Taxonomy

- Focuses in naming and describing species and groups of species
- general tenet: classification should somehow reflect evolutionary history

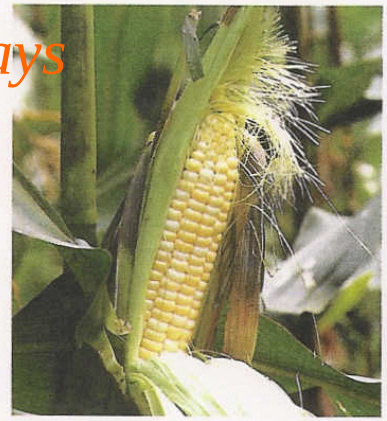
Species Names

- Binomial system: two-part name developed by Linnaeus to identify species (scientific name)

- For example red oak is named *Quercus rubra*
  - Note use of italics to write species name
  - First word on name is capitalized and corresponds to the genus
  - Latin is the standard language

corn

Zea mays

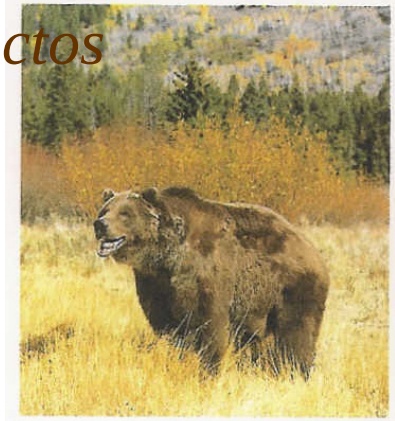


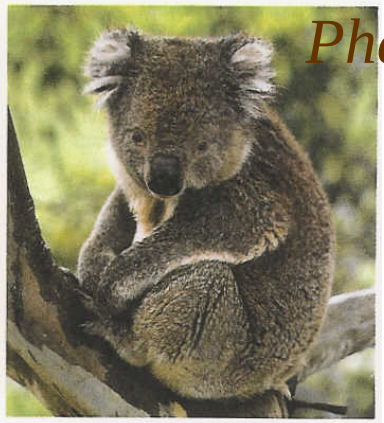
Triticum aestivum

(a)

bear

Ursus actos



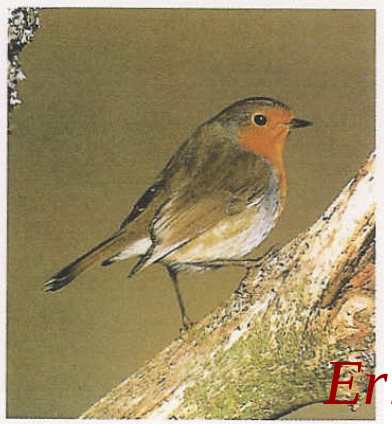


Phascolarctus cinereus

(b)

robin

Turdus migratorius

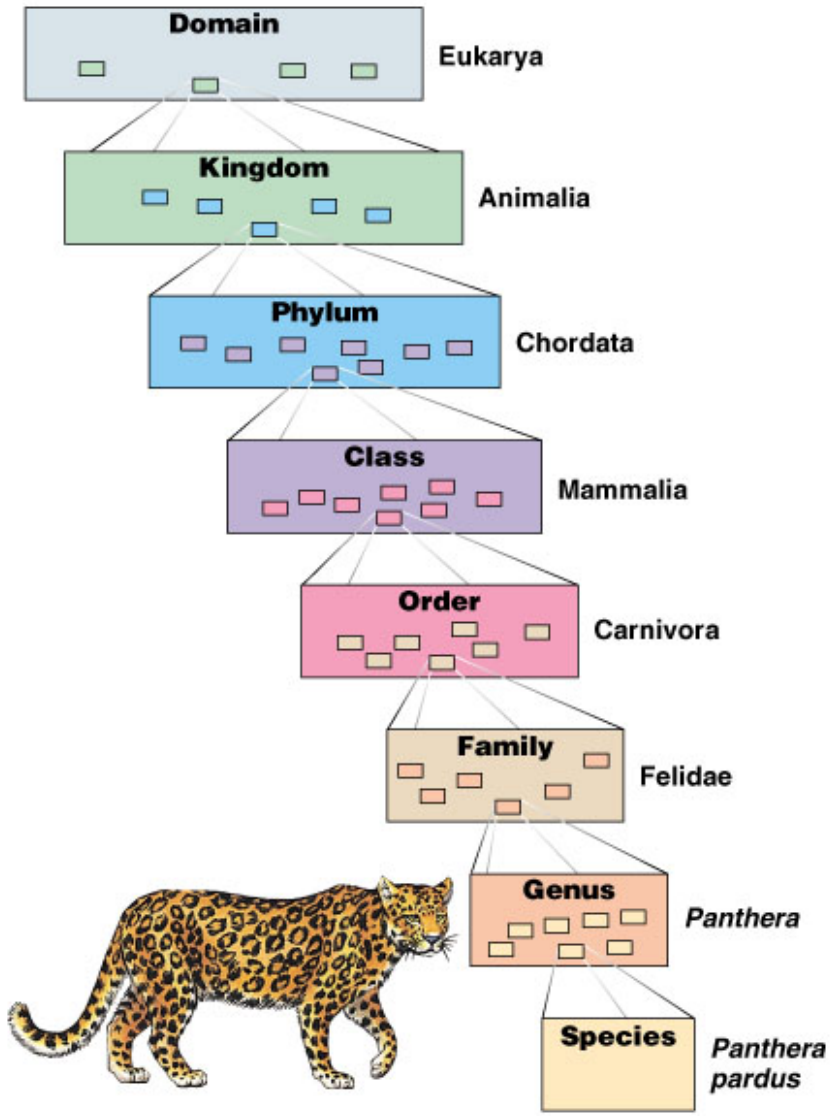


Erithacus rubecula

Hierarchical classification

- We need more than two categories to classify all living things → broader/higher
- First step of classification built in binomial name
- Keep on clustering groups based on common characteristics/properties
- Taxon (plural taxa): a group of organisms at a particular level of classification

"**K**indly **p**ay **c**ash or **f**urnish **g**ood **s**ecurity"

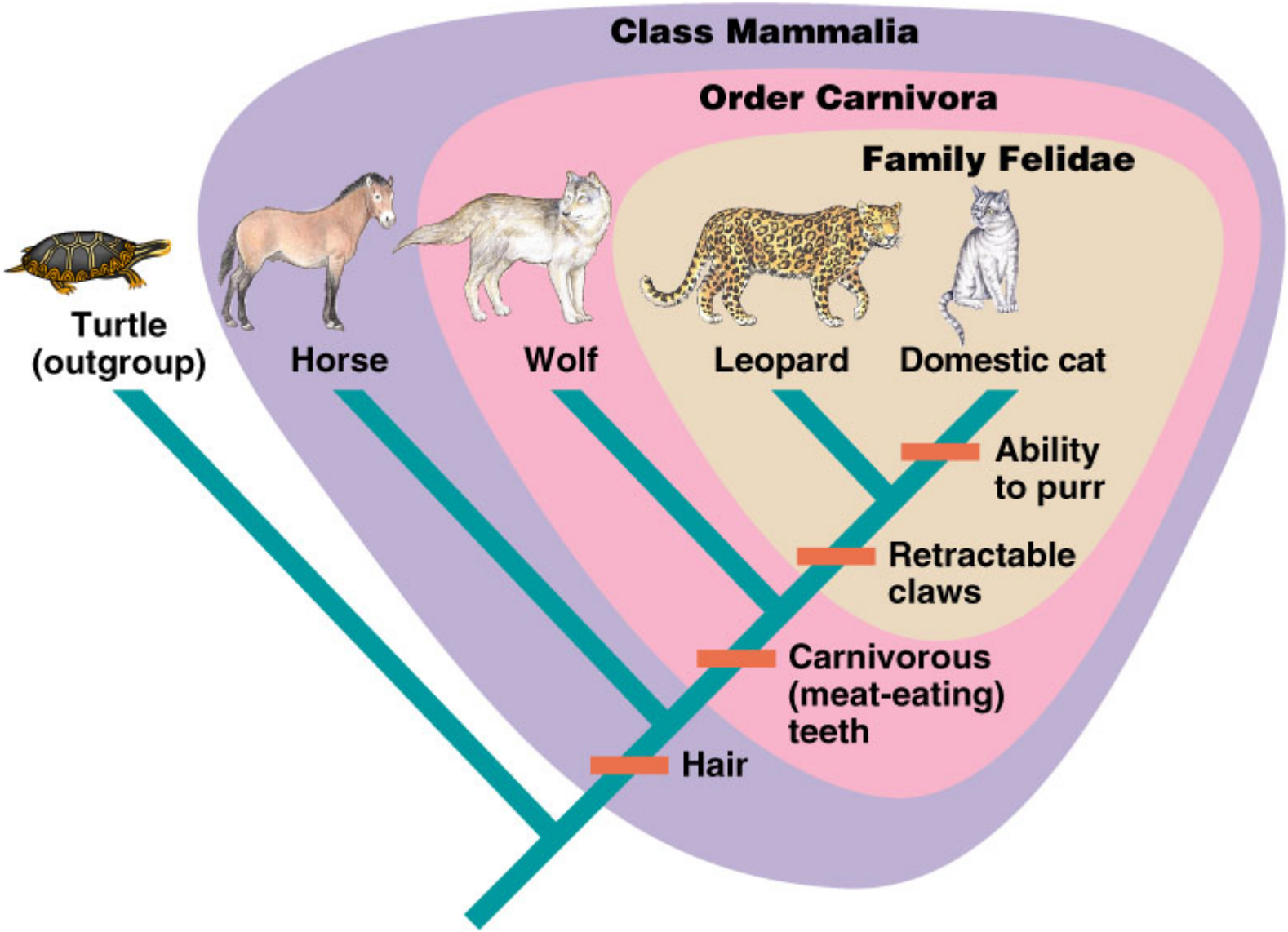


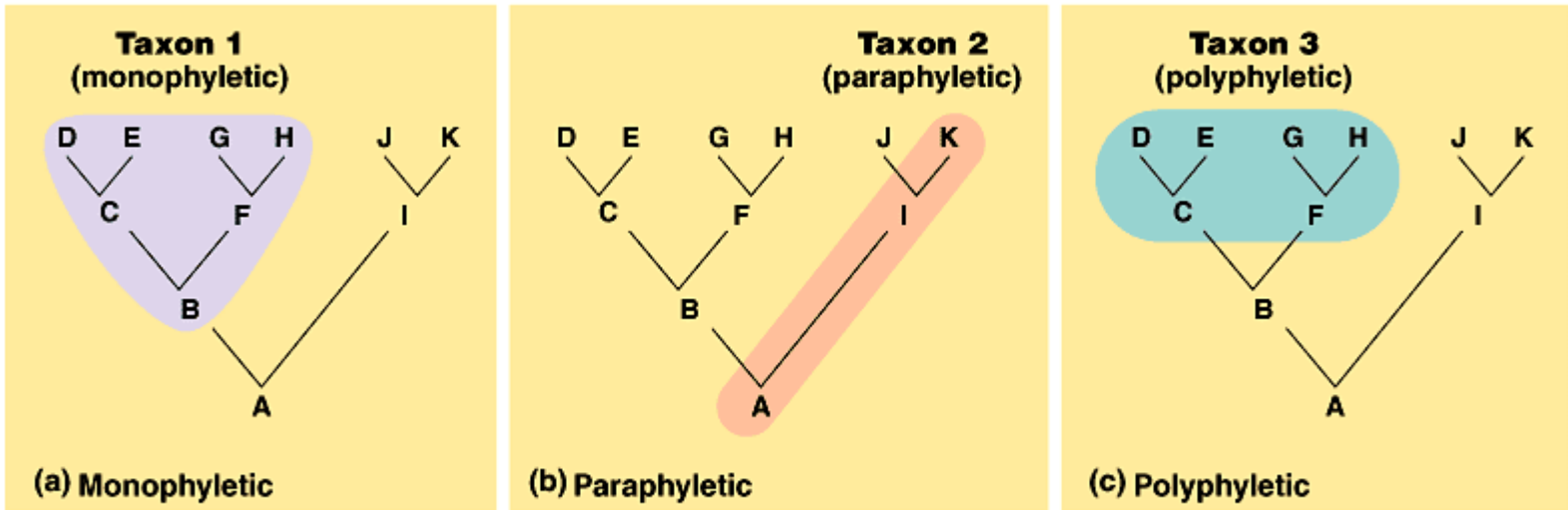
Systematics

- Defined as the study of the history of biological diversity
  - Organizes diversity according to relationships and similarities; now generally refers to the inference or estimation of phylogeny

Inferring phylogeny

- Phylogeny: evolutionary history of a species or group of related species
- Phylogenetic inference: the estimation of history through the proposition and testing of phylogenetic hypotheses
  - Cladistic approach – shared derived characters
  - Phenetic approach – similar characters





Cladistic methods: Parsimony

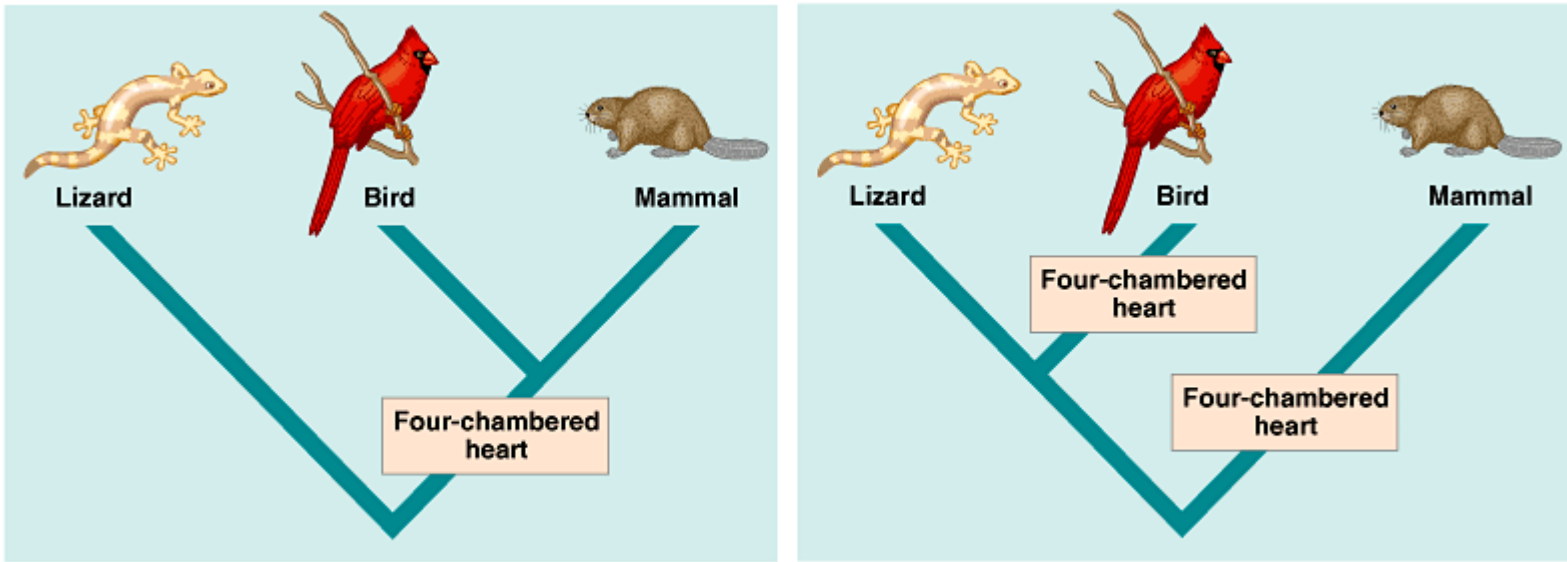
1. Assumption: characters states will be shared *more often* because of shared ancestry than because of independent changes (homoplasy)
2. Justifications:
   a. Changes are fairly rare (heredity works)
   b. Independent changes that are the same are expected to be even rarer
3. Principle (criterion) of parsimony is then used to evaluate many different **phylogenetic hypotheses** (all if possible); the hypothesis that best explains the data is the one (or one of the set) that requires the least number of changes from common ancestral sequences

Analogous characters can cause homoplasy

Ocotillo in US SW

Allauidia in Madagascar

Effect of homoplasy in phylogenetic inference



(a) Mammal–bird clade

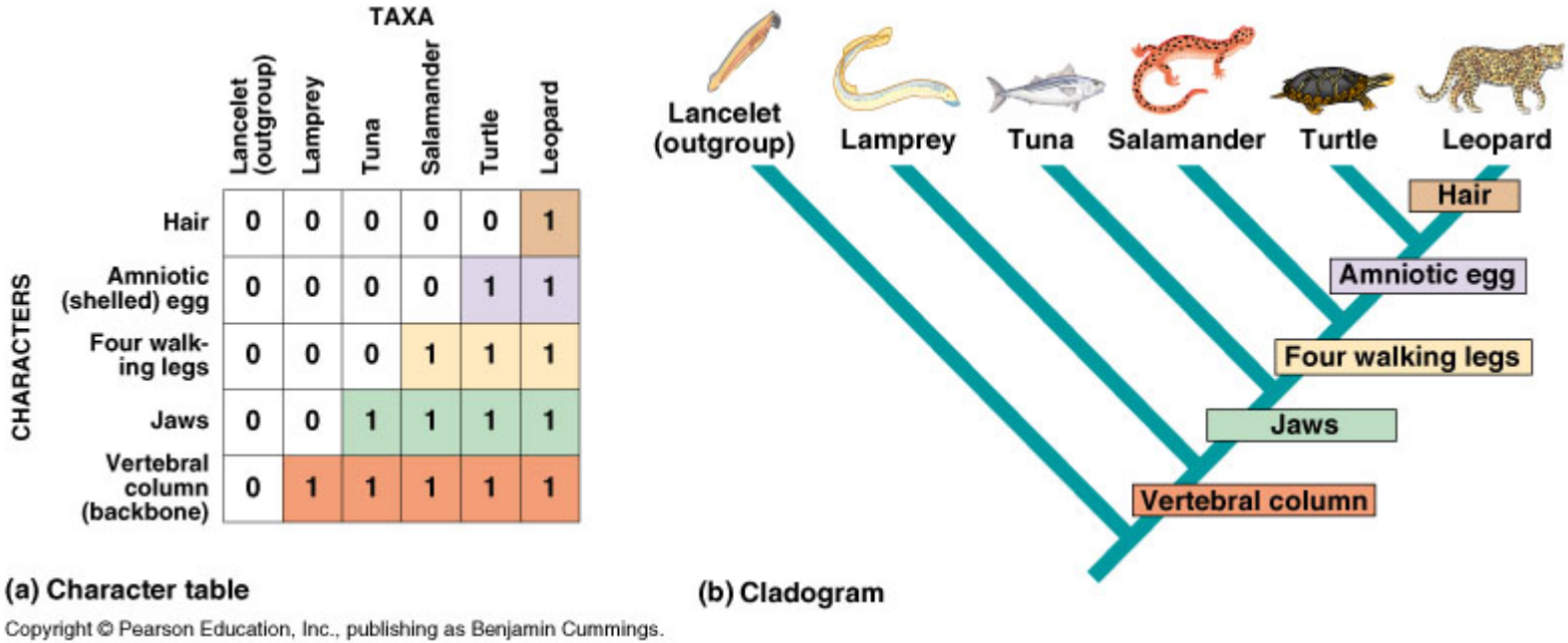
(b) Lizard–bird clade

How to avoid homoplasies: use suite of characters to increase chances of getting several homologous characters

Inferring direction of evolutionary change

- Requires at least a cladogram and an ancestral state
- OUTGROUP often helps to define primitive state (does not necessarily mean that the primitive state is the one in the outgroup or that the primitive state is the one that is possessed by most of the taxa)

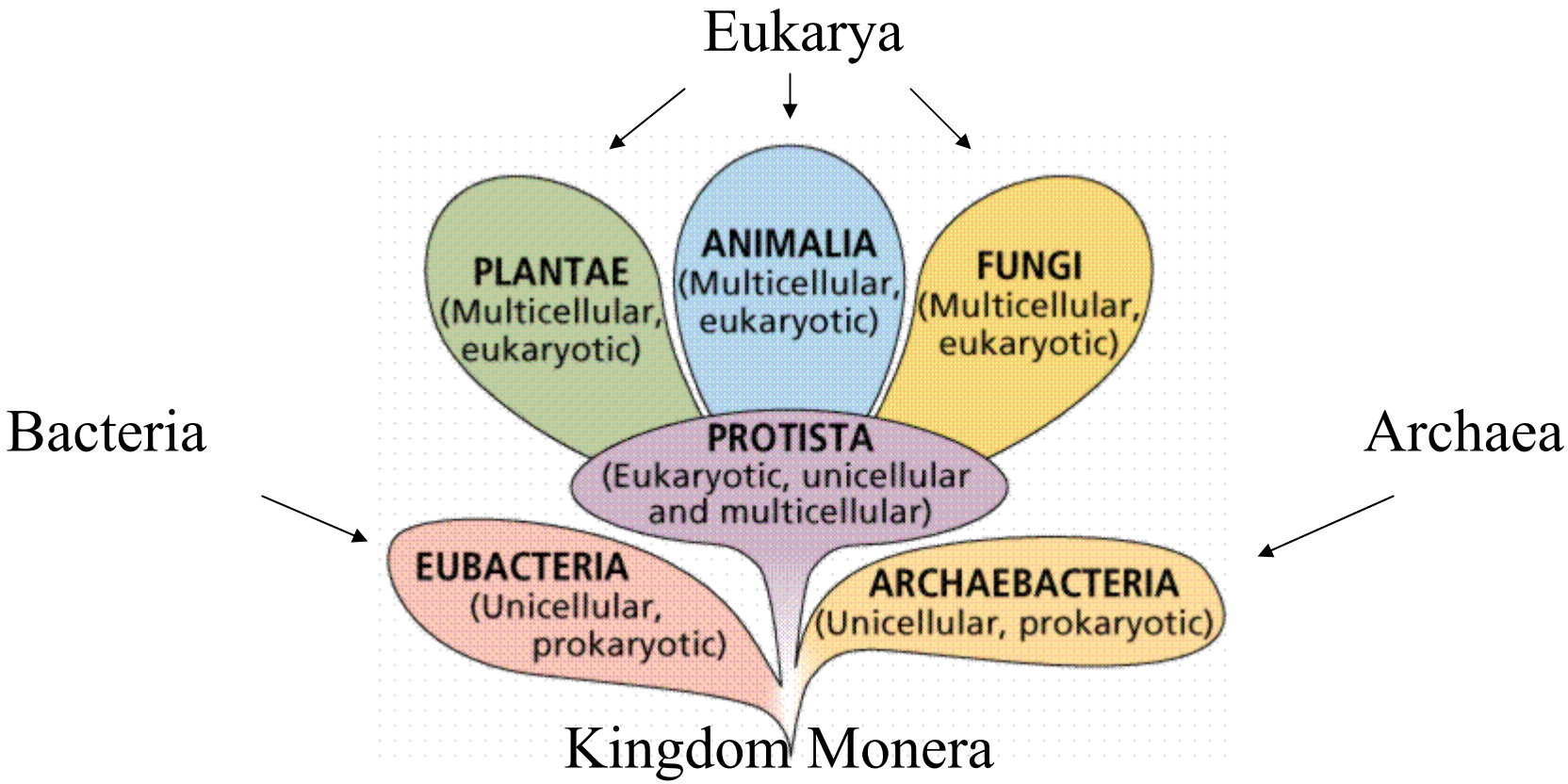
Example



(a) Character table

(b) Cladogram

Kingdoms and domains



From 5 – 30 million species in the world. All organized in this scheme

Bacteria

Archaea

Protista

Plantae

Fungi

Animalia