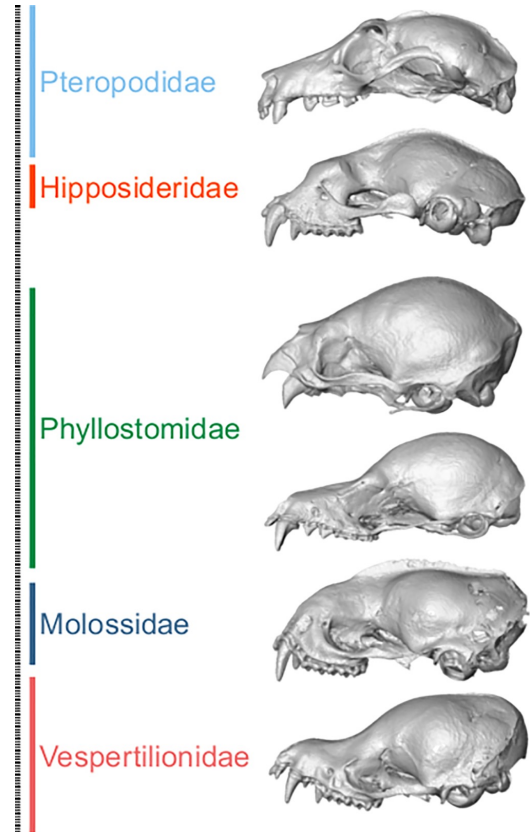


Onchonycteris finneyi

What is *Morphology*?

Description and analysis of organismal form

- How organism's **function** and how diverse phenotypes **evolved**
- Can shed light on mechanisms that allow change during evolution
- Historically, morphological structures were used to create phylogenies of a group and predict how taxa is related.

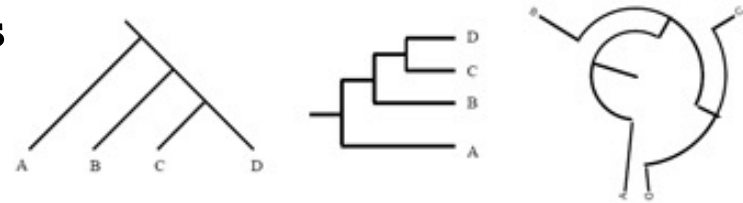


Shi et al., 2018

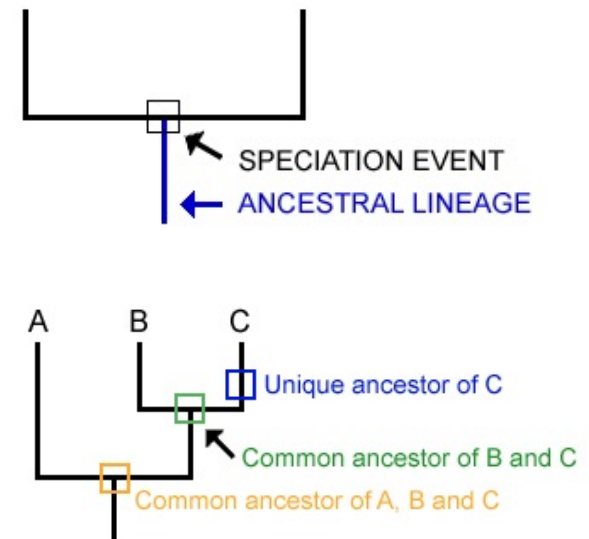
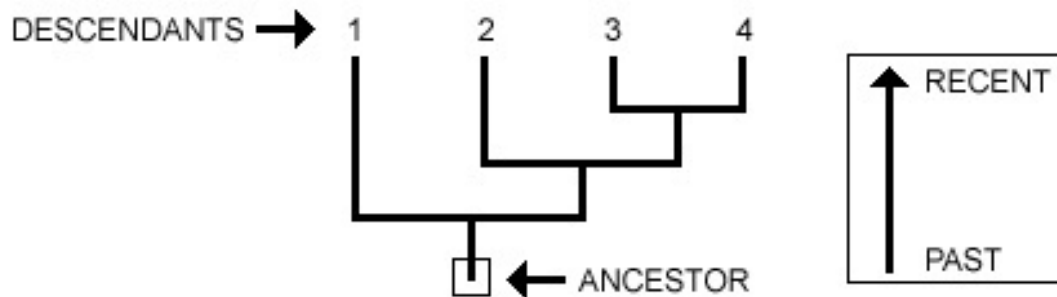
How Do We Know Who is Related to Whom?

■ Using **Evolutionary (Phylogenetic) Trees**

- Based on shared derived characters
- Organize biological diversity
- Structure classifications
- Show pattern of evolutionary descent from common ancestor
- Identify speciation events



Types of phylogenetic trees



Phylogenetic terminology and figures from
evolution.berkeley.edu

Phylogenetic Trees

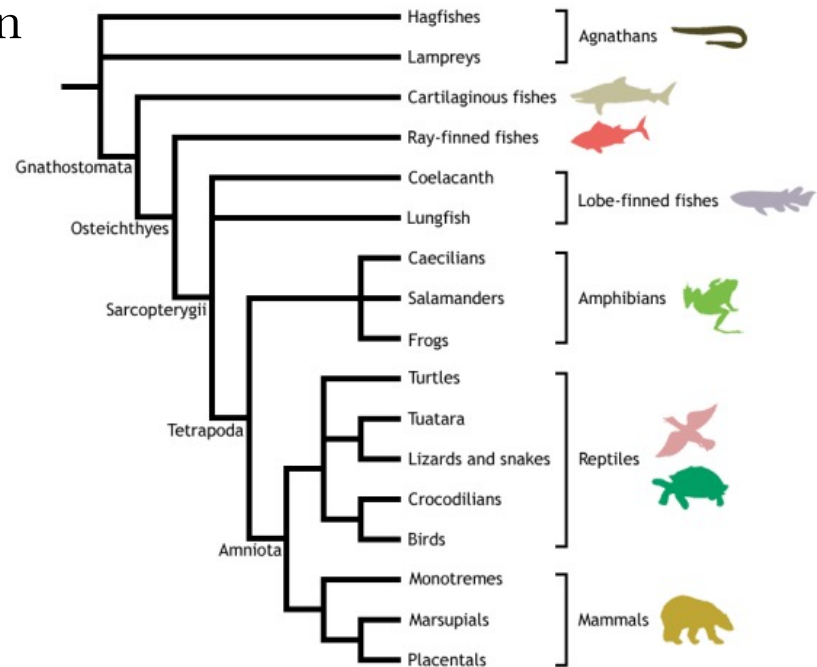
- Shows hypothesized evolutionary relationships
- Depicts evolutionary descent of different organisms from a Common ancestor
- Strong evidence supporting evolution

- Types of Character Datasets

- Morphological
 - Palaeontological (*we will get to this*)
- Molecular (genetics)
- Sometimes behavioral

- Principle of Parsimony

- Simplest explanation preferred over complicated



Vertebrate Phylogeny
Adapted from Meyer & Zardoya (2003)

Data Used in Phylogenetic Studies

- Character datasets can be: Morphological, Molecular, or Behavioral
- Traits or features of an organism are used to form a phylogenetic tree
 - Character is a feature that is observable in an organism
 - Character states are within a character, they are different forms or appearances
- Phylogeny reconstruction has historically used morphological data
- With recent innovations in comparative genomics over the last 40 years, molecular data has taken over phylogenetic analysis
- Since then, evolutionary trees have changed dramatically

Molecular Data in Phylogenetic Studies

Current Phylogenetic studies use mainly Molecular Characters

- Highlight prevalence of convergent evolution of phenotypic traits
- DNA (genetic code) contains instructions for building an organism
- Every nucleotide position is a Character with four States (A, T, C, G)
- Mutations in an organism's DNA are the raw material of genetic variation

Offer *many* more Characters than morphology = stronger trees

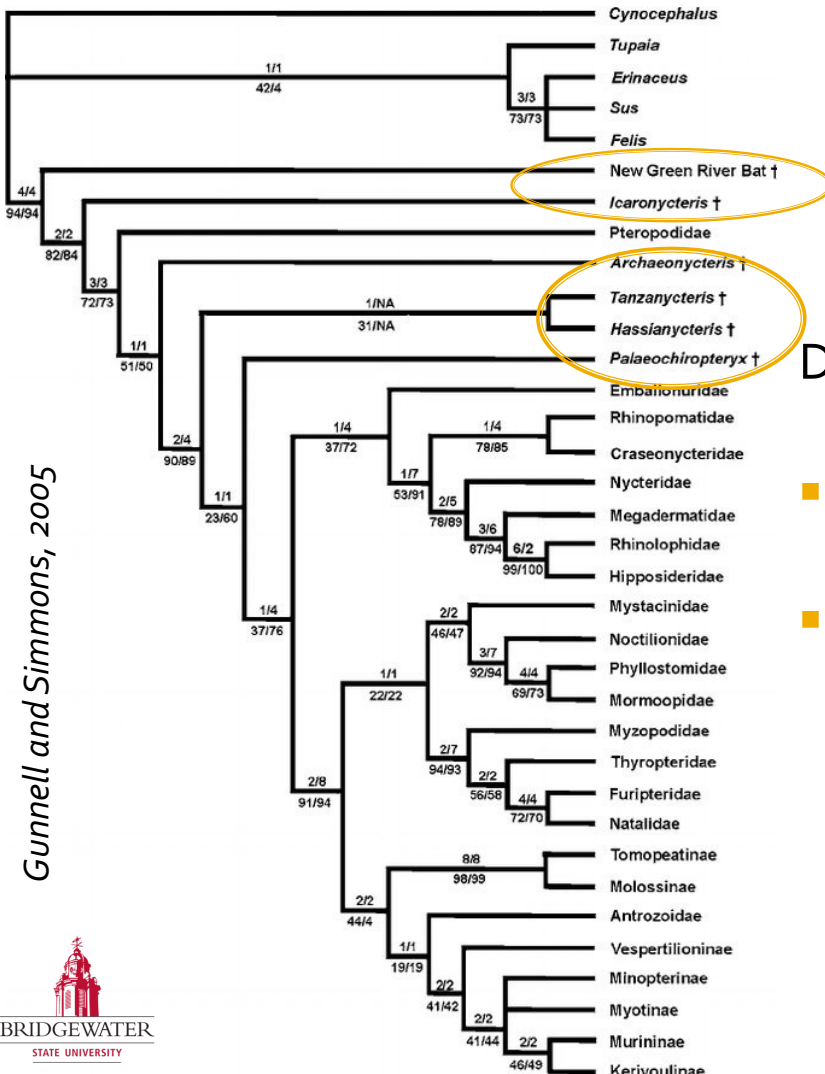
Ra	1	CCCCA	G	G	G	T	G	G	T	G	G	C	T	G	G	G	G	G	C	A	G
Rb	2	CC	T	C	A	T	G	G	T	G	C	T	G	G	G	C	G	C	A	A	
Rc	3	CCCC	A	T	G	G	T	G	G	C	G	C	T	G	G	G	G	A	C	A	G
Rd	4	CCCC	A	T	G	G	T	G	G	C	G	C	T	G	G	G	G	A	C	A	G
Re	5	CC	T	C	A	T	G	G	T	G	C	T	G	G	G	C	T	C	A	A	

Are Morphological Characters Still Important?

ABSOLUTELY!

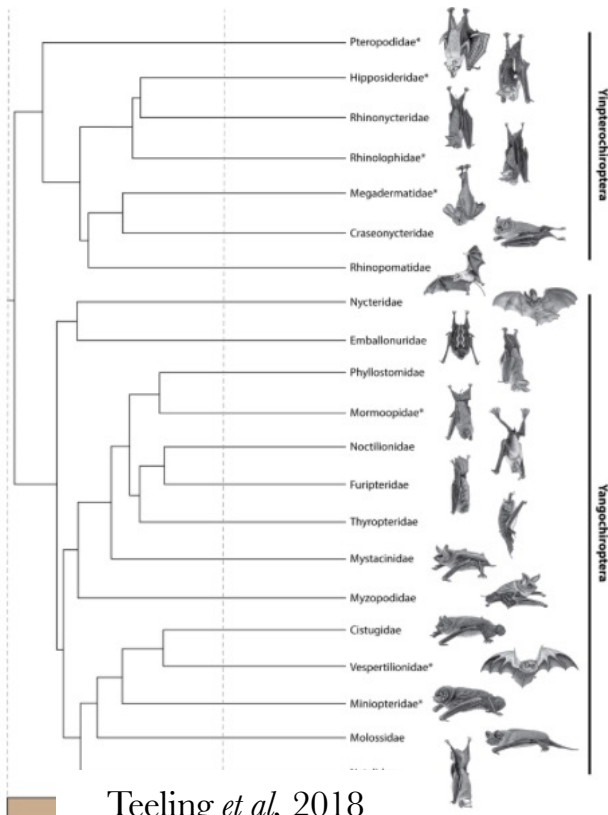
Datasets allow for **time scaling** of phylogenies

- Because of morphology we have dated trees
- Fossil phenotypes (Palaeontological Data)
 - Largely inaccessible to genetic data but provide best view of extinct biodiversity and evolutionary dynamics



Current Bat Phylogenetic Tree

Using Molecular Dataset



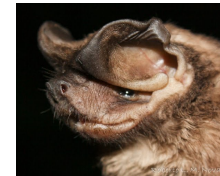
Teeling *et al*, 2018



Yinpterochiroptera



Yangochiroptera

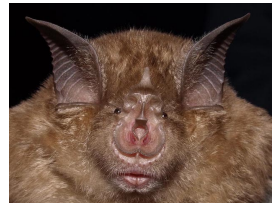
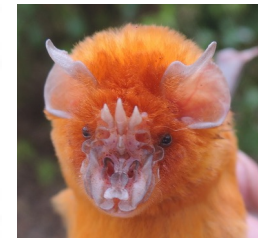
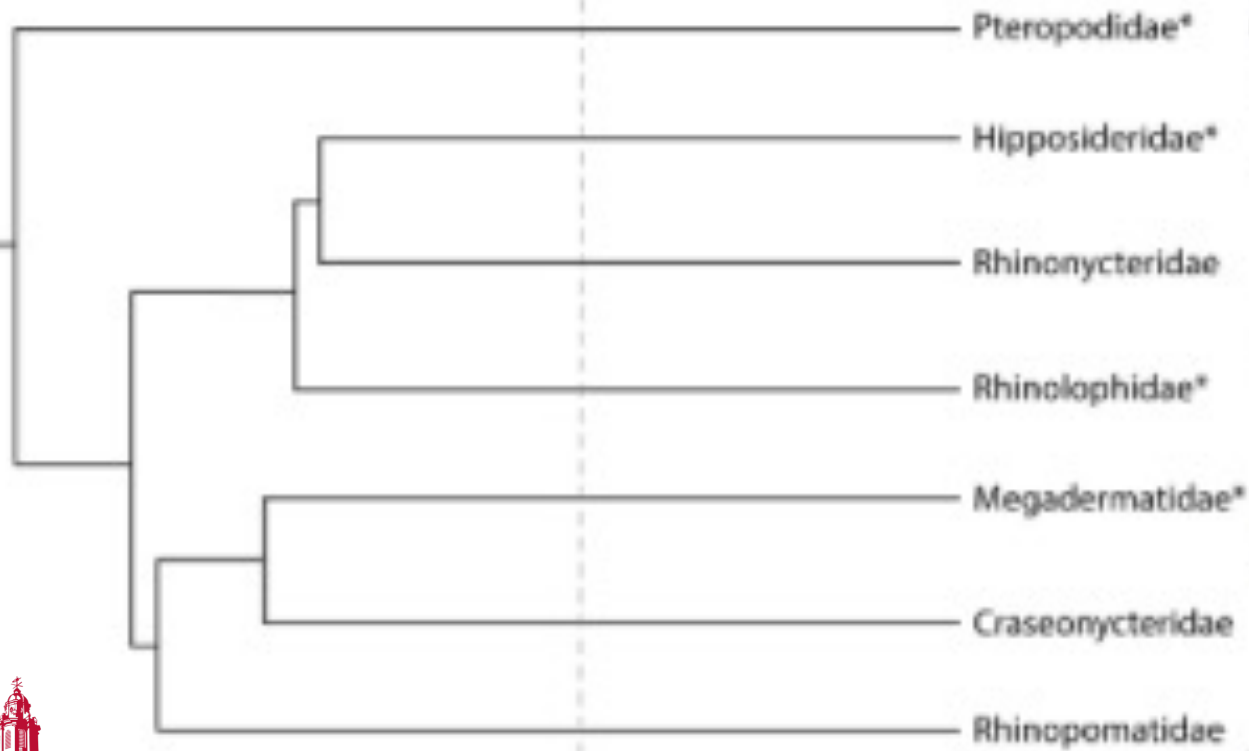


- 2 Suborders
- 20 Extant Families
- 1,400+ Species

Suborder Yinpterochiroptera

Species: 420

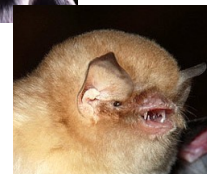
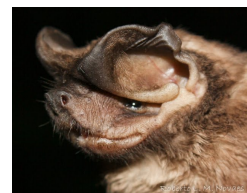
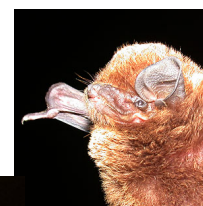
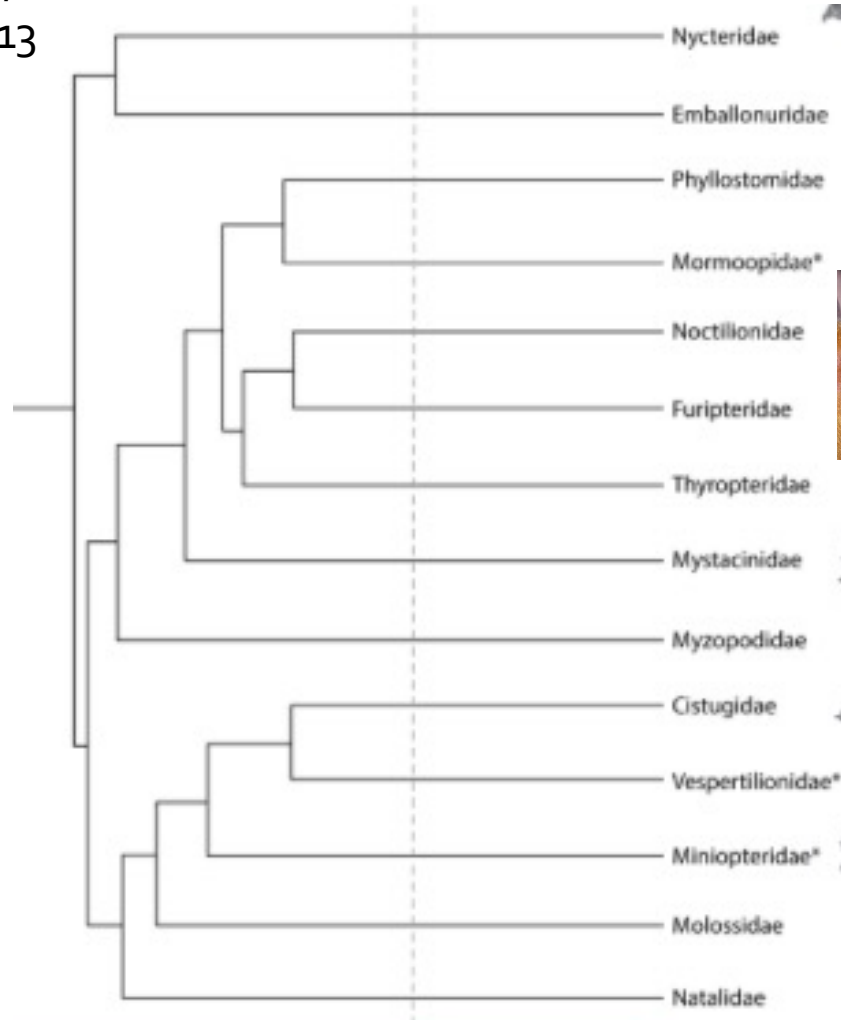
Families: 7



Suborder: Yangochiroptera

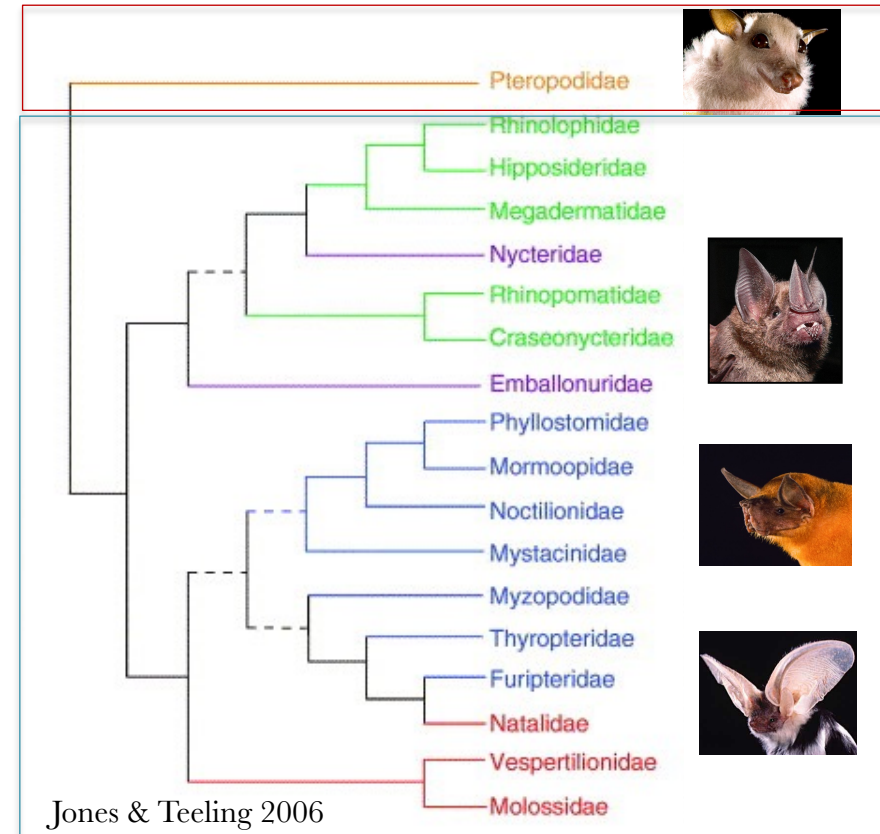
Species: 1,012

Families: 13



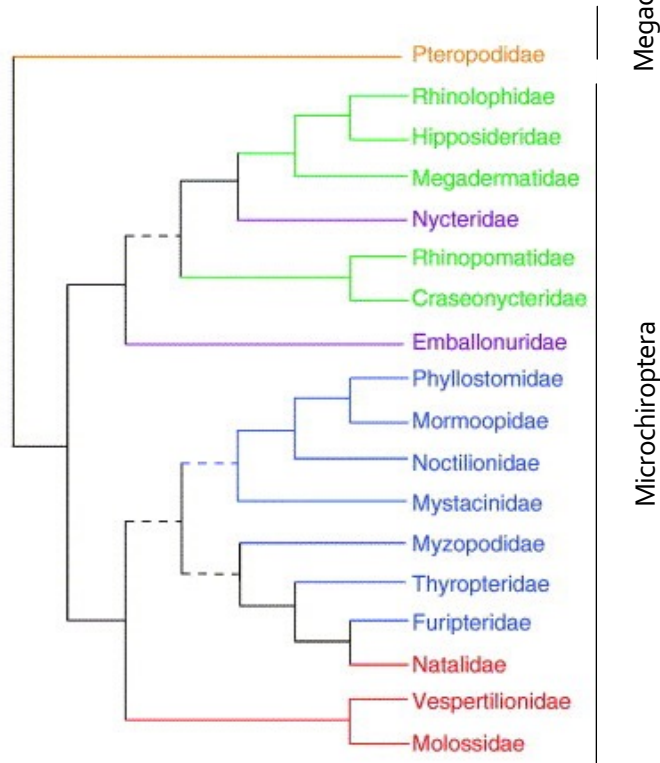
A Warning About Using Only Morphological Data

- Bat Morphological Tree
 - OLD Suborders: **Mega** and **Micro**
 - Based on Echolocation ability from larynx
- Leads to homoplasy
 - Shared similarity not due to a common ancestor, but is the result of convergent evolution or reversal

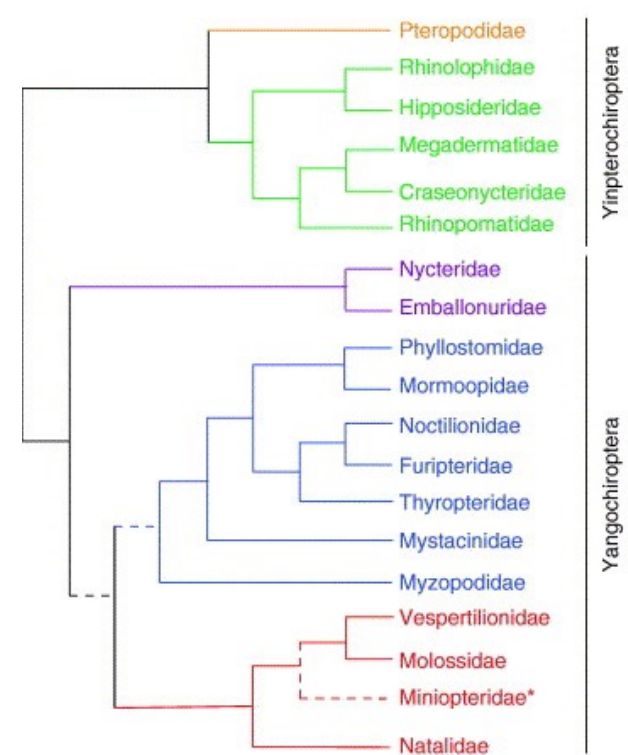


Major Changes in the Bat Tree

Morphological Data Tree



Molecular Data Tree



Jones & Teeling 2006

Activity:

Cladistic Analysis & Character Mapping

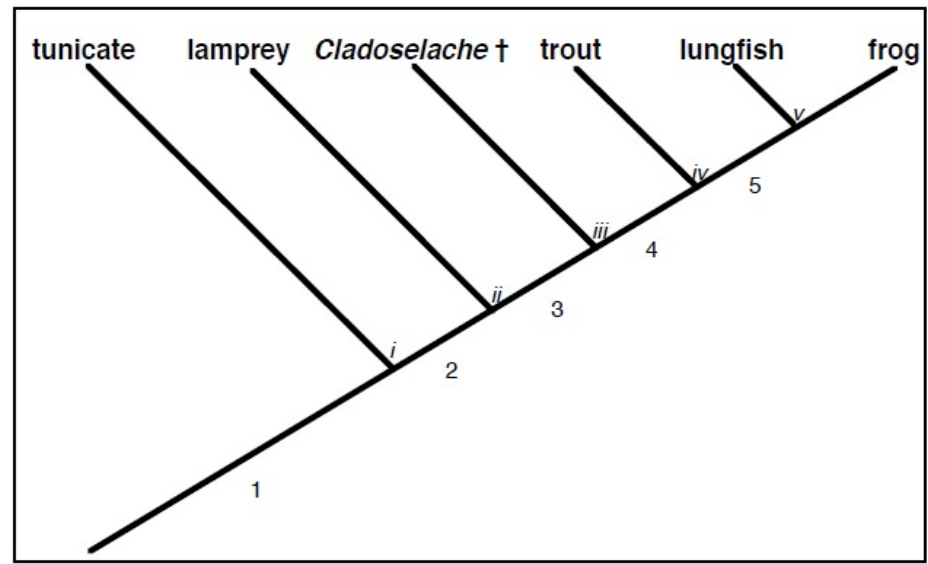
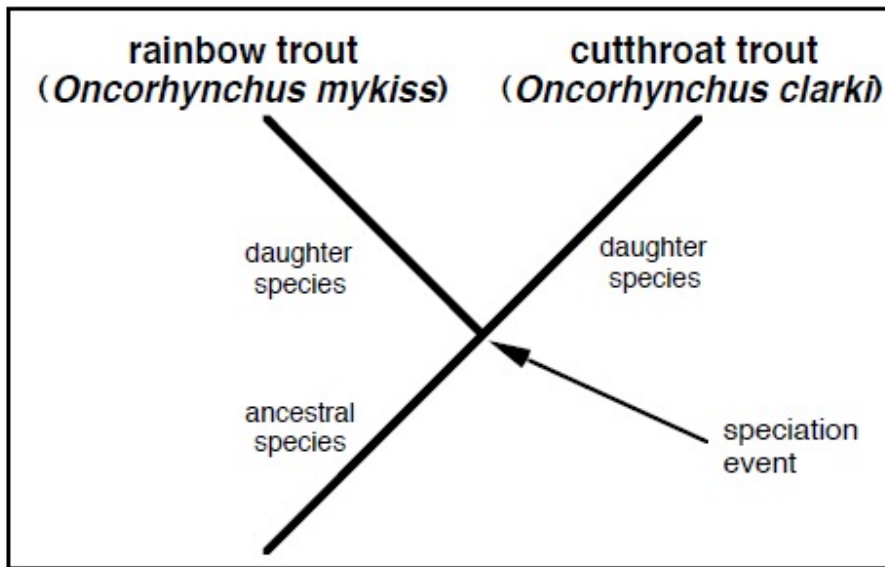
- Method introduced by Willi Hennig in 1950
- Used to hypothesize relationships among organisms
- Gives information about relative timing of speciation events
 - Lacks absolute time axis, can't tell year occurred
- It is a hypothesis, not a fact!

Assumptions:

1. Any group of organisms are related by descent from a common ancestor
2. There is a bifurcating pattern of cladogenesis
3. Change in characteristics occurs in lineages over time

Cladogram

- Results in the form of branching diagram
- All taxa under study are on the “tips” of the cladogram
 - Taxa used must be clades = monophyletic taxon
- Branches illustrate common ancestry relationships



Cladograms from Department of Integrative Biology, University of California-Berkeley

Characters and their States

- Traits or features of an organism that are used to form a cladogram
 - Morphological, Molecular, or Behavioral
- **Character** is a heritable trait that is observed in an organism
- **Character states** are the different forms or appearances of a character
 - “Nails present” vs. “Nails absent”
- The more characters used in a cladogram, the stronger the tree

Character	1	2	3
	Presence of Hair	Ocular	Patagium / Interdigital Membrane
Character States	(0) Lacks true hair (1) Has true hair	(0) Complex, large eyes (1) Small, simple eyes	(0) Absent (1) Continuously attached between digits

Data Matrix

- Characters can be coded into a matrix by assigning a number to each State
- This is the Polarity of the character and can be ancestral or derived
 - **Plesiomorphic** state: primitive or ancestral
 - **Apomorphic** state: derived, specialized or advanced
- Transformation series – former character evolved into the latter
- How does one identify states as being ancestral or derived?
 - Outgroup Comparison

Character	1	2
	Presence of Hair	Ocular
Character States	(0) Lacks true hair (1) Has true hair	(0) Complex, large eyes (1) Small, simple eyes
Taxa		
Carnivora	1	0
Emballonuridae	1	1
<u>Megadermatidae</u>	1	1
<u>Molossidae</u>	1	1
<u>Natalidae</u>	1	1
<u>Noctilionidae</u>	1	1
<u>Phyllostomidae</u> (<u>Desmodus rotundus</u>)	1	1
<u>Phyllostomidae</u> (<u>Uroderma bilobatum</u>)	1	1
<u>Pteropodidae</u>	1	0
<u>Rhinolophidae</u>	1	1
<u>Vespertilionidae</u>	1	1

Outgroup Comparison

- Asks the question:
 - Which character state is plesiomorphic and which are apomorphic?
- Outgroup should be the most closely related taxon, but not ancestor of set taxa under study (called the ingroup)
- Assumption: common ancestor of both groups has only ancestral characters and they are prevalent in the outgroup
- So...Any state displayed by OUTGOUP must be PLESIOMORPHIC (ancestral)

Character State =

0 is the PLESIOMORPHIC state

1 (2, 3) are the APOMORPHIC states

Character	1	2
	Presence of Hair	Ocular
Character States	(0) Lacks true hair (1) Has true hair	(0) Complex, large eyes (1) Small, simple eyes

Kinds of Apomorphies

Reminder **Apomorphic** state: derived, specialized or advanced

■ **SYNAPOMORPHIES:**

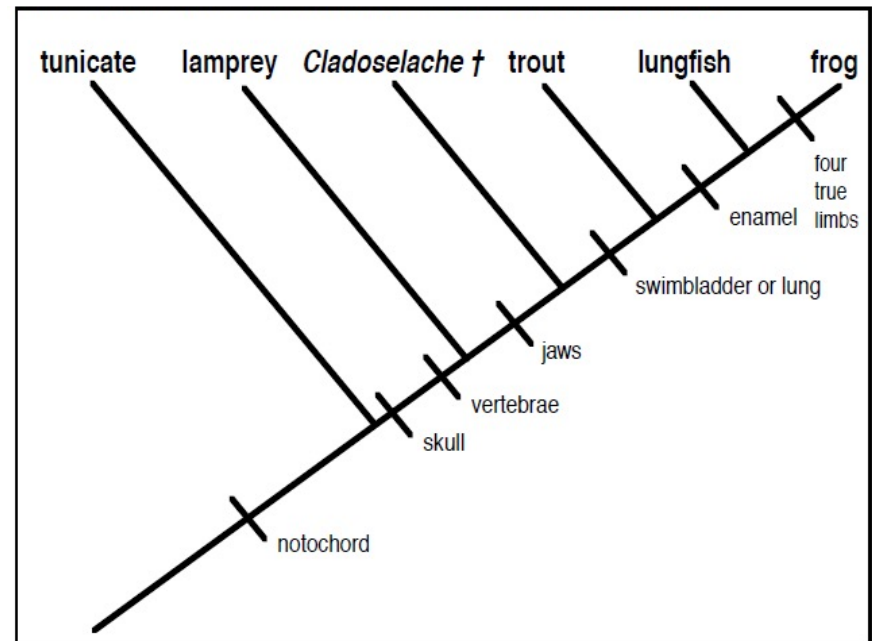
shared derived character

- Occurs in two or more taxa
- Points out clades
 - i.e. Notochord, skull, vertebrae...

■ **AUTAPOMORPHIES:**

occur in only 1 taxon

- Demonstrate the uniqueness of the taxa but do not help develop clades
 - i.e. Four true limbs



Principle of Parsimony

- Alternative cladograms – have no way of knowing which (if either) is correct evolutionary history
- PP allow researcher to decide which cladogram is more acceptable
 - Look at the number of innovations that have occurred
 - Synapomorphies and autapomorphies
 - Sometimes requires evolutionary reversal

The simplest explanation of the data is preferable over more complicated explanations

Cladogram with fewest branches is probably most accurate

Example Using Morphological Characters

- Phenotypic features of an organism used to form a phylogeny
 - Character is a feature that is observable
 - States within that character are different forms or appearances and are scored (0, 1, 2, 3...) to form a dataset

Hand	Eyes	Leg membrane	Body Hair	Ears
(0) fingers separate, (1) long with membrane	(0) large and complex, (1) small and simple	(0) absent, (1) present	(0) Sparse, (1) Solid brown, (2) brown and tan, (3) spots, (4) solid white	(0) small, (1) large

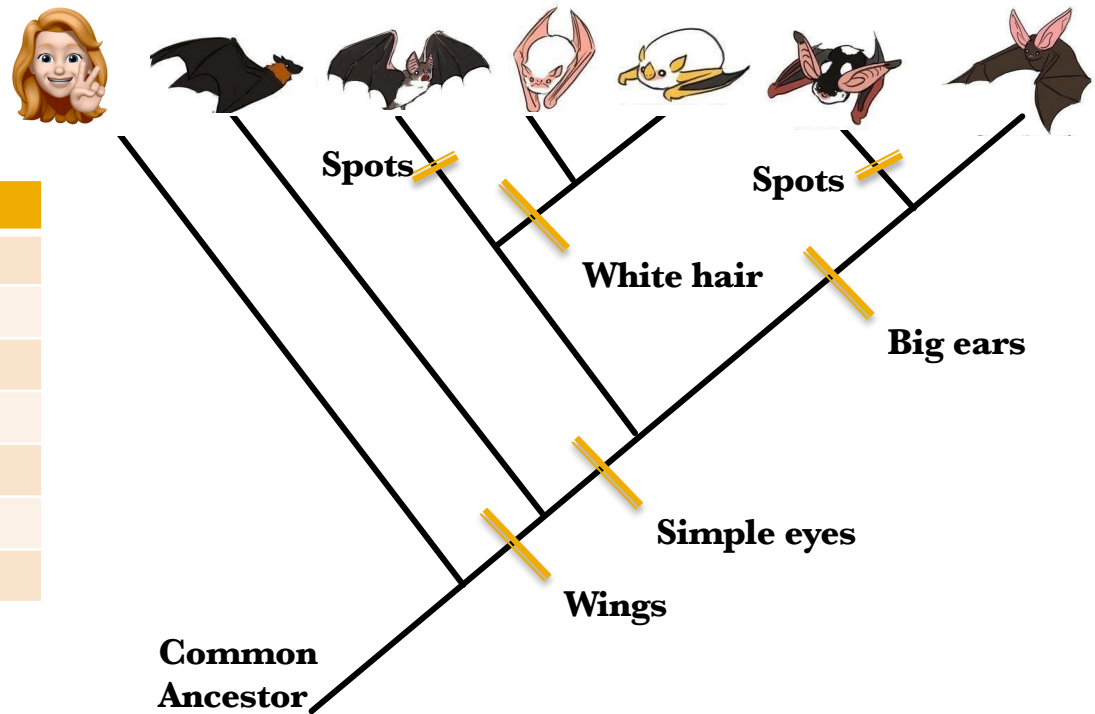


- Outgroup: helps root the tree, closely related to group of interest

Character Matrix to a Cladogram

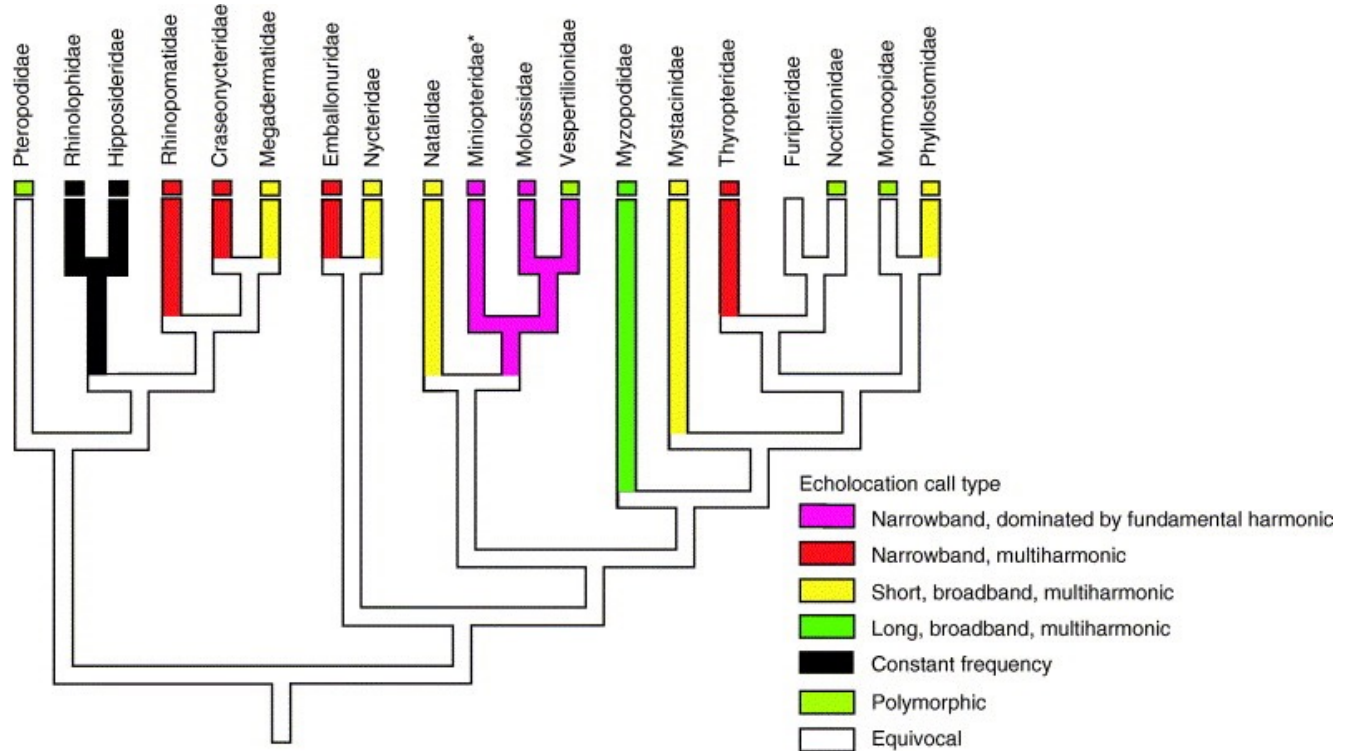
Morphological Character Matrix

	Hand	Eyes	Legs	Hair
Flying fox	1	0	0	2
Spotted	1	1	1	3
Long-eared	1	1	1	1
Ghost	1	1	0	4
Vampire	1	1	0	3
White bat	1	1	0	4
Human	0	0	0	0



Character Mapping

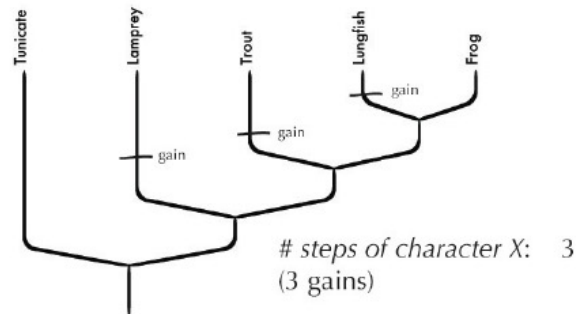
- Mapping a morphological structure onto molecular tree identifies convergence



Character Mapping

CHARACTER MAPPING, METHOD 1 - only evolutionary gains

Taxon	Character X
Tunicate	<i>absent</i>
Lamprey	<i>present</i>
Trout	<i>present</i>
Lungfish	<i>present</i>
Frog	<i>absent</i>



■ Gains:

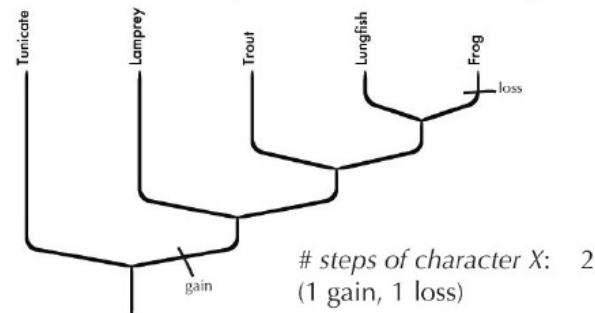
- Trait modified
- Character state moves up
0 to 1 to 2

■ Reversals:

- Trait is lost
- Character state goes down
from 2 to 1 to 0

In this example, character mapping method 2 provides a more parsimonious explanation of the data than method 1. The first method proposes three independent gains of Character X, whereas the second method proposes one gain and one loss of the character. Method 2 is more parsimonious because it only requires two evolutionary changes, whereas method 1 requires three.

CHARACTER MAPPING, METHOD 2 - with evolutionary reversal



Cladistic Analysis and Character Mapping Group Activity

- Groups will gather data by looking at images and reading about different bat taxa. Throughout this activity ask yourself the question:

“Based on morphology alone, how are these taxa related?”

In this Activity each student group will:

1. Create a data matrix by scoring a set of 6 morphological characters on 10 bat clades (monophyletic taxa) and 1 outgroup (coyote/carnivora)
2. Build 2 hypothesized cladograms by grouping taxa by synapomorphies
3. Perform Character Mapping with 2 characters
4. Present group's cladistic results to the class

Follow directions in the handout to build your cladograms and perform character mapping. Answer the questions and prepare to present your findings to the class.

Use Informational Cards to Score Data Matrix

- Includes figures of taxa: profile illustration, full body image, and skull image
- Back of cards includes written information on that taxa from Mammalian Species Accounts

