

# Phylogenetic estimation

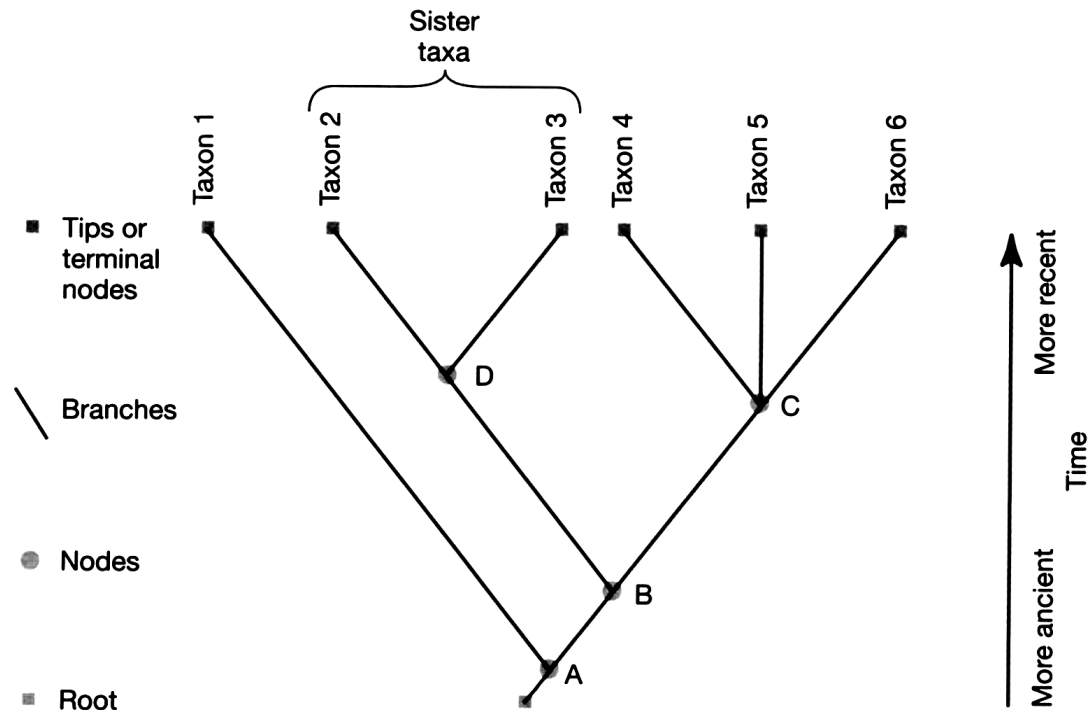
- Reconstructing evolutionary history
  - Phylogeny building
  - Parsimony
  - Other methods
- Using phylogeny in evolutionary analysis
  - Rates of change
  - Classification
  - Hypothesis testing

# Phylogeny and Evolution

- The evolutionary relationships among groups of organisms
  - Reflects single unique history of life
  - Pictured as a phylogeny or ‘cladogram’
    - ‘clade’ is related group of organisms

# Phylogenetic tree

- Nodes
- Branches
- Taxa
- Clade



# How to make a tree

- Principle of parsimony
  - Less complicated explanations more likely to be correct
  - In evolutionary biology, phylogenies that require fewer evolutionary transitions more likely to be correct

# Cladistic methods

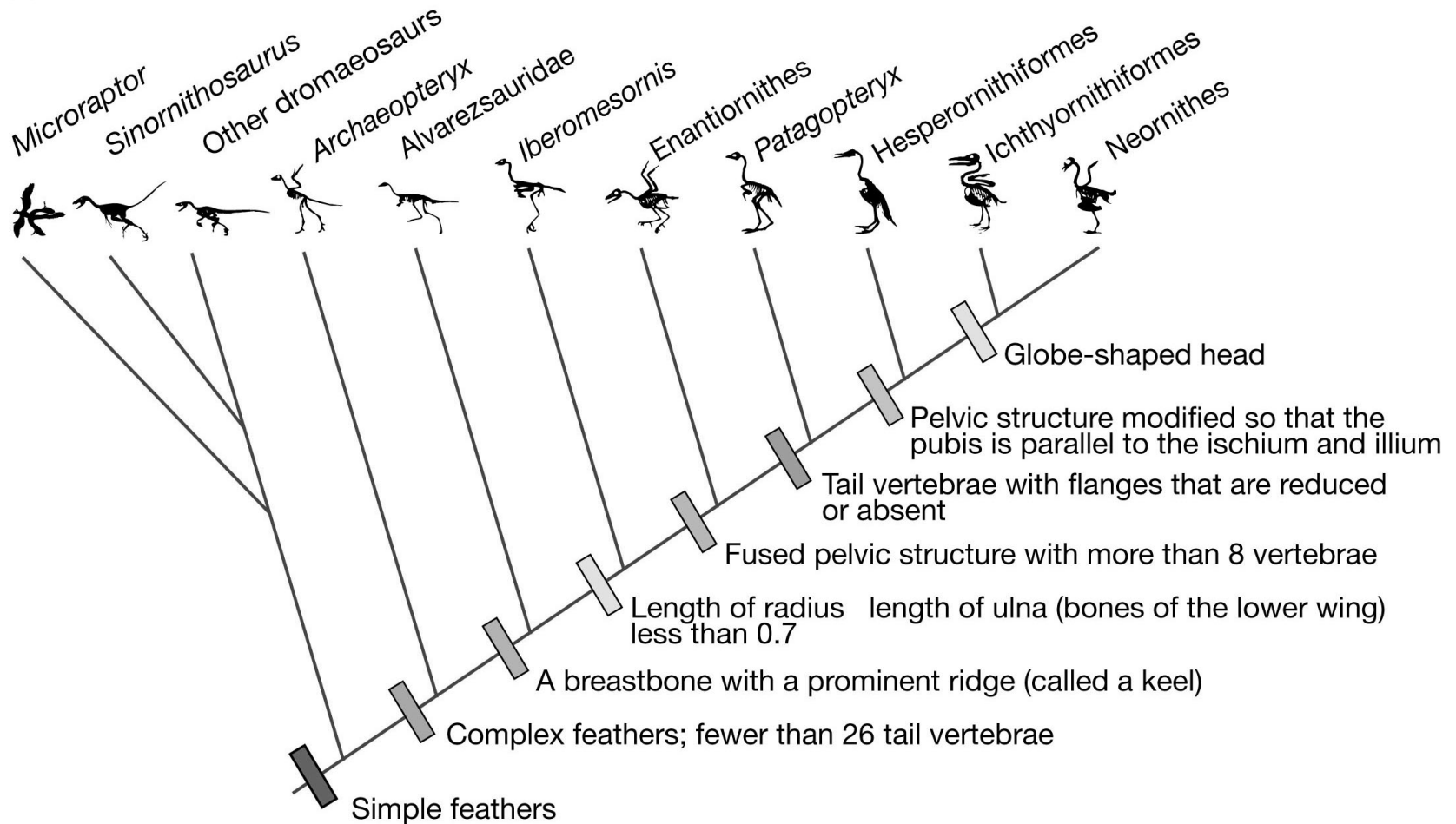
- Synapomorphy = shared derived traits
  - E.g. mammals and hair
  - Reflect true evolutionary history
- Homoplasy = ‘noise’ character similarity does not reflect evolutionary relationships
  - trait reversals
  - Convergent evolution

# Applying cladistic methods

- Identify synapomorphic traits
  - Homology: structural, developmental, genetic
- Code taxa for traits
- Use parsimony to infer phylogenetic relationships
- Validating and assessing tree

# Synapomorphy in bird evolution

(b)

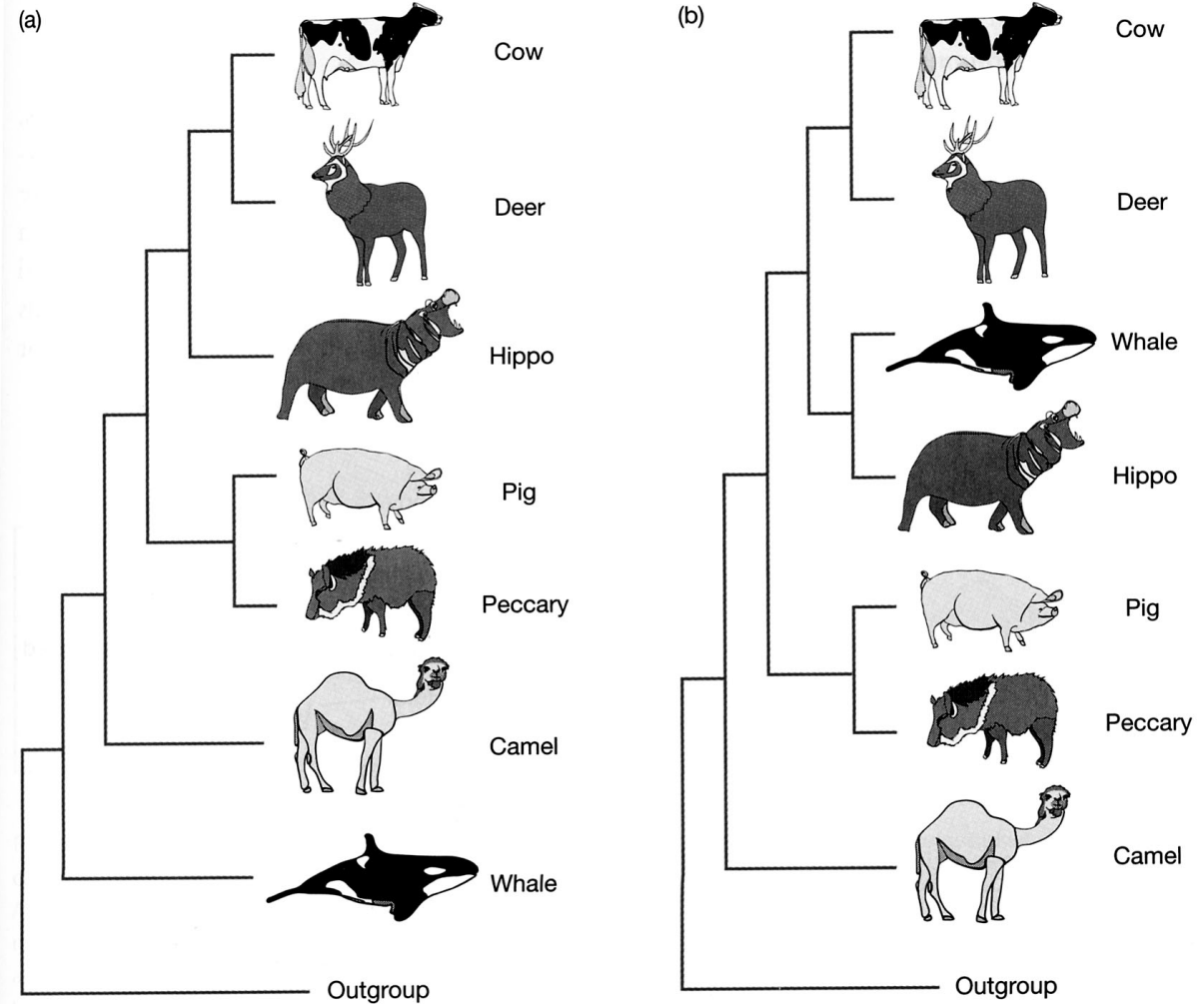


# Example: the evolutionary relationships of whales





# A phylogeny is a hypothesis



# What data might test these hypotheses?

- Morphology, including fossils
  - 55 mya fossil ankle bones, resembled fossil mammals called mesonychians
  - Morphologically resemble extant Artiodactyls
- DNA sequences
  - Suggest relationship to Hippopotami

# Advantages and limitations: morphology

- Only data available for fossils (+)
- Can reduce homoplasy through study of development (+)
  - But convergent evolution may still cause a false sense of relatedness (-)
- Very slow (-)

# Advantages and limitations: DNA

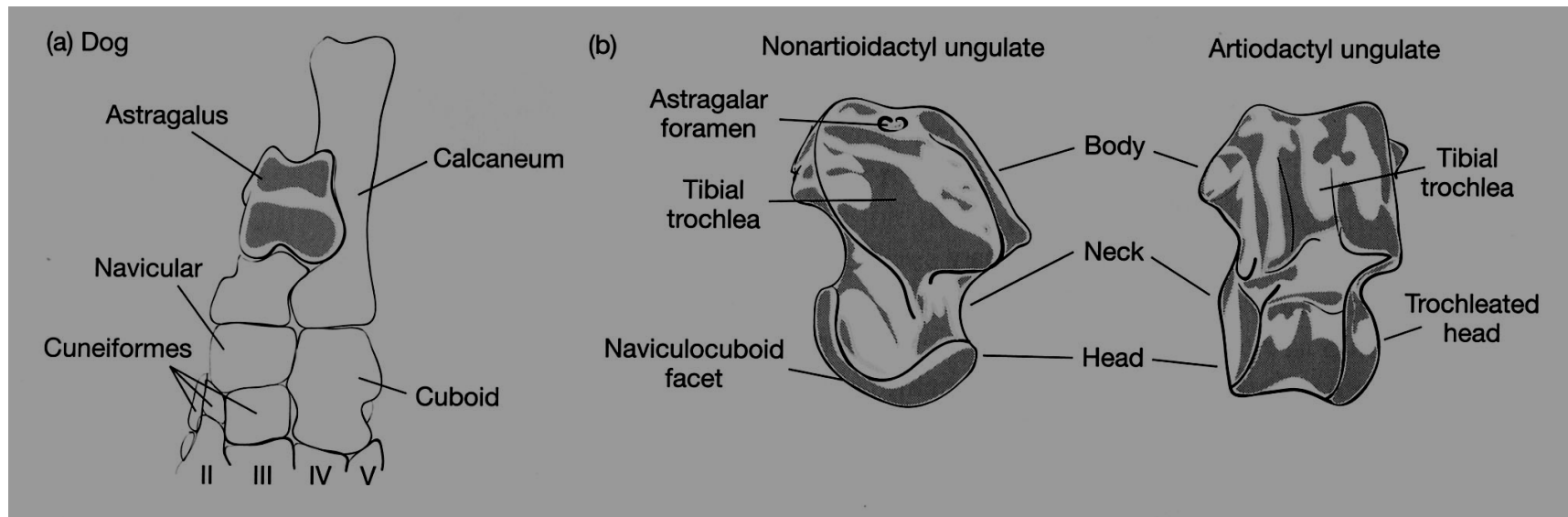
- Fairly fast and easy (+)
- Homoplasy not independently tested (-)
- Few character states (A, C, T, G)
  - Reversals more likely (-)
  - ‘saturation’ = no new changes possible (-)
- Problems and usefulness depends on how fast DNA evolves and age of taxa analyzed
  - Fast evolving good for species, populations, even ‘DNA fingerprinting’
  - Slowly evolving good for more distantly related taxa

# Often best approach combines

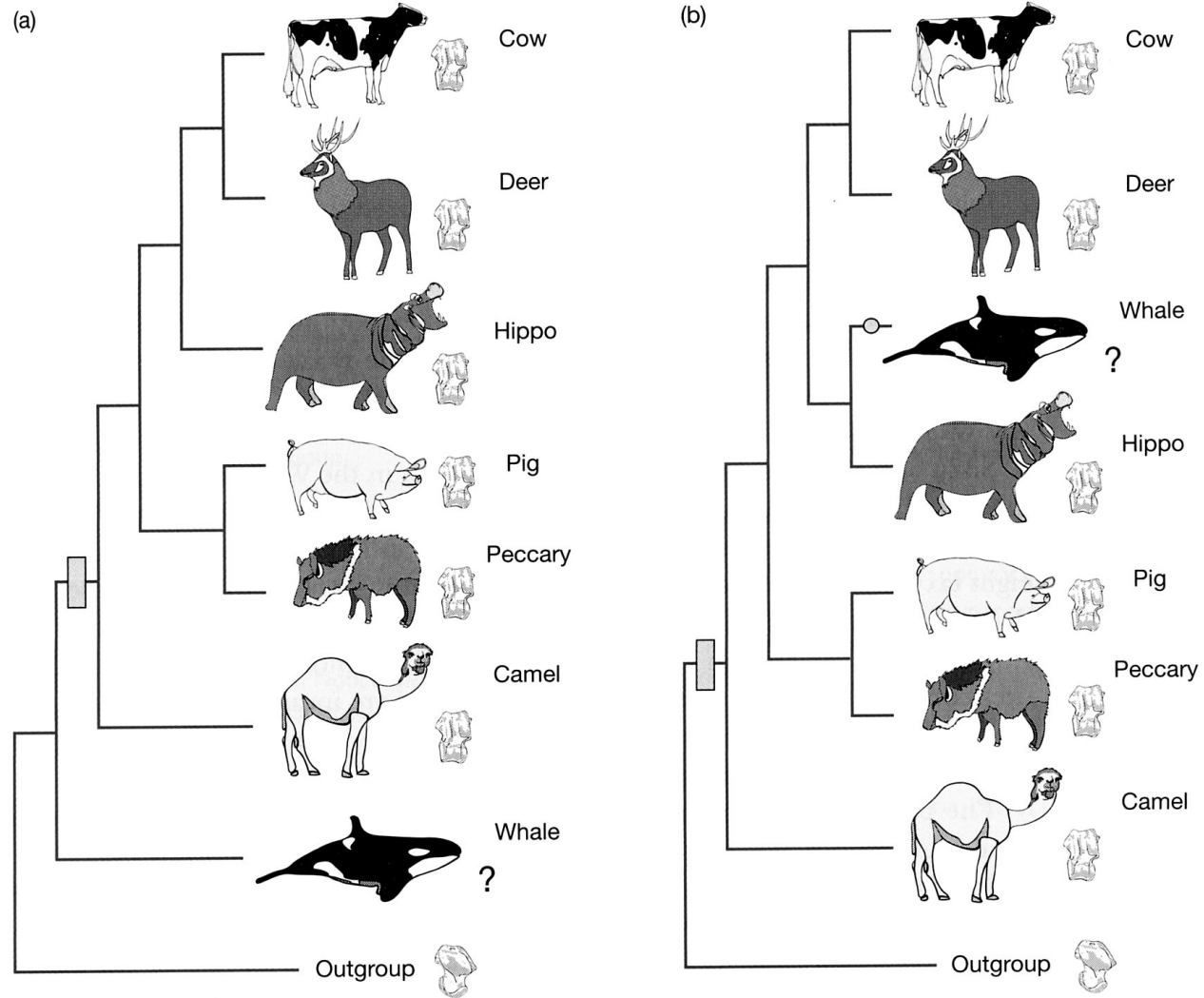
- morphology
- Uses different sections of DNA
  - Mitochondrial
  - Nuclear
  - Coding v non-coding

# Astragalus ankle-bone evidence

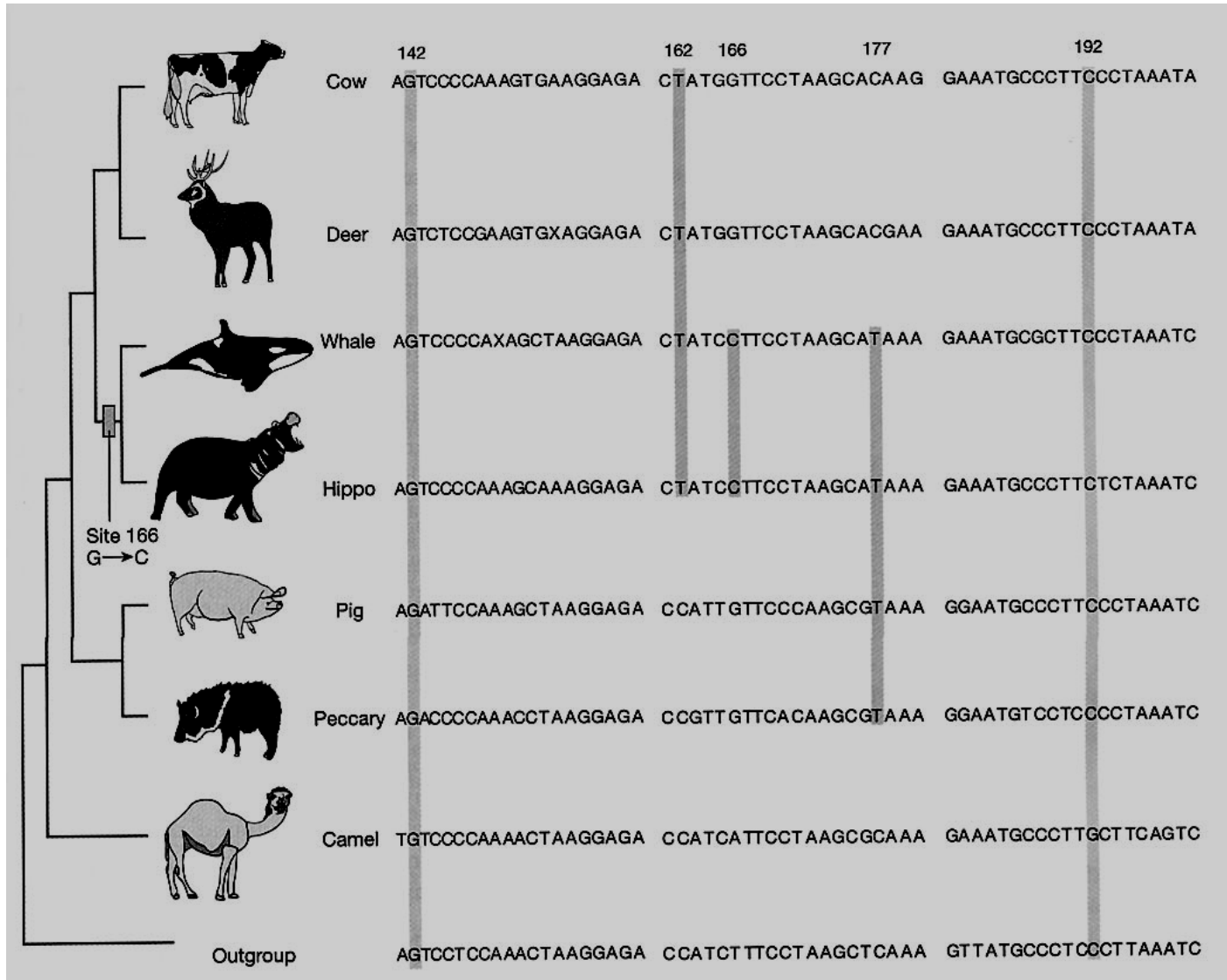
- Single morphological character
- All Artiodactyls have pulley shaped and smooth astragalus on both ends



# Whales, parsimony, and astragalus



# Parsimony with molecules





# Comparing trees and their support

- Many different trees are possible
  - For four taxa, 3 possible trees
  - For five taxa, 15 possible trees
  - Six taxa -> 105 possible
  - Seven -> 945
  - Eight -> 10,395
- Often not possible to evaluate every possible tree

# Tree evaluation

- Could be several equally most parsimonious trees
- Branches in agreement are well supported
  - Strict consensus tree
  - Majority rule consensus tree
- Resample data, called ‘bootstrapping’
  - Estimates support for branches

# Comparing different methods

- Parsimony and bootstrapping support whales + hippos scenario
- Other methods do too
  - Distance matrix methods
  - Maximum likelihood

# Overall support

- Confidence in a phylogeny increases if:
  - Diverse data sets agree
  - Different analysis methods agree
  - Statistical support strong
- A phylogeny is always a working hypothesis, subject to further testing

# What good is a phylogeny?

- Analyzing rates of change
  - Molecular clock
- Classification
- Testing hypotheses

# Molecular clock

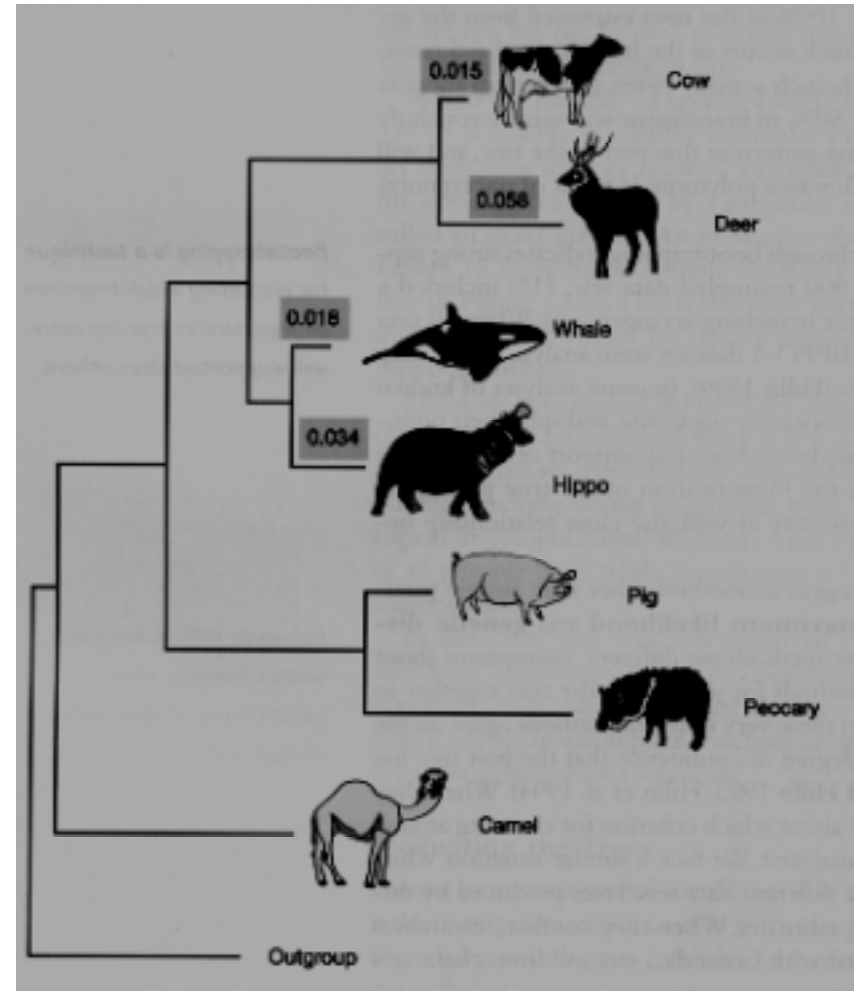
- Basic idea
  - If mutation rates are about constant
  - And if generation time is about constant
  - Then nucleotide changes should accumulate in proportion to time
- Then you could estimate date of divergence of taxa from the nucleotide data

# DNA clock calibration

- Calibrate to known divergence time
  - E.g. geological ages based on radiocarbon or other dating techniques
- Calibrate molecular clock for
  - Type of organism working with (generation time)
  - Type of DNA working with
- E.g., vertebrate mitochondrial DNA clock estimates average about 2% divergence per million years
  - Or 1% change per lineage

# Phylogenetic classification

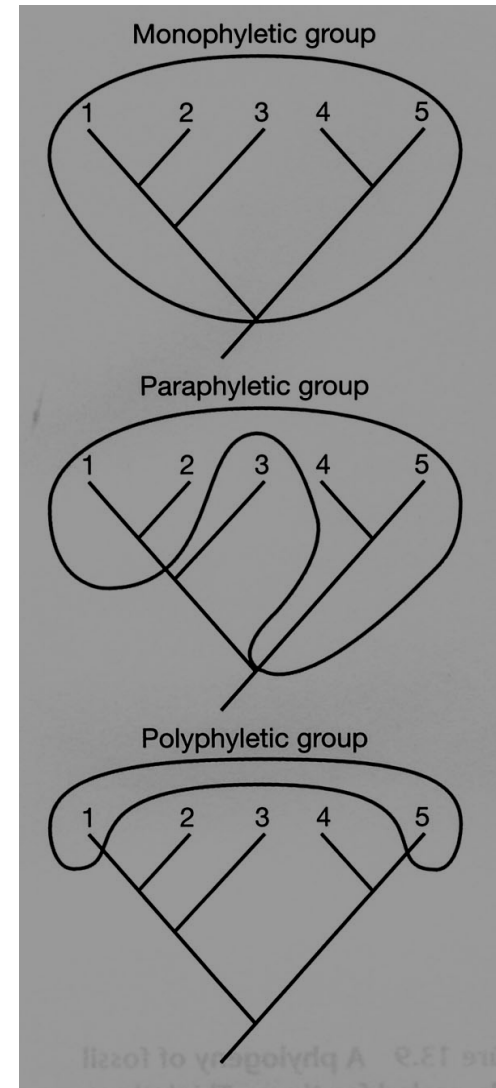
- We discussed problems with species concepts.
- But worse, what is a ‘genus’ a ‘family’ or other higher taxonomic category?
- If Artiodactyla is an Order, then why aren't whales considered Artiodactyls?





# Phylogenetic systematics

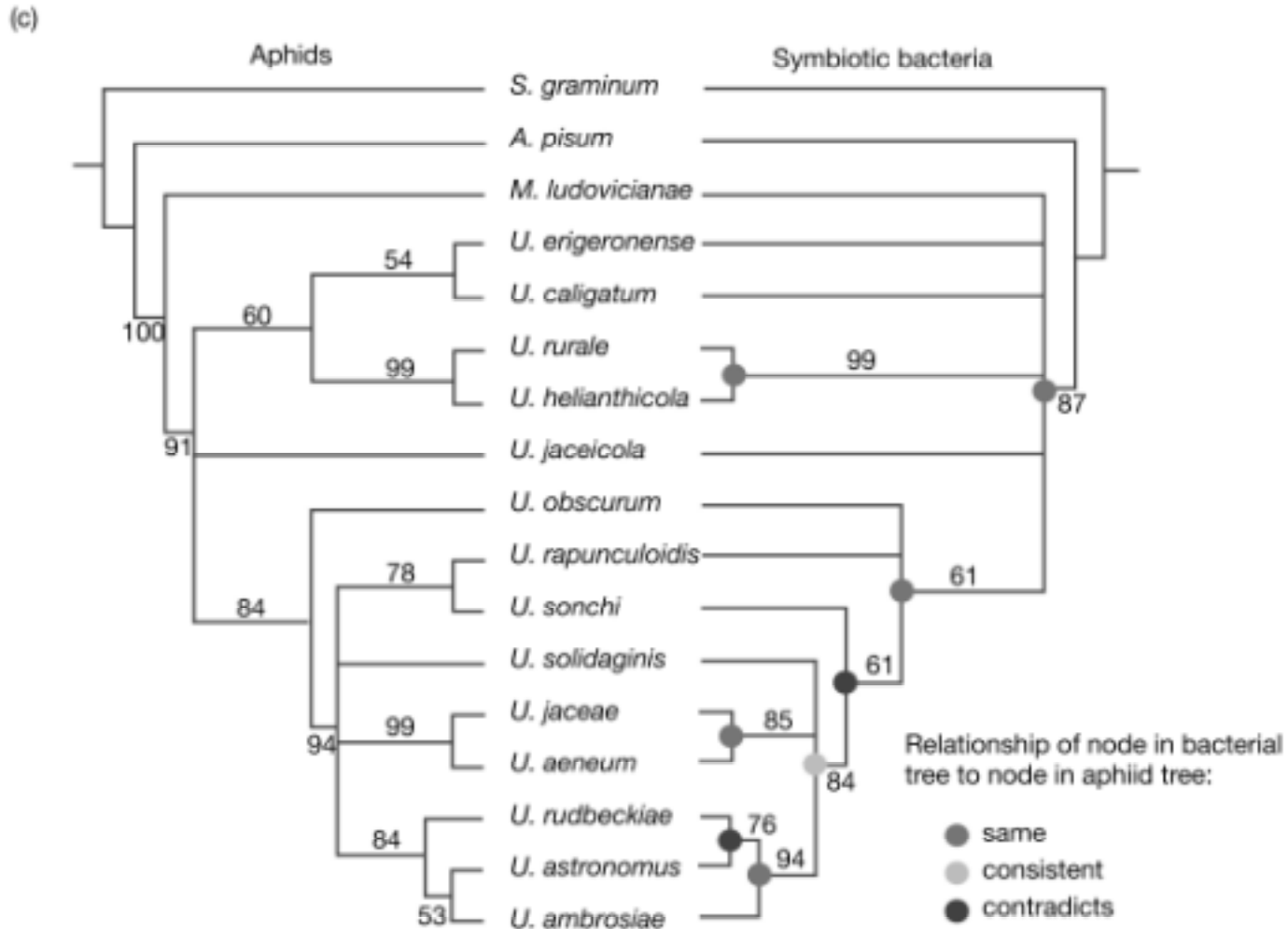
- Only monophyletic groups should be named
- Monophyletic groups contain common ancestor and all of its descendents
- Paraphyletic has common ancestor, but not all descendents
- Polyphyletic does not have recent common ancestor



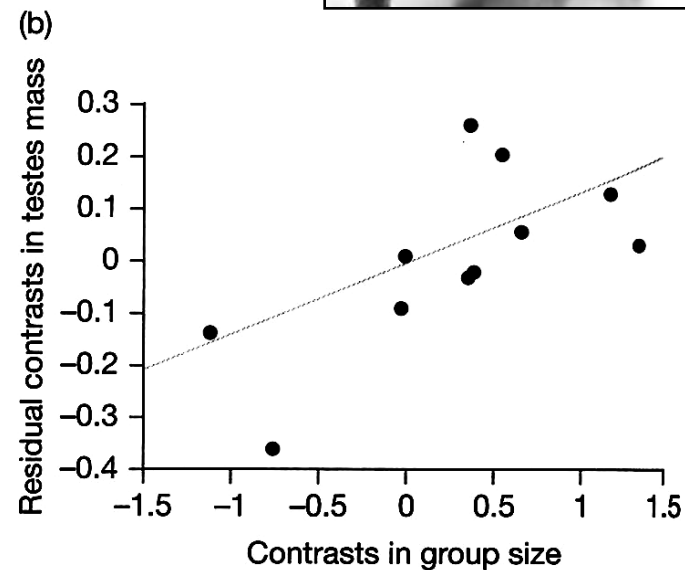
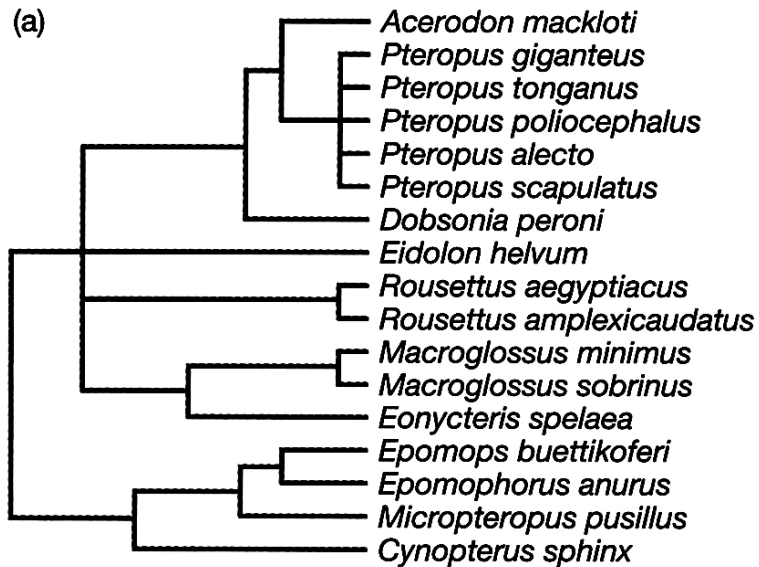
# Studying coevolution

- Coevolution = interactions between species that result in reciprocal adaptation
  - We might expect that repeated interaction over time would lead to specialization
  - Specialization might lead to co-speciation
    - When one partner speciates, the other gets dragged along

# Aphids and endosymbiont bacteria co-speciation



# Testing adaptive hypotheses



# Informing public health policy

- Major reforms in physician-patient contact initiated after demonstration that a dentist transmitted HIV to patients

