
Lecture 1.1

Introduction to Molecular Phylogenetics

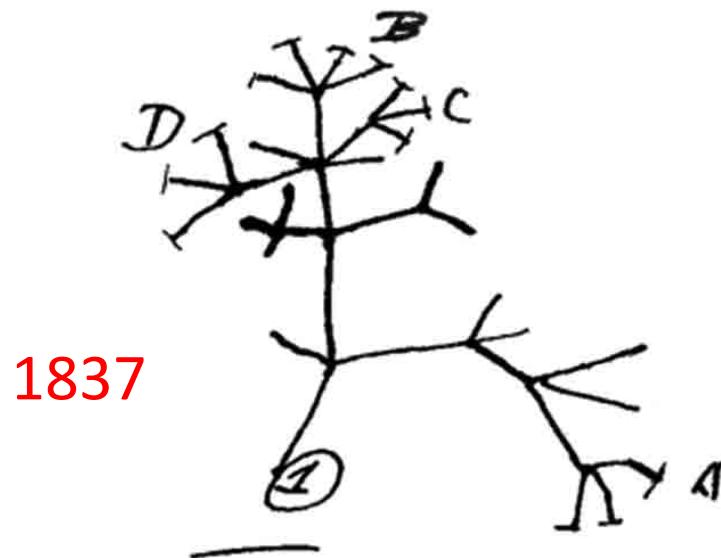
Phylogenetic Trees

What is a phylogenetic tree?

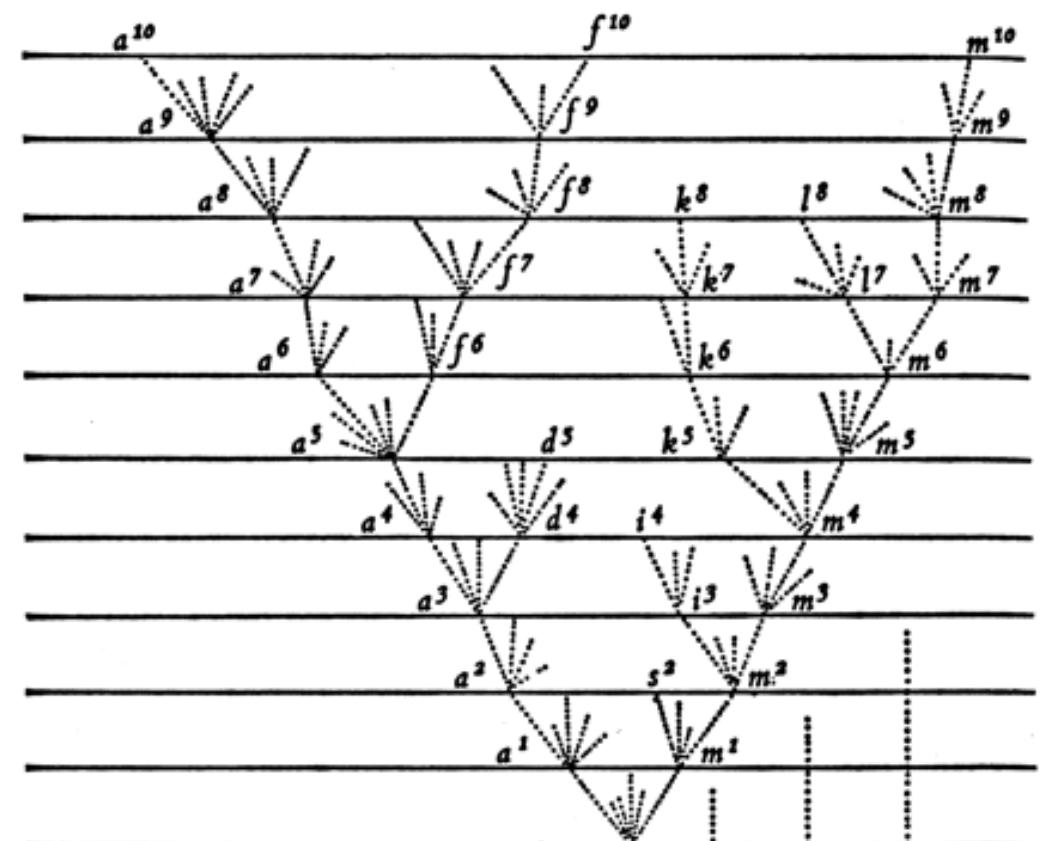
Phylogeny

evolutionary relationships
among a set of organisms

I think



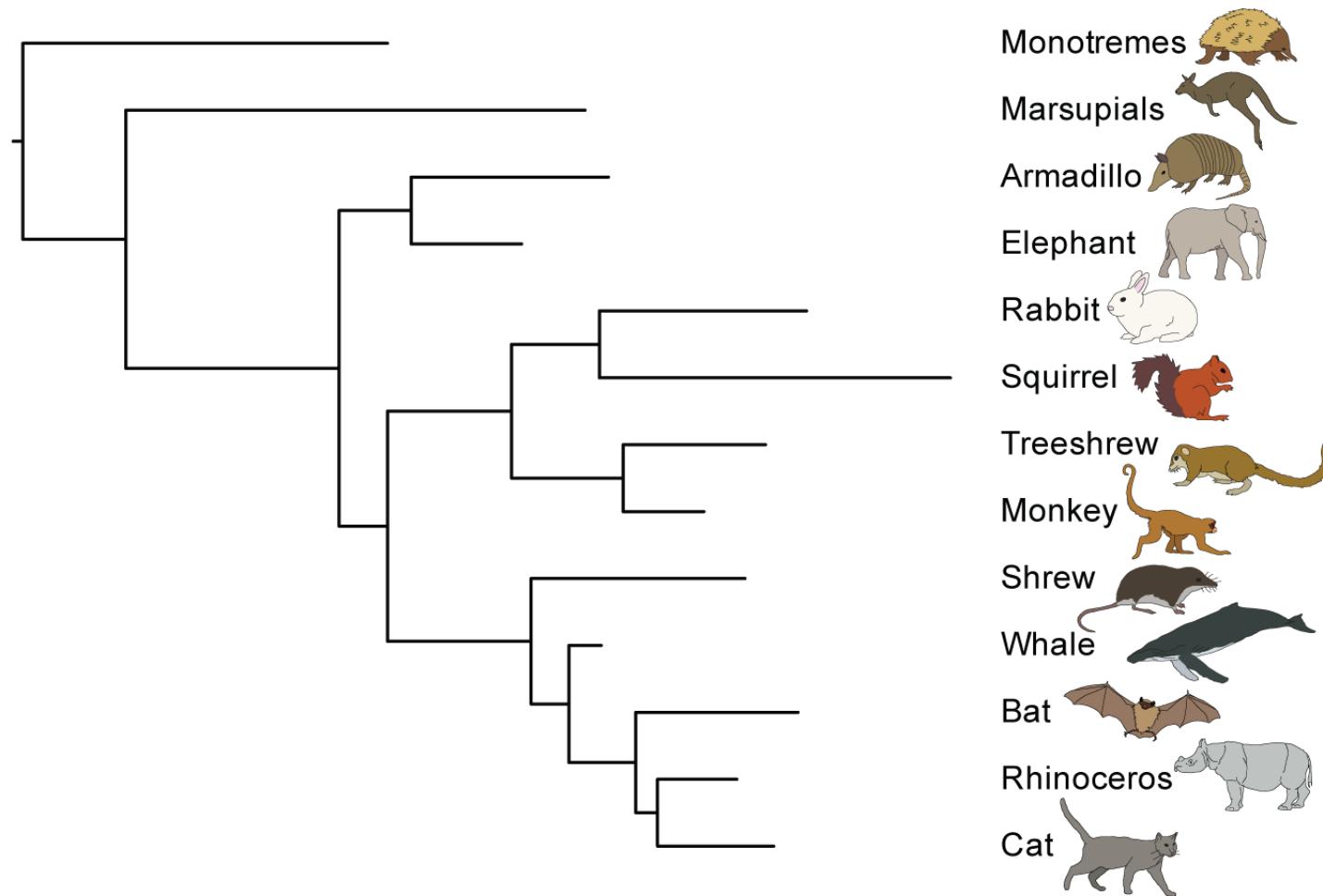
1837

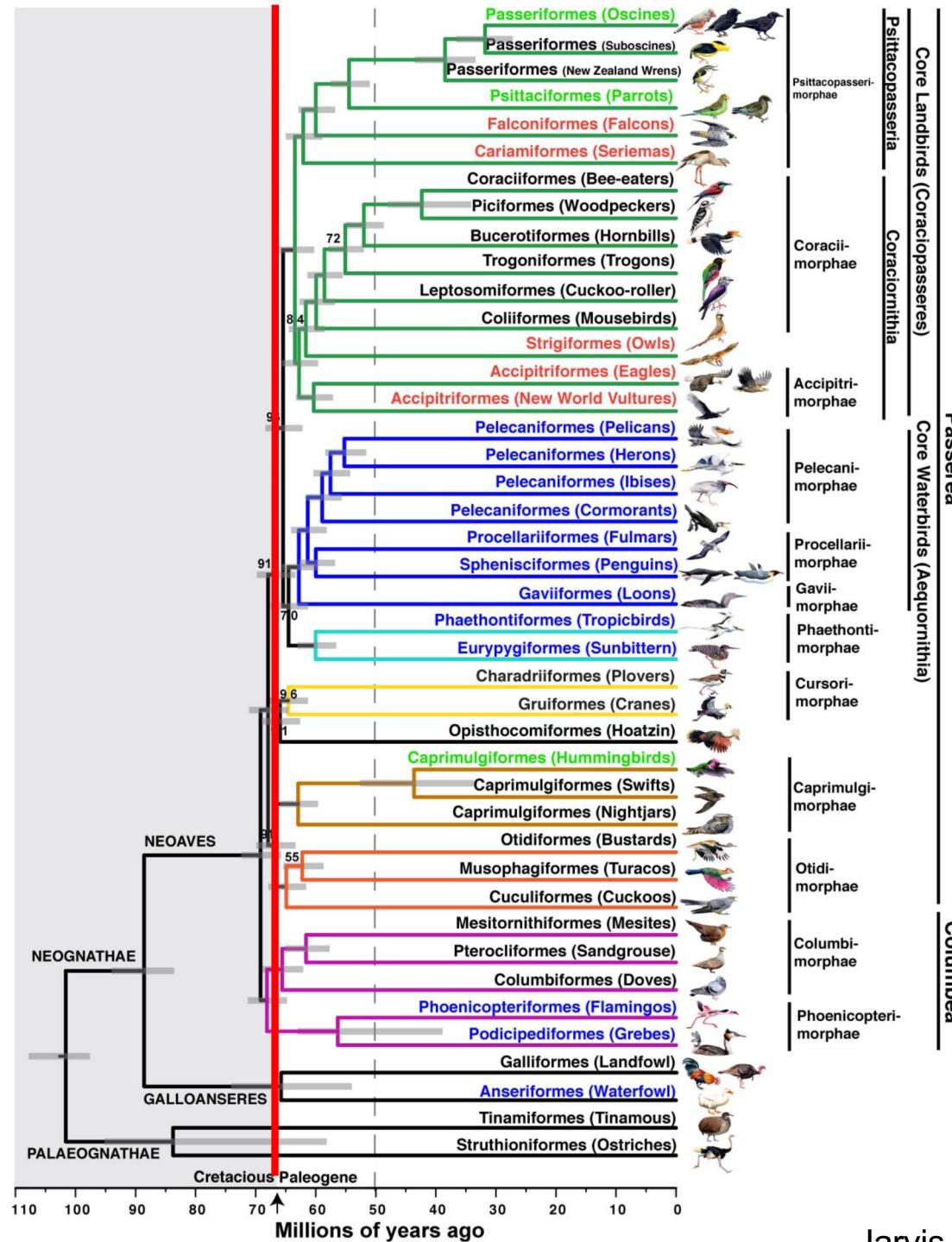


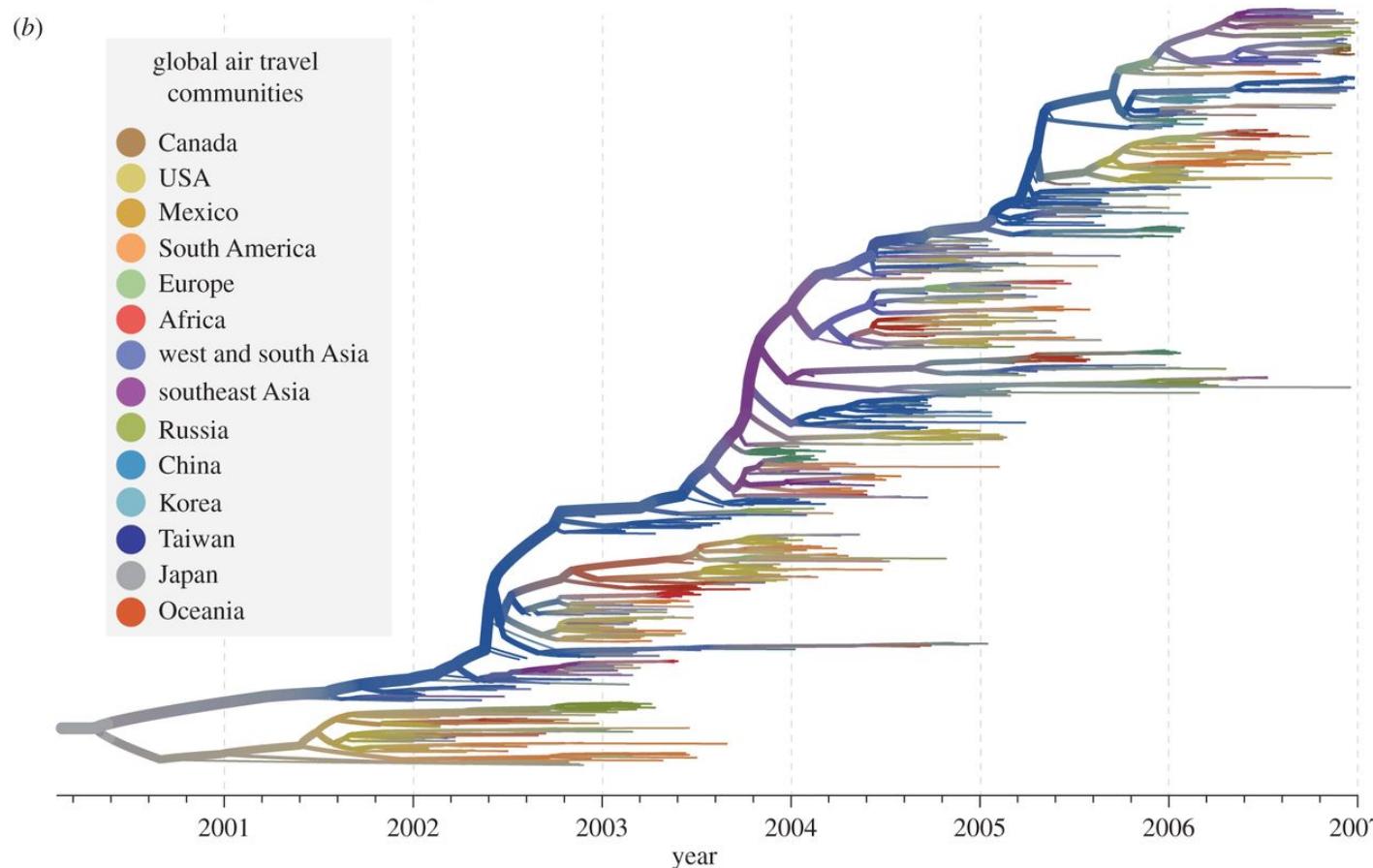
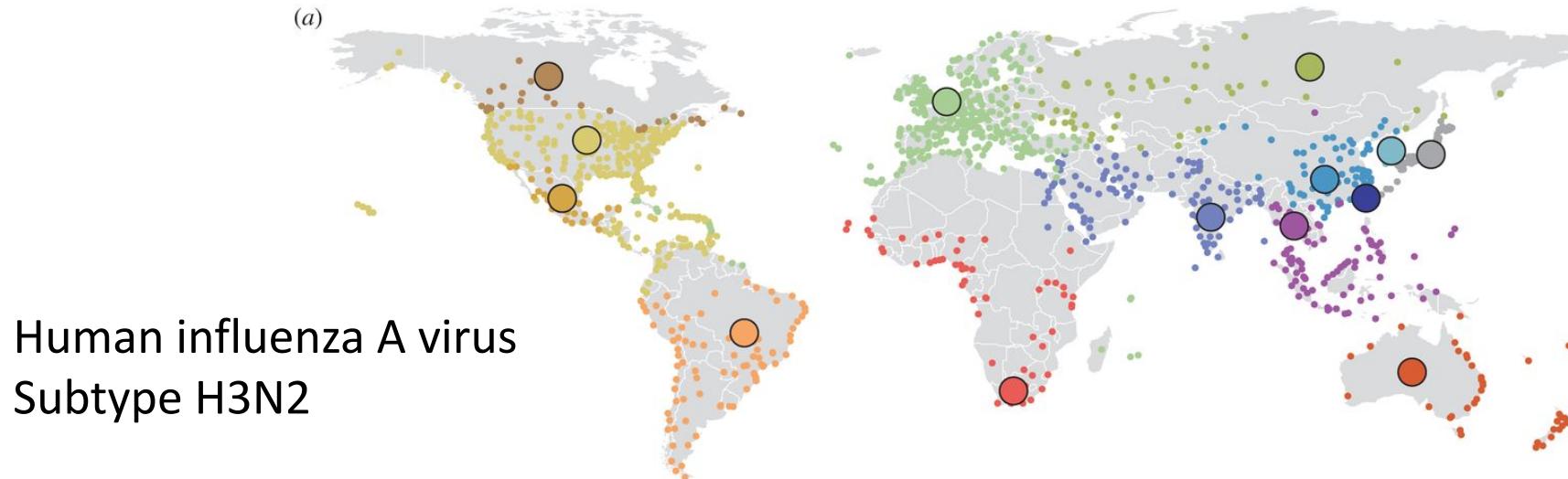
1859

Phylogenetic trees

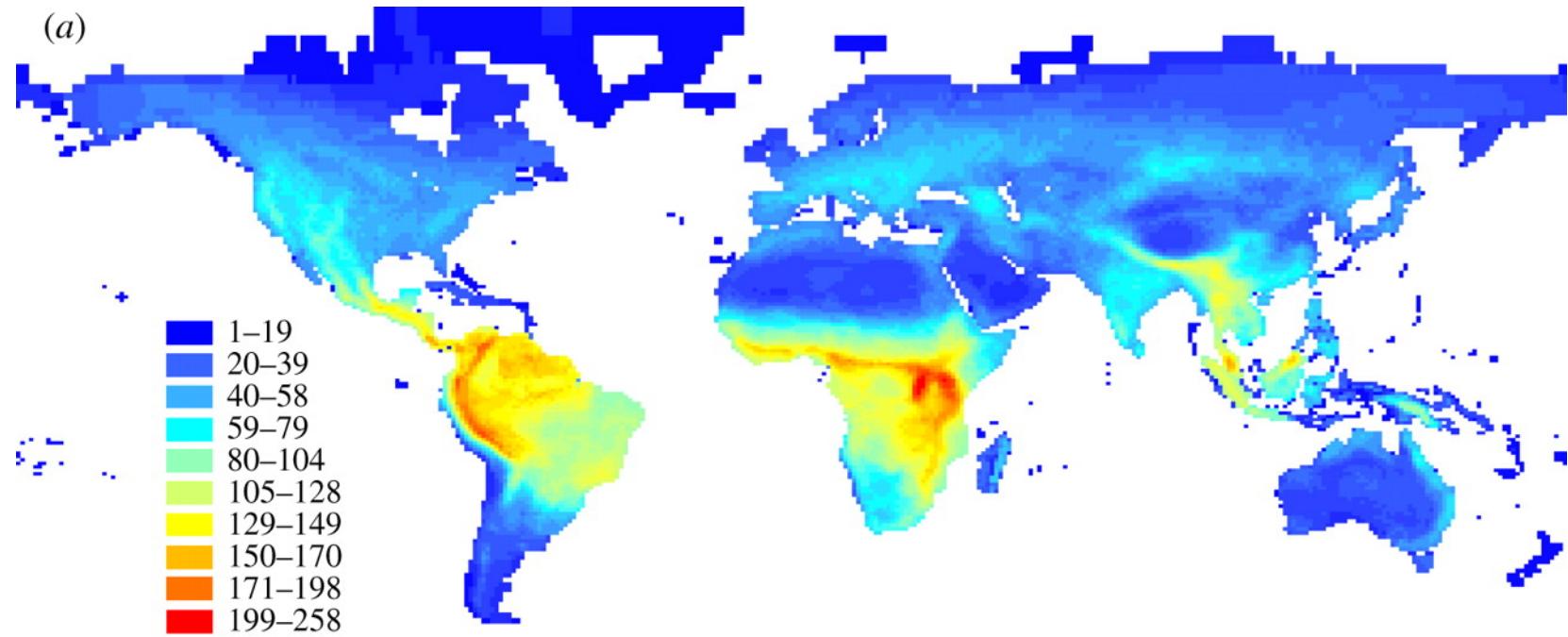
- Topology (relationships)
- Branch lengths (amount of evolutionary change or time)



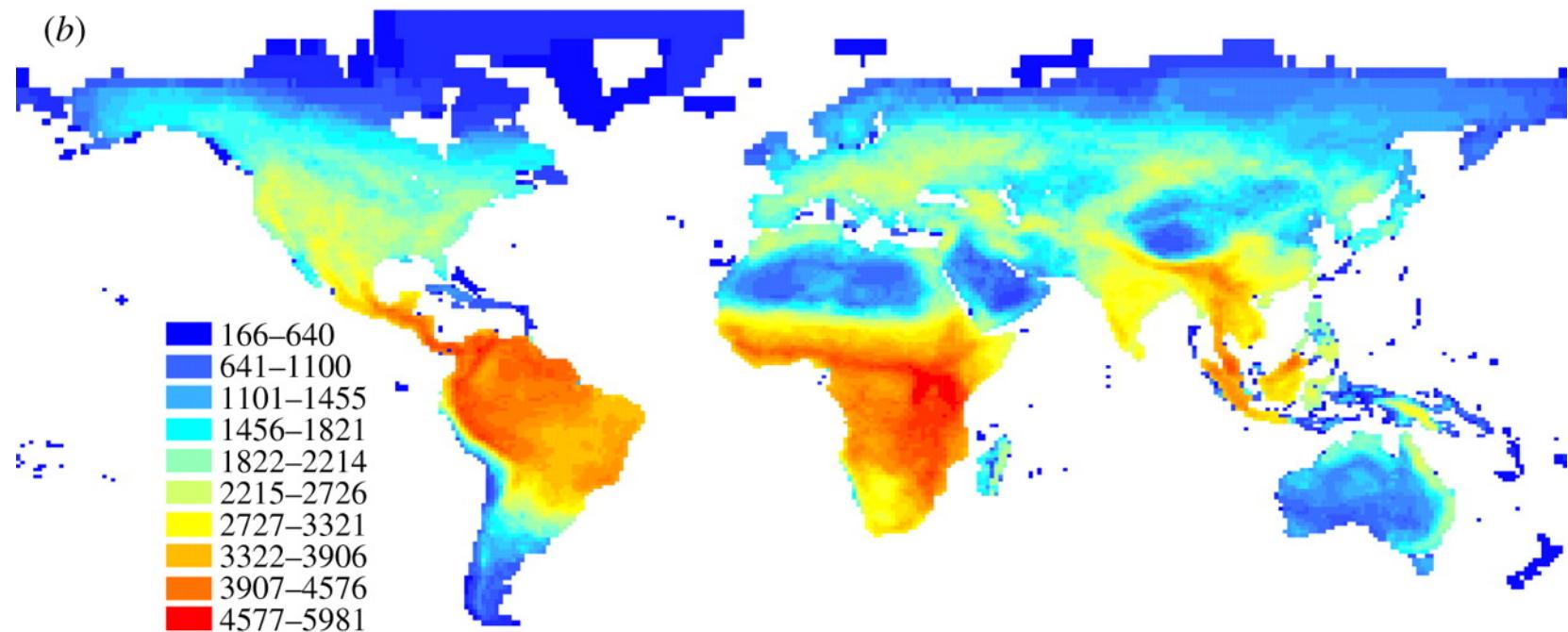




Mammal
species
richness

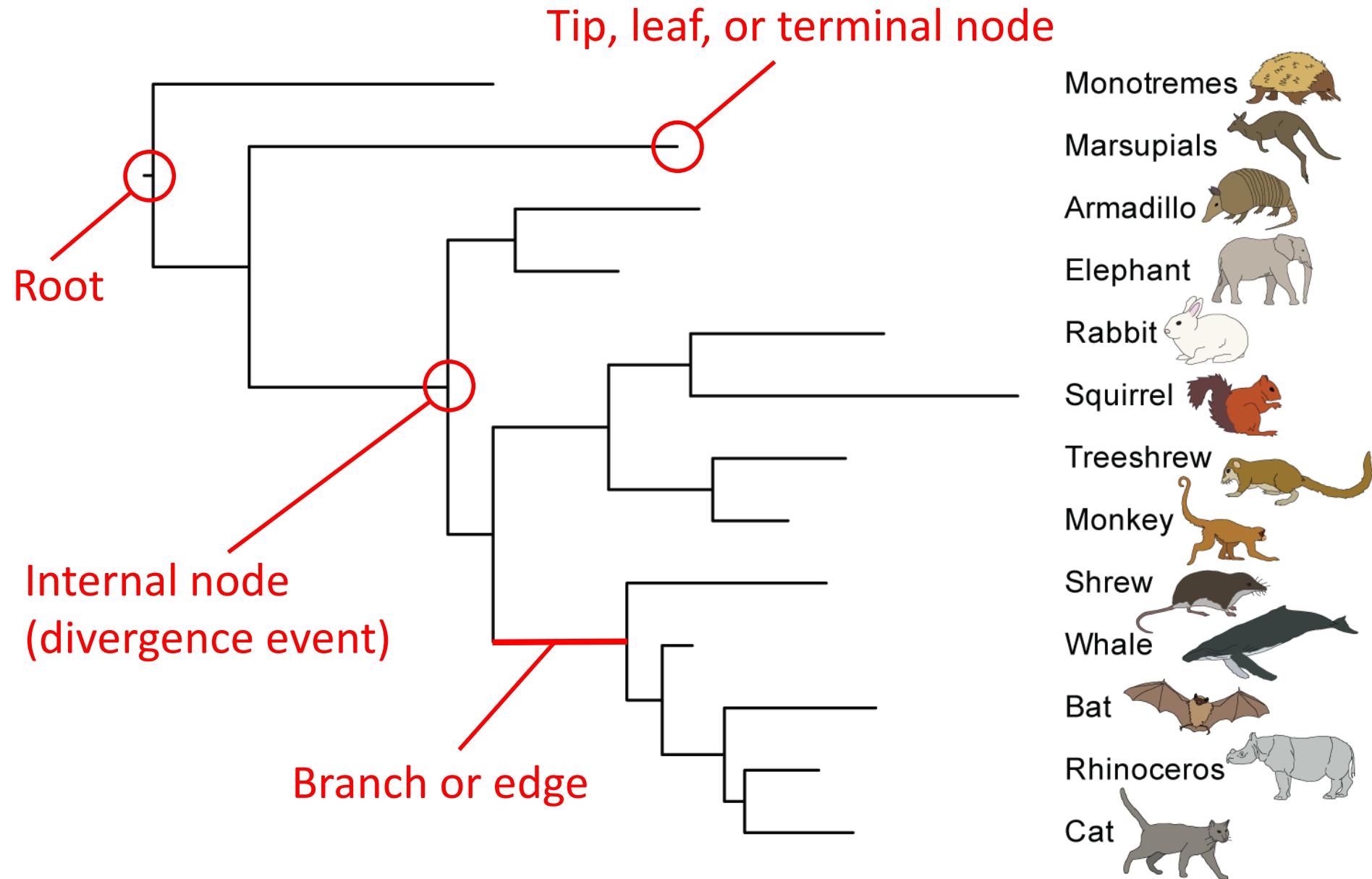


Mammal
phylogenetic
diversity

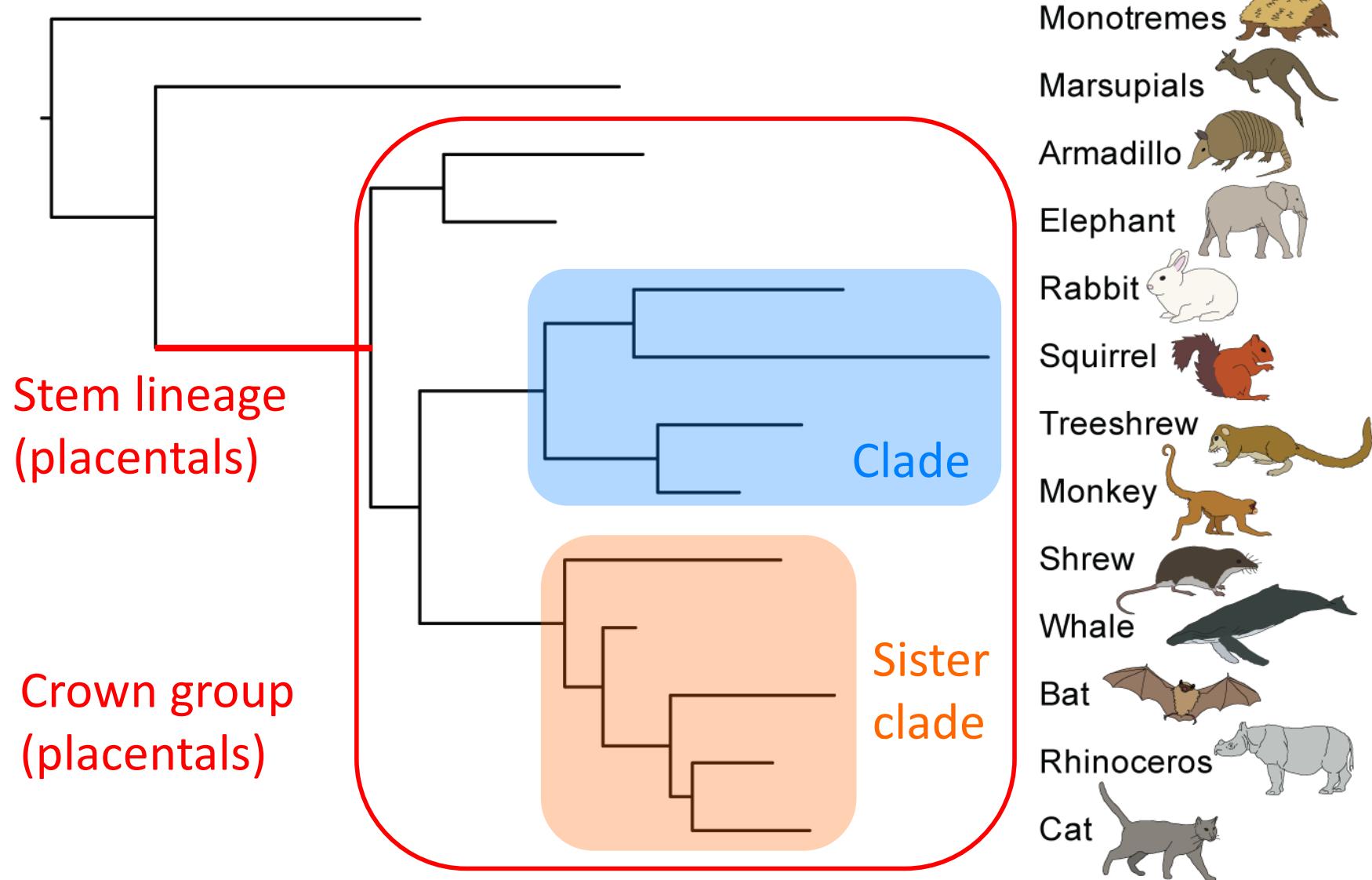


Tree Thinking

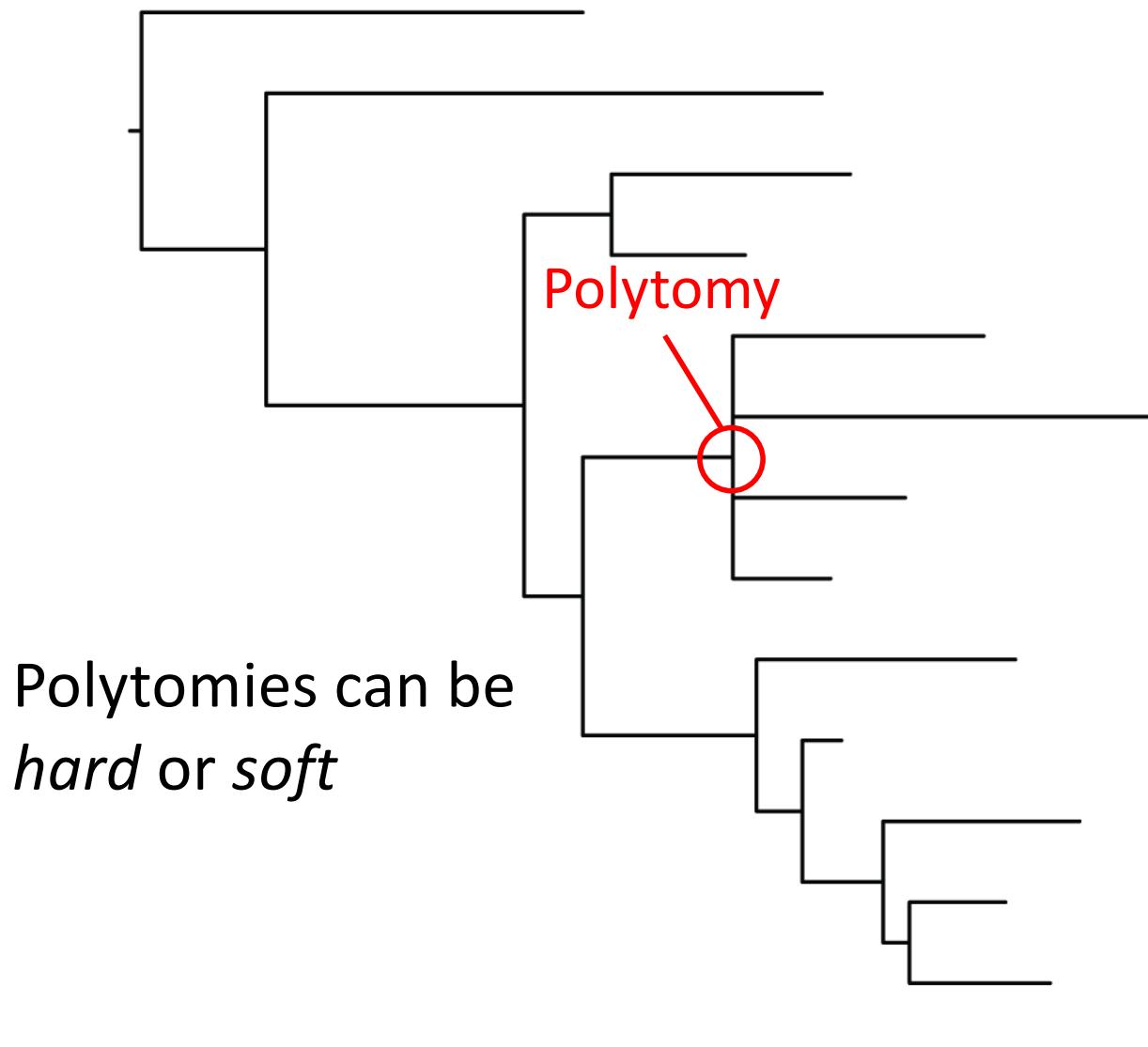
Phylogenetic trees



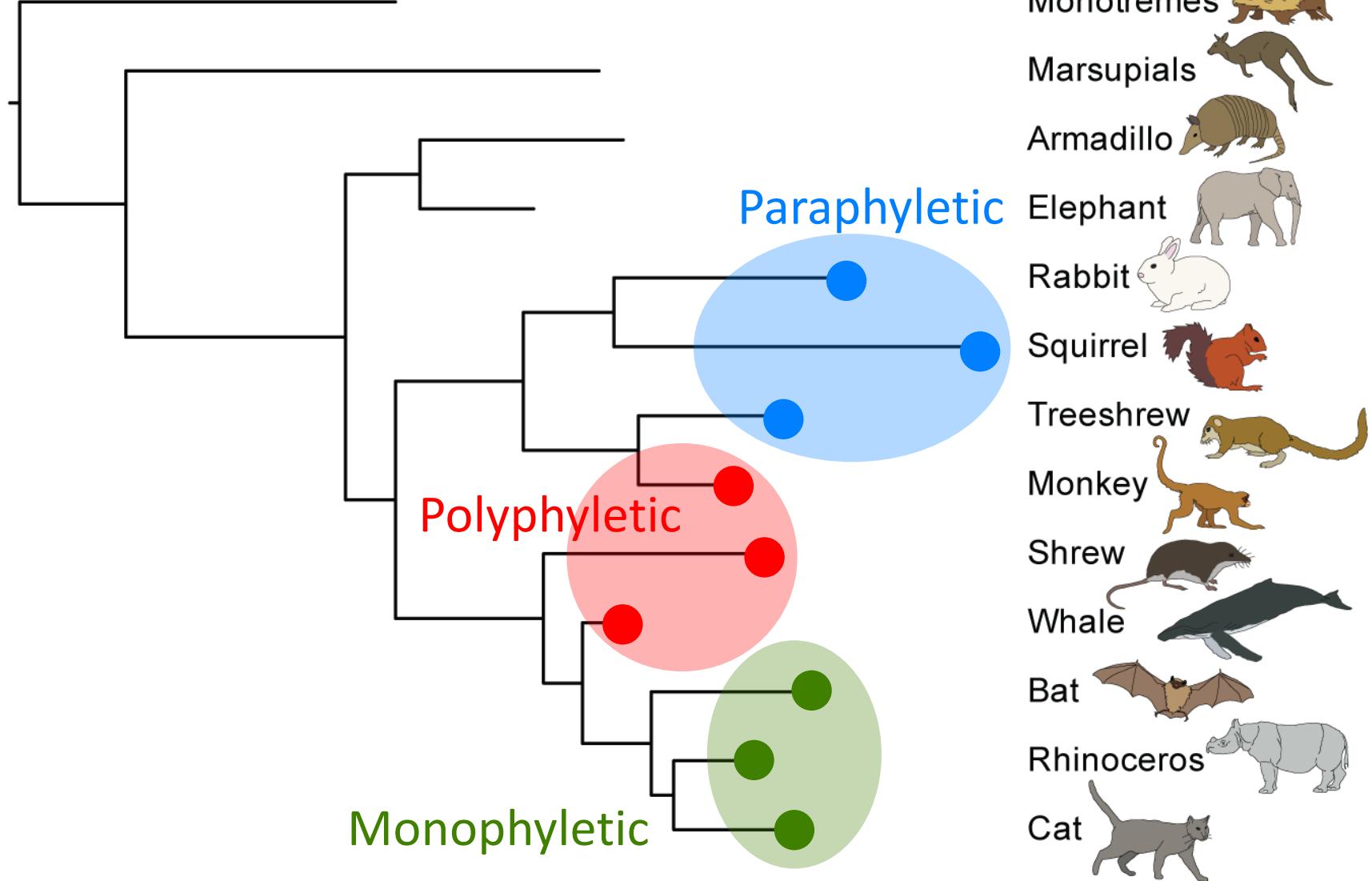
Phylogenetic trees



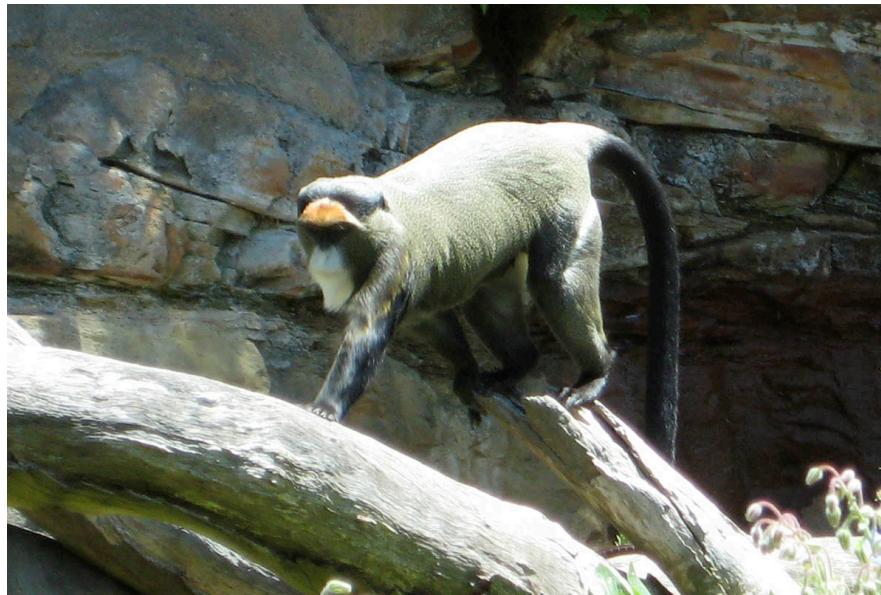
Phylogenetic trees



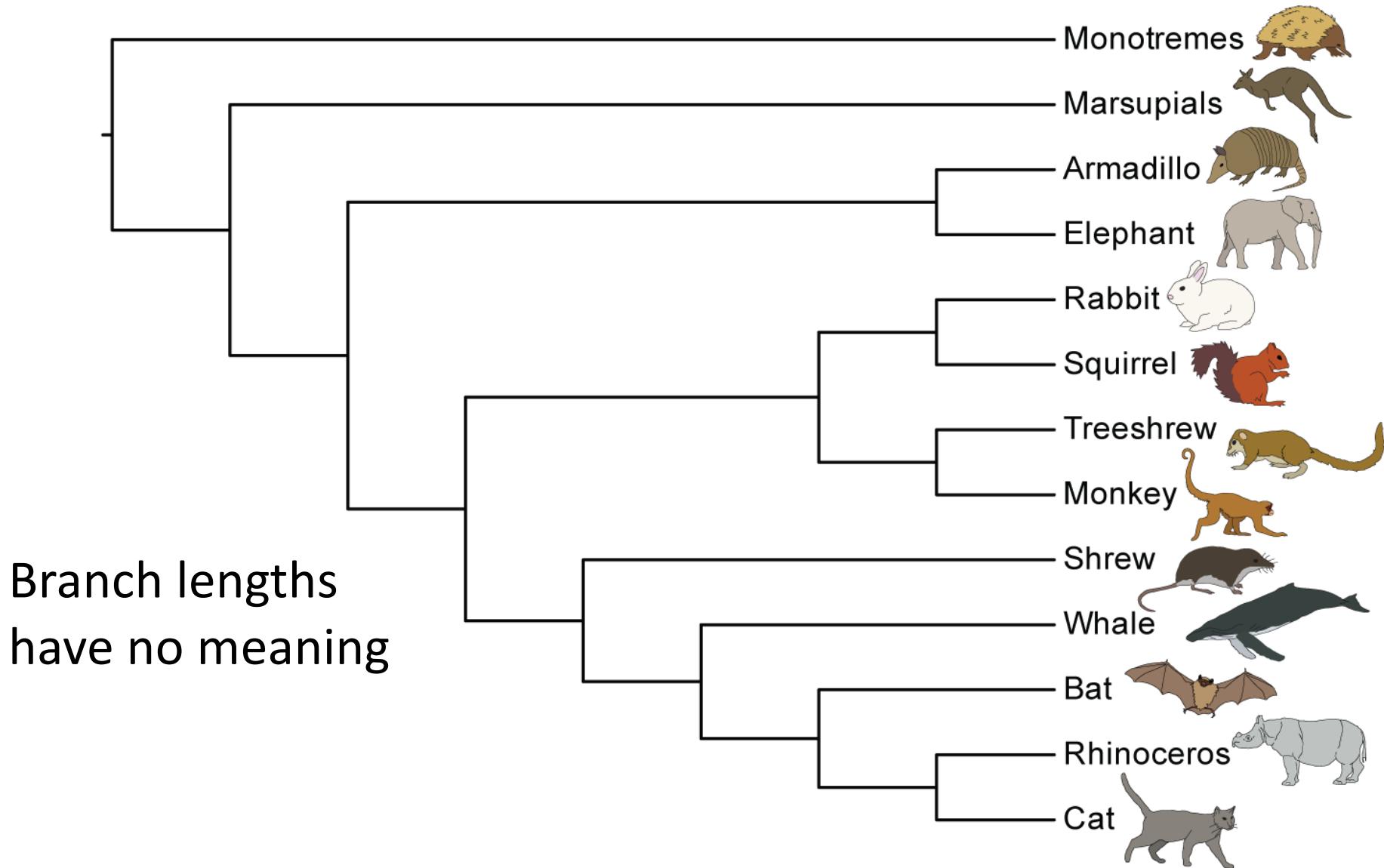
Cladistic terms



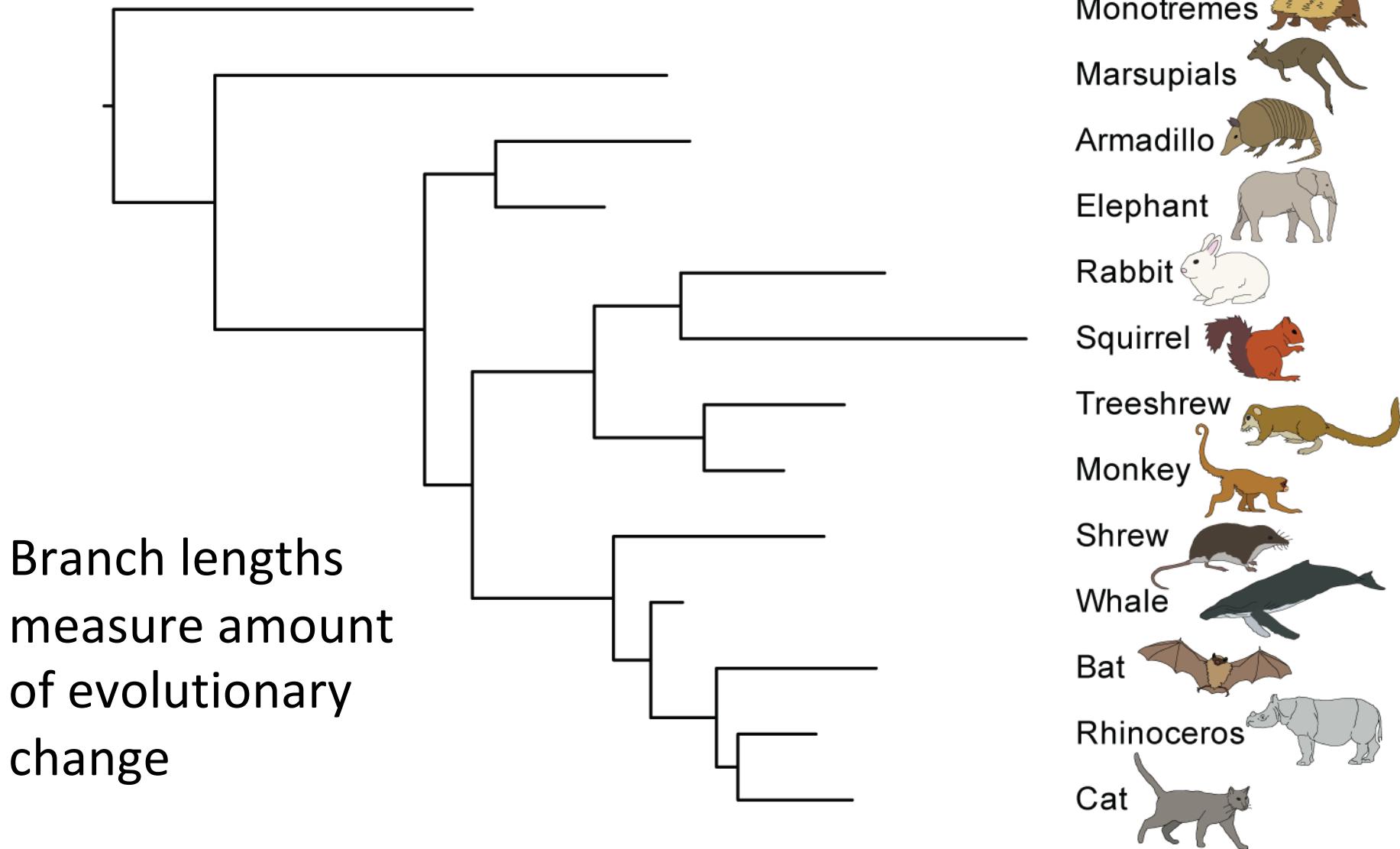
Paraphyletic groups



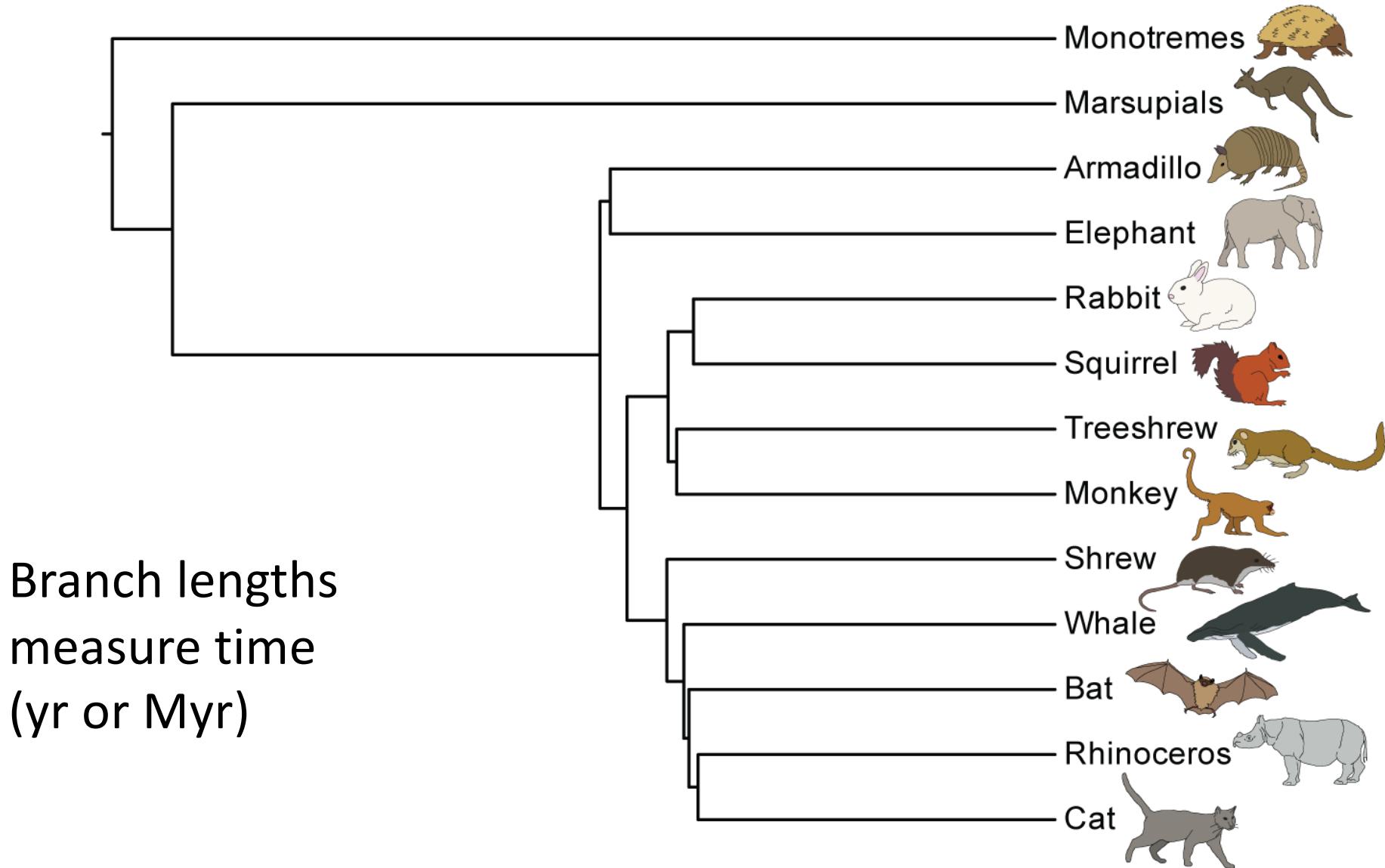
Trees: Cladogram



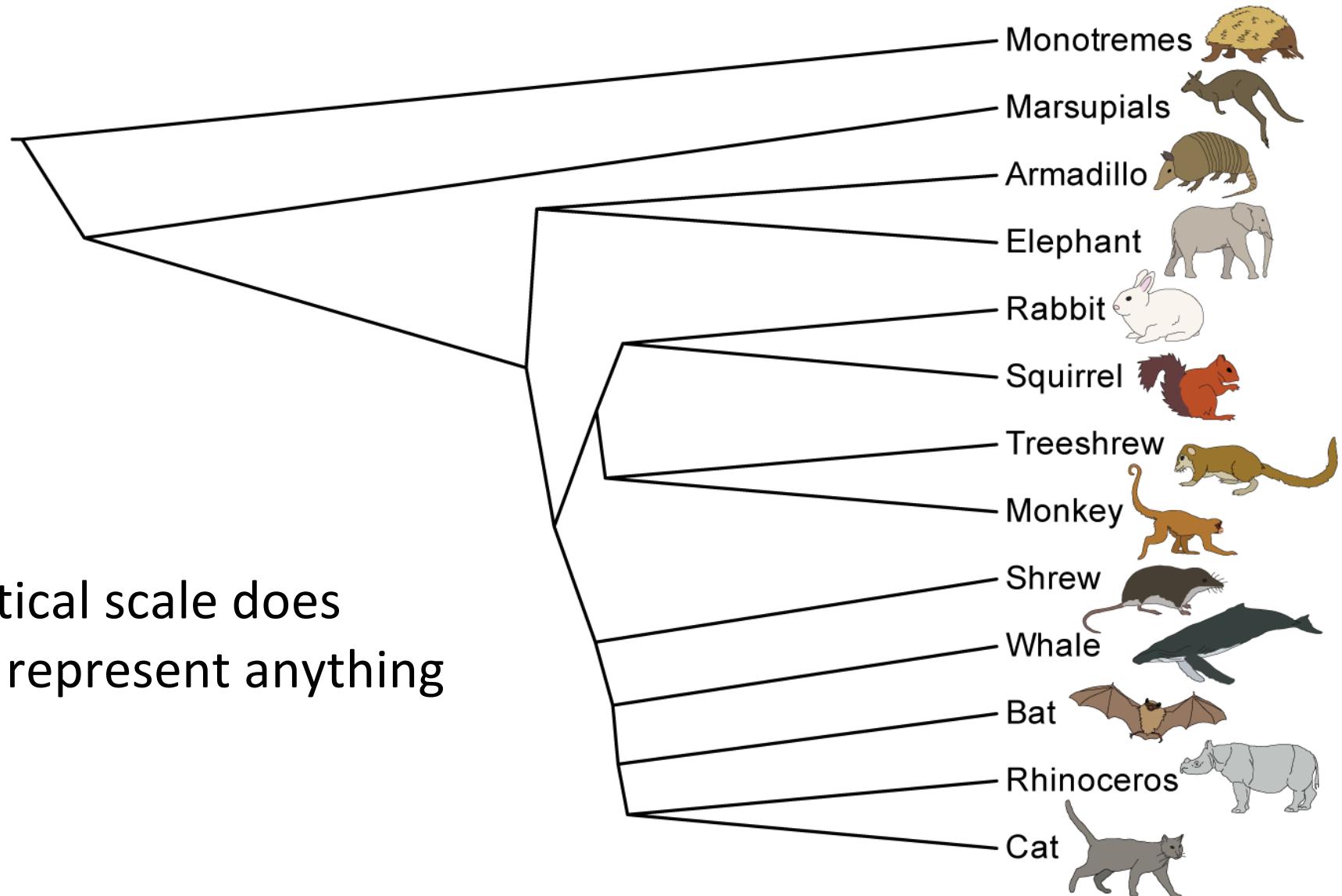
Trees: Phylogram



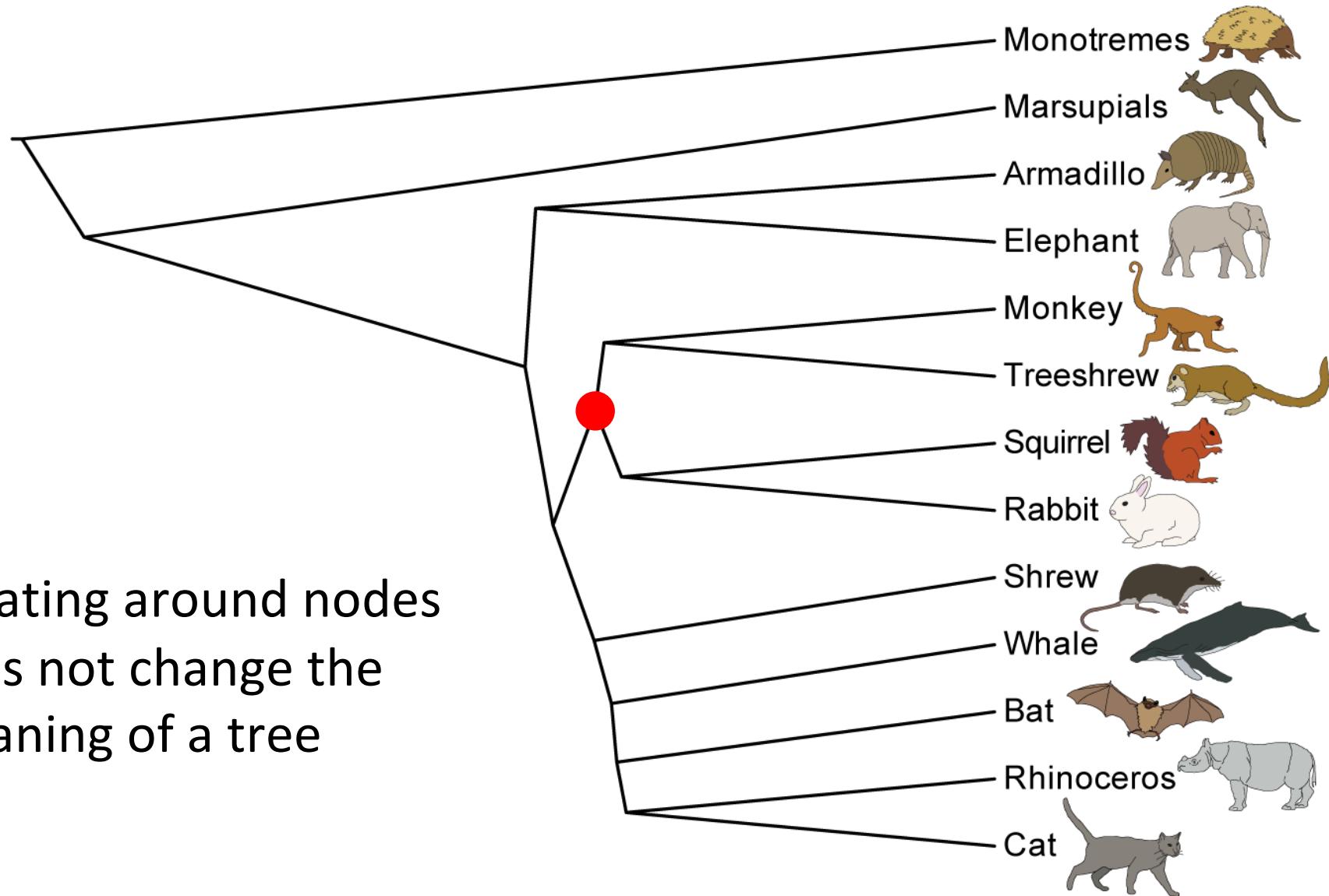
Trees: Chronogram or time-tree



Phylogenetic trees



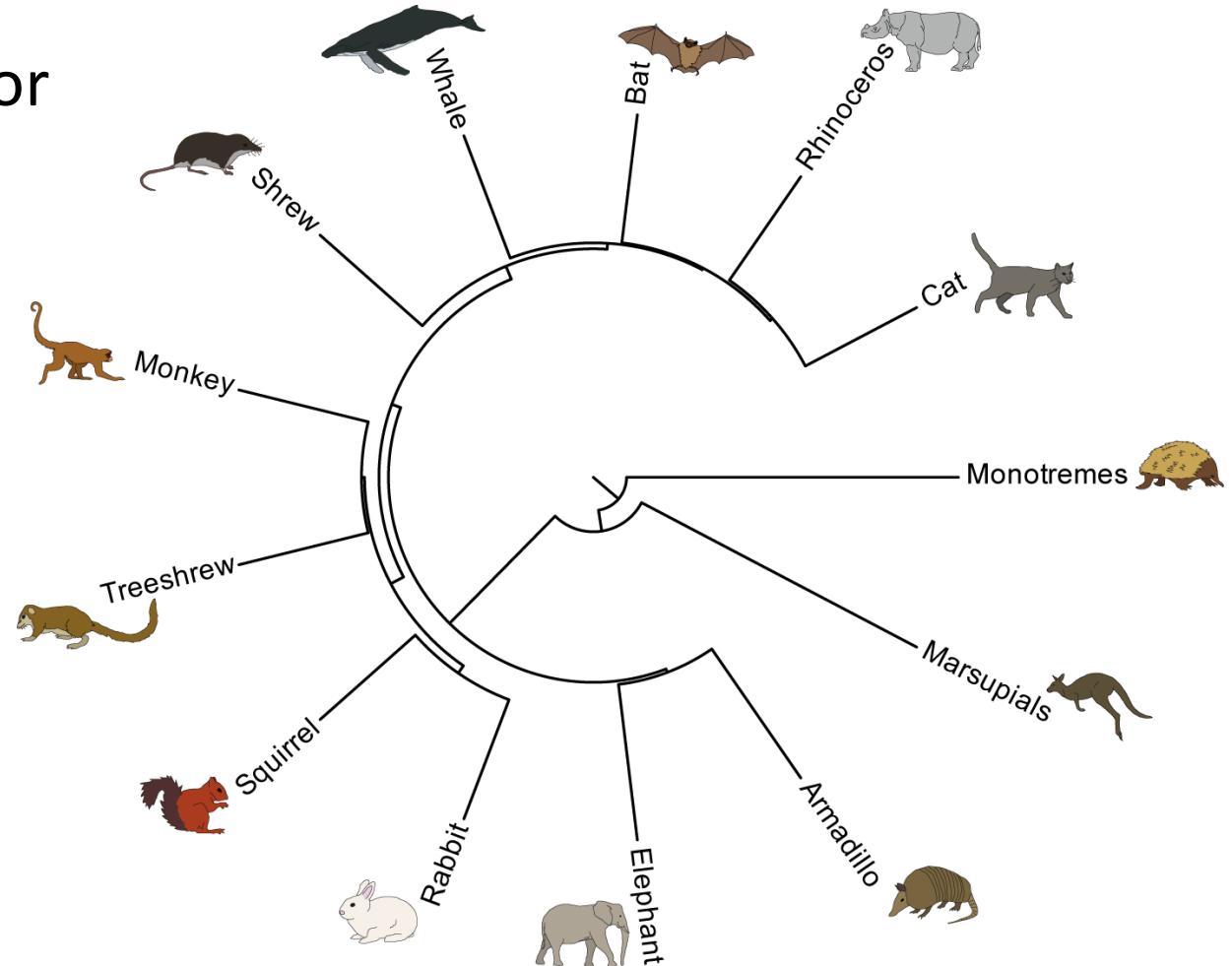
Phylogenetic trees



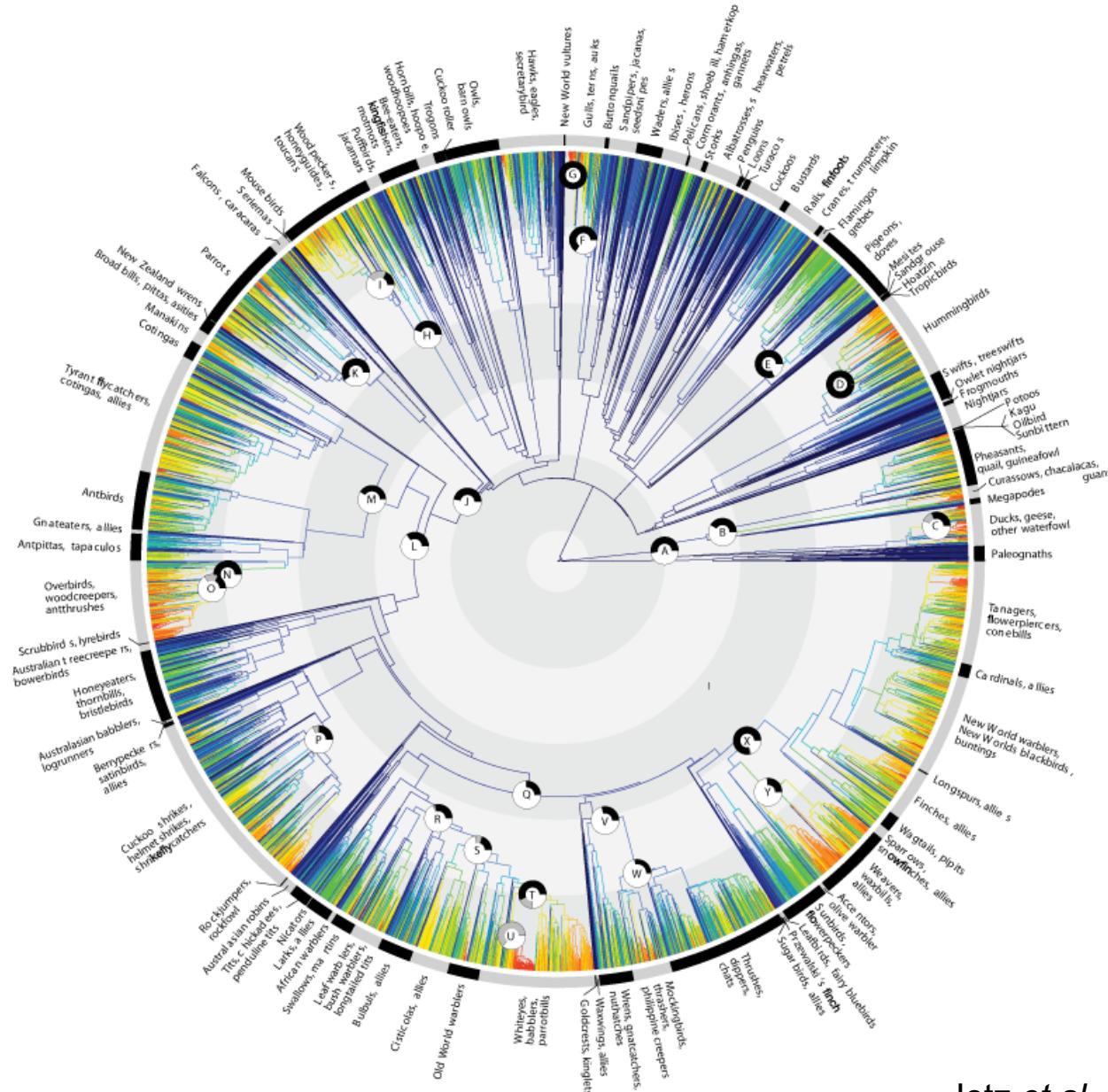
Rotating around nodes
does not change the
meaning of a tree

Phylogenetic trees: Circular

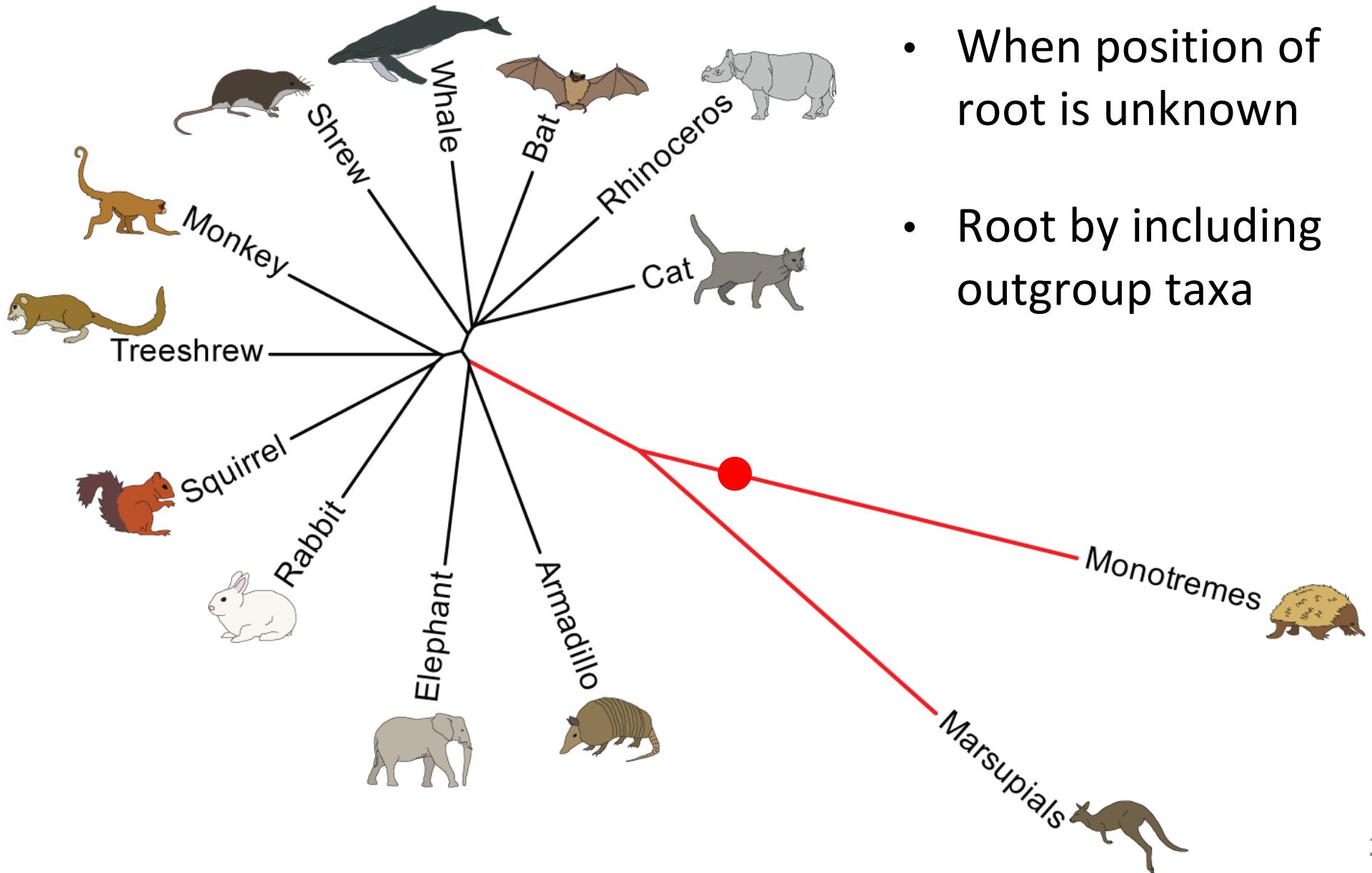
- Root is placed in centre
- Cladogram, phylogram, or chronogram
- Often used to display large trees
- Difficult to interpret



Phylogenetic trees: Circular



Phylogenetic trees: Unrooted



- When position of root is unknown
- Root by including outgroup taxa

Rooting

- **Include outgroup taxa**
 - Taxon closely related to ingroup
 - Taxon is not part of ingroup
- **Root at midpoint**
 - Highly unreliable if internal branches are short
- **Use a molecular clock**
 - Automatically estimates position of root

Phylogenetic trees: Newick format

- Without branch lengths (cladogram):
 - (Monotremes,(Marsupials,((Elephant,Armadillo),(((Squirrel,Rabbit),(Monkey,Treeshrew)),(Shrew,(Whale,(Bat,(Cat,Rhinoceros)))))));
- With branch lengths (phylogram/chronogram):
 - (Monotremes:12.0,(Marsupials:11.0,((Elephant:1.0,Armadillo:1.0):9.0,((Squirrel:1.0,Rabbit:1.0):2.0,(Monkey:1.0,Treeshrew:1.0):2.0):5.0,(Shrew:4.0,(Whale:3.0,(Bat:2.0,(Cat:1.0,Rhinoceros:1.0):1.0):1.0):1.0):4.0):2.0):1.0):1.0);

Molecular Phylogenetics

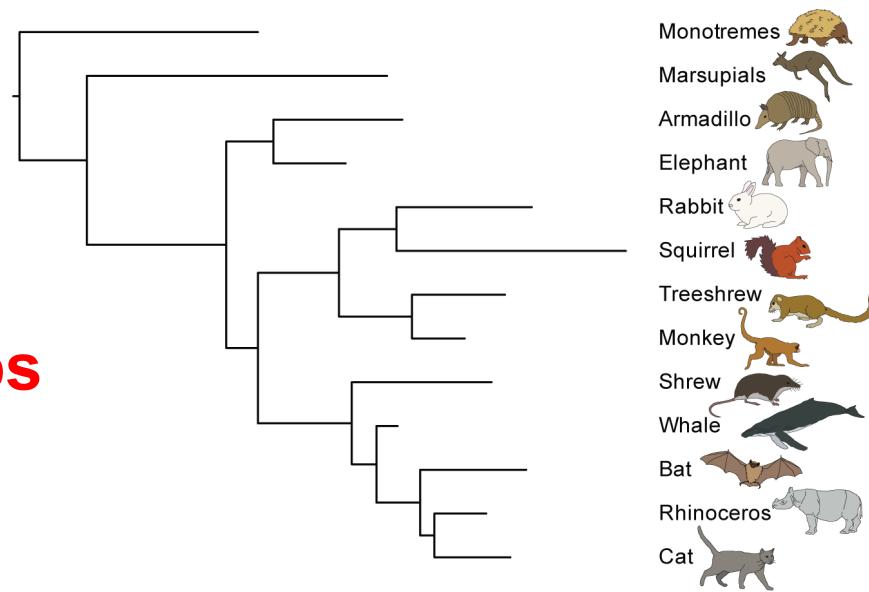
Phylogenetic analysis

- Sometimes we know the phylogeny
 - Viral transmission histories
 - Pedigrees (humans, domesticated animals, lab organisms, etc.)
- Usually we do not know the phylogeny but we can estimate it
 - Morphological data
 - Molecular data

Fundamental assumptions

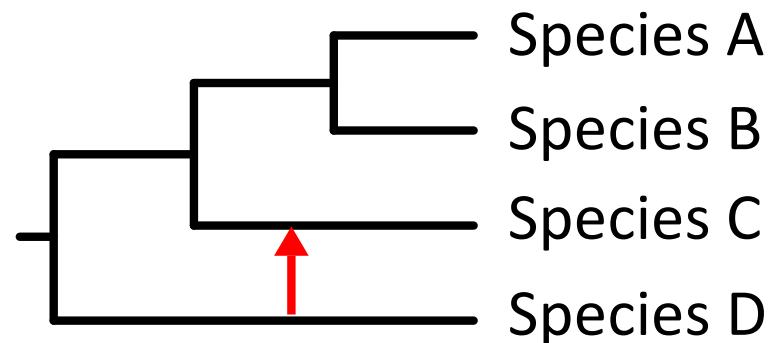
- Phylogenetic methods make several fundamental assumptions:
 - Relationships among taxa can be represented by a tree
 - Homologous characters are being compared
 - Characters are mutually independent
 - Lineages evolve independently

**When might relationships
not be treelike?**

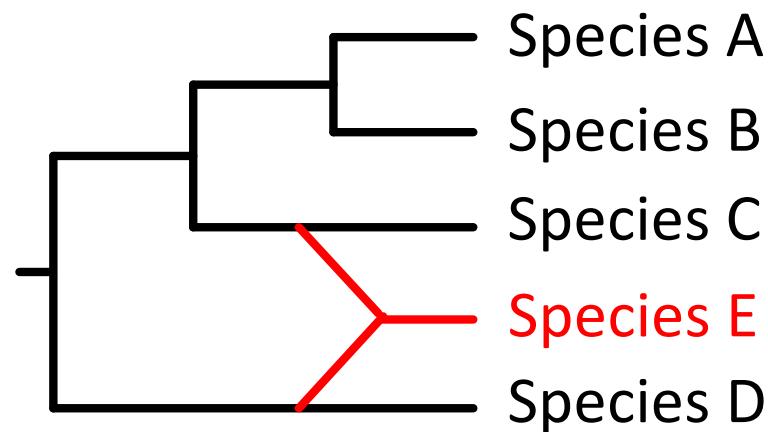


Non-treelike evolution

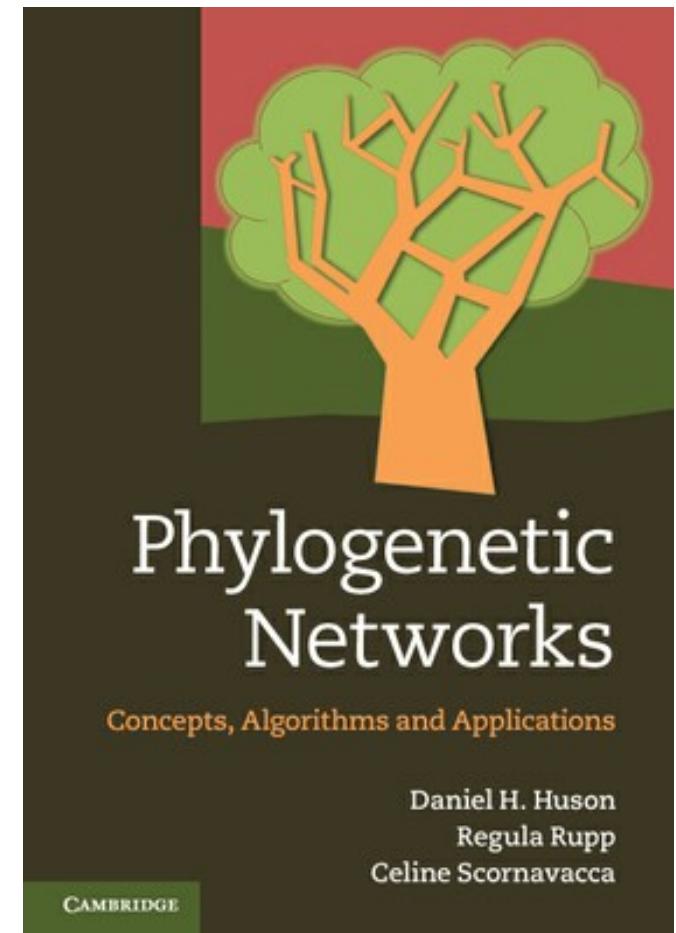
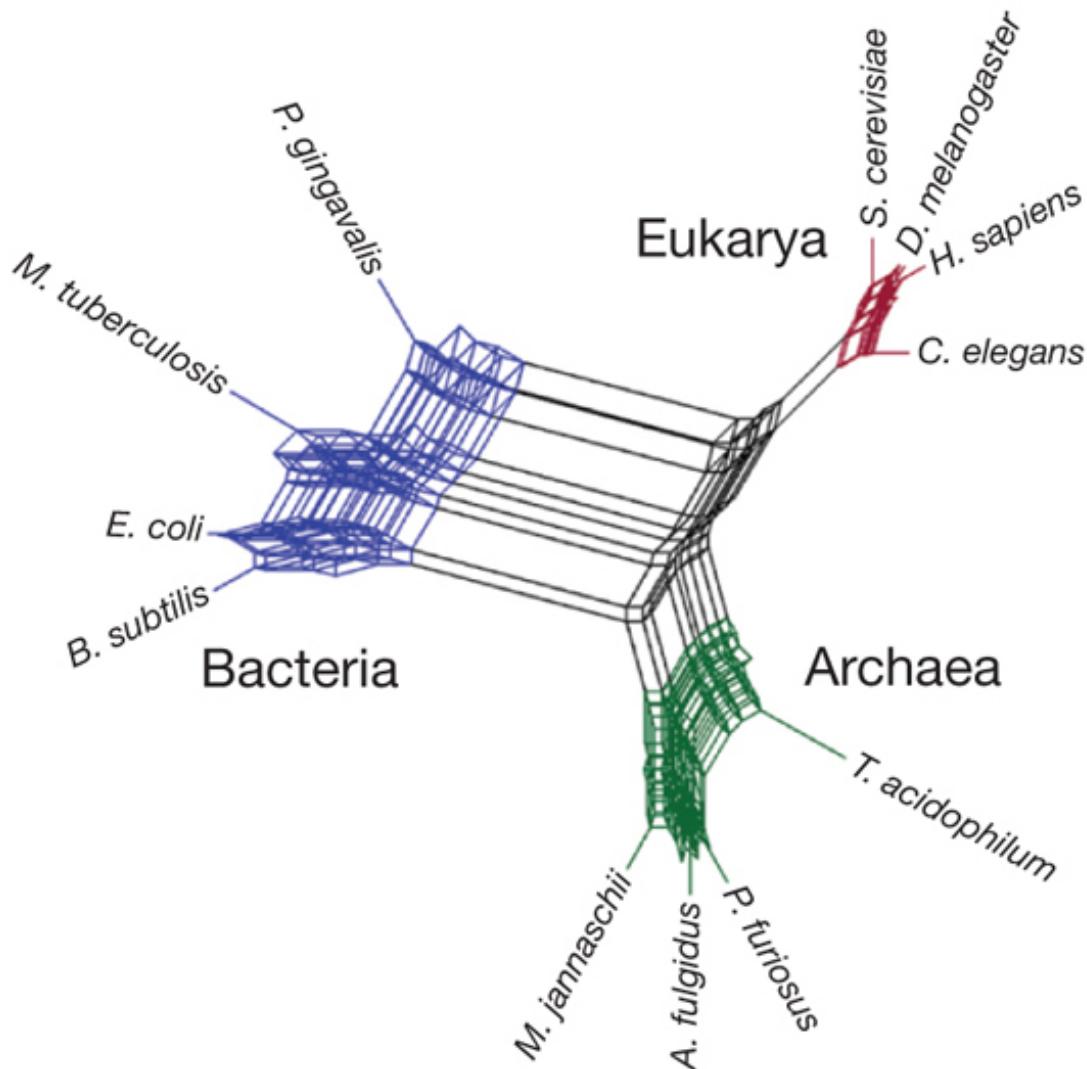
Horizontal gene transfer



Hybrid speciation

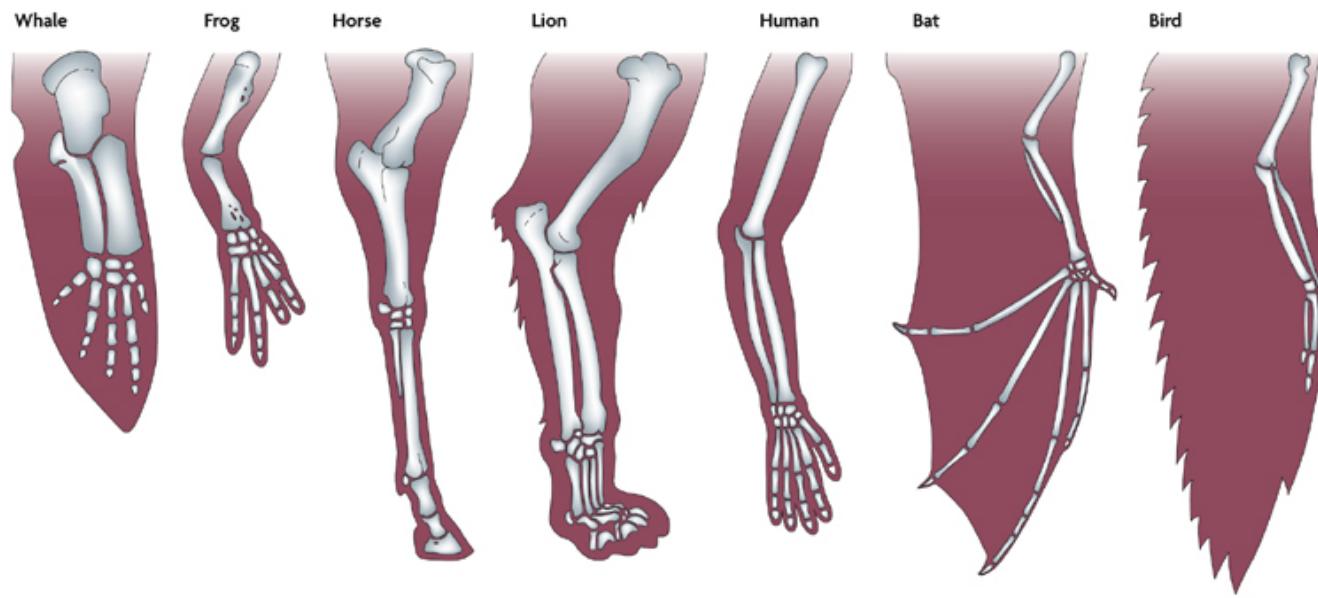


Phylogenetic networks



Fundamental assumptions

- Phylogenetic methods make several fundamental assumptions:
 - Relationships among taxa can be represented by a tree
 - Homologous characters are being compared
 - Characters are mutually independent
 - Lineages evolve independently



Character homology

- Comparing strings of nucleotides
- Each nucleotide site is a character
- But DNA sequences can vary in length

blue whale

CGTTAGTACACT

humpback whale

CGATAGTTCACT

gray whale

CGTTAGTTACC

fin whale

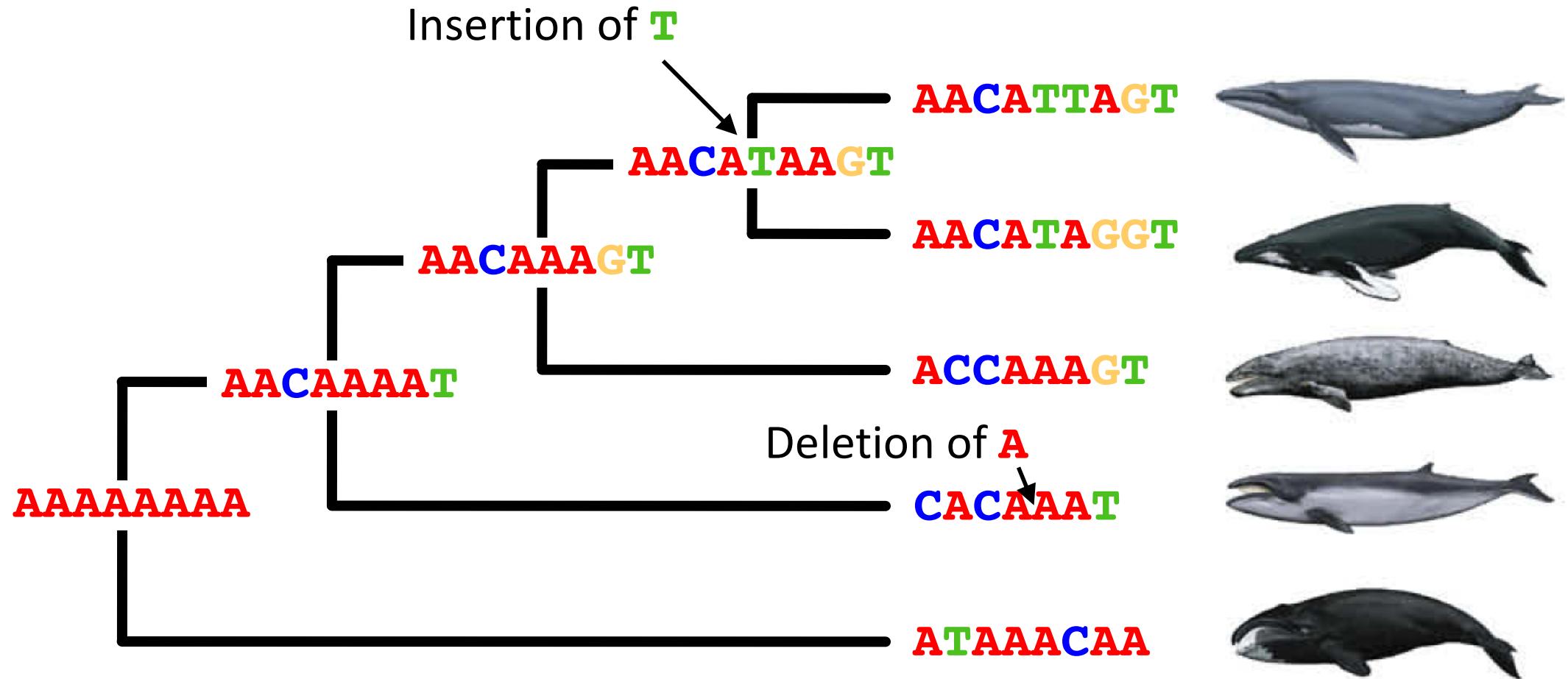
CATTGGATTACT

right whale

CATTGGTTACT



Example: Whales



DNA sequence alignment



AACATTAGT

AACATAGGT

ACCAAAAGT

CACAAAT

ATAAACAA



AACATTAGT

AACATAGGT

ACCA-AAGT

CACA--AAT

ATAA-ACAA

DNA sequence alignment

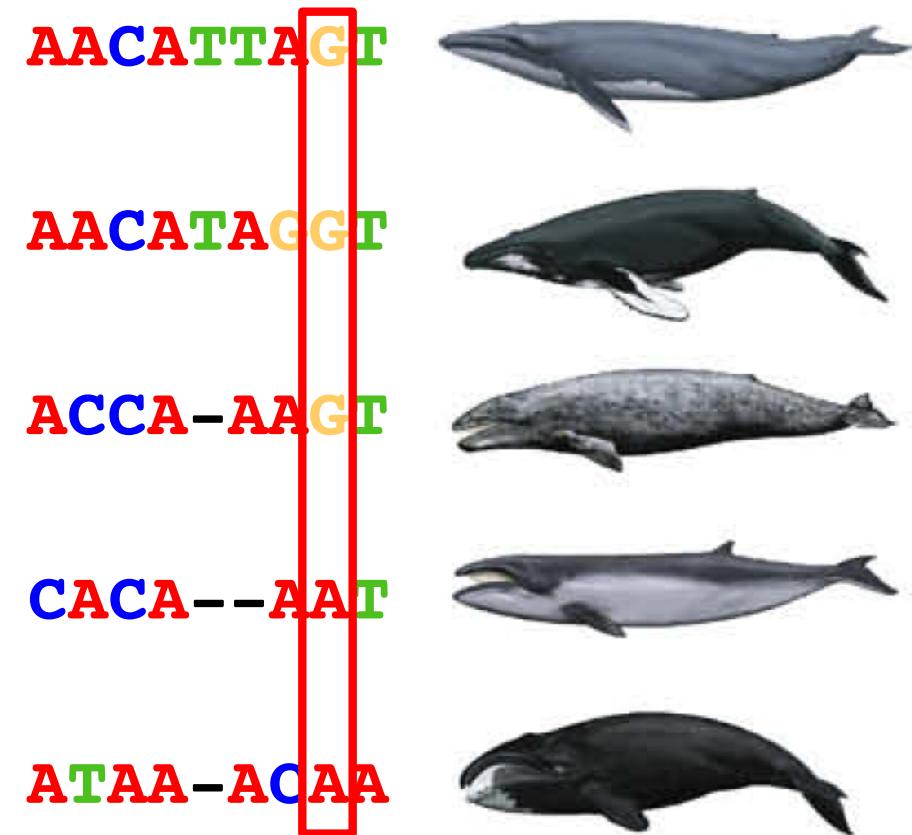
- Homologous site
- Inherited from the common ancestor of all sequences in the alignment
- The aim of sequence alignment is to maximise the number of sites for which you can infer homology

AACATTAGT
AACATAAGT
ACCA-AAGT
CACAA--AAT
ATAA-ACAA



DNA sequence alignment

- Groups together the first 3 sequences
- Groups together the last 2 sequences
- Informative for all phylogenetic methods



DNA sequence alignment

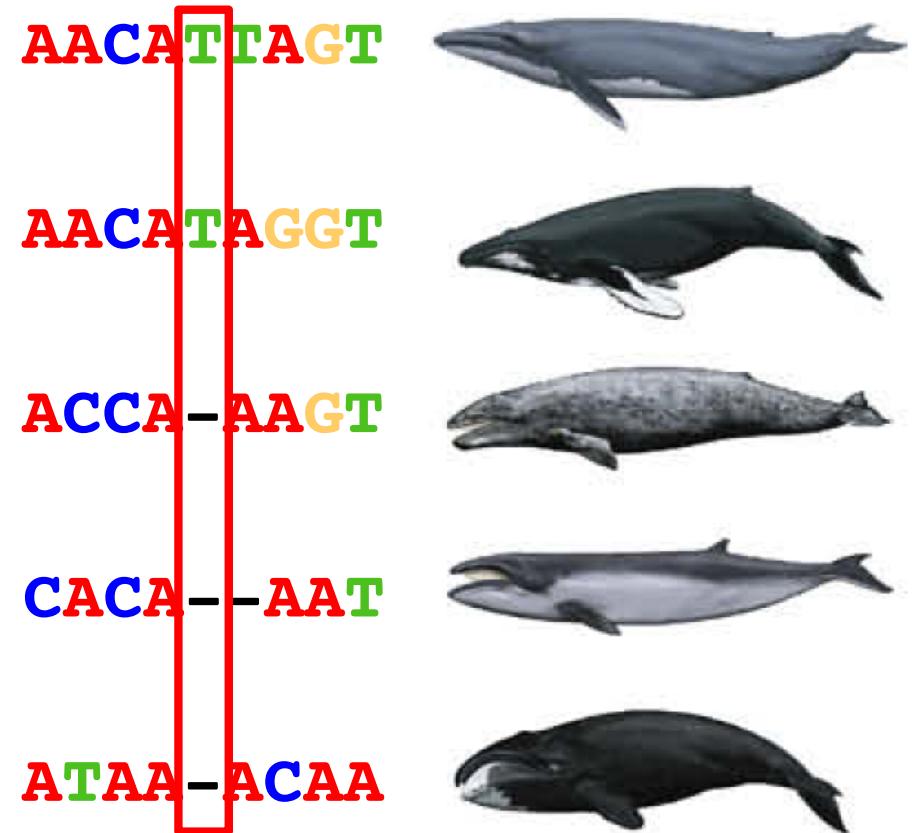
- Does not group any sequences
 - Not useful for maximum parsimony
- But informative for estimating amount of evolutionary change
 - Useful for other methods

AACATTAGT
AACATAAGT
ACCA-AAGT
CACAA--AAT
ATAA-ACAA



DNA sequence alignment

- Indel – insertion or deletion
- Potentially informative
- Most phylogenetic methods do not really use indel data



A practical approach

Align sequences using automated methods

CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice

Julie D.Thompson, Desmond G.Higgins⁺ and Toby J.Gibson*

Software

Open Access

MUSCLE: a multiple sequence alignment method with reduced time and space complexity

Robert C Edgar*

MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform

Kazutaka Katoh, Kazuharu Misawa¹, Kei-ichi Kuma and Takashi Miyata*

A practical approach

Align sequences using automated methods



Adjust alignments by eye

CTATGTGGCACCCAGCCCCATGCA--AGC

ATATGTGGCA-----CCCAGGGCA--AG-

ATATGTGGCACCCAGCCCCATGCATT--

A practical approach

Align sequences using automated methods



Adjust alignments by eye



Delete sites with uncertain homology

CTATGTGGCACCCAGCCCCATGCA -- AGC

ATATGTGGCA ----- CCCAGGGCA -- AG - ?

ATATGTGGCACCCAGCCCCATGCA TTT --

Useful references

