The diversity of life is great. To communicate about it, there must be a scheme for organization.

There are many species that would be difficult to organize without a scheme based on consistent criteria.
Classification - an organized scheme for grouping organisms - a tool for communication -

Taxonomy - the practice of naming and classifying organisms.

Linnaeus developed the classification scheme we use today.

Species have **binomial** names (*Genus species*) and are arranged in a hierarchical classification - Linnaeus saw a genus as a general kind of organism and a species as a more specific kind of organism. Linnaeus grouped organisms by their degree of similarity (as he saw it). “God creates, Linnaeus organizes”

Hierarchical - a series of successive and inclusive rankings

The major categories used in our current hierarchical classification are **Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species** - many intermediate subcategories are necessary for organizing the diversity within groups with many species.
Hierarchical System of Organism Classification

- Eastern gray squirrel
  - *Sciurus carolinensis*
Ever since Darwin the hierarchical organization of living things has been seen as a product of evolution

- **anagenesis** - change within a lineage through time
- **cladogenesis** - the origin of new lineages
- **extinction** - the termination of genetic lineages
Evolution has produced the diversity of living things today, which can be represented as a tree.

The currently used classification has 3 Domains - two prokaryotic and one eukaryotic.
Each branch on the overall tree can be further subdivided to different taxonomic levels - phyla, classes, orders, families, genera, species, or populations.
Biologists have used many approaches to estimating the evolutionary history of organisms and using that history to construct classifications.

Willi Hennig developed the techniques that form the basis for the modern methods of estimating evolutionary history and then using that history for classification. He called his method **phylogenetic systematics**.
The process of developing an estimate of the evolutionary history of a group of organisms is called **phylogenetic inference**.

The unit of data used in phylogenetic inference is the **character** or **trait**. Characters are any measurable or identifiable aspect of a group of organisms. They can be anatomical (morphological), behavioral, physiological, biochemical, molecular.

Characters may be useful for phylogenetic inference if they come in alternate **character states** - different shapes of the same bone, enzymes that differ in their amino acid sequence, genes that differ in their nucleotide sequence, etc.
Characters with multiple states can be used to construct a phylogeny

1. A T C ... C G A C
2. A T C ... C G A T
3. T T C ... C G A C
4. T A C ... C G A T
5. T A C ... C G A C
6. A T T ... C G A T

Infer phylogenetic relationship from DNA sequences

After a phylogeny has been constructed using one set of characters a different set of characters can be mapped onto the tree to develop hypotheses about the pattern and process of evolution.
Two different ways of representing the same pattern of evolutionary history
The tips of the branches represent taxa used to construct the tree.

The overall tree is a hypothesis of evolutionary relatedness of taxa used to construct the tree.

The branch points or nodes represent hypothetical common ancestors of taxa used to construct the tree.
The same pattern of evolutionary relationships can be represented by a variety of trees that can be formed rotating branches at their nodes.

Although they look different, they are equivalent presentations of relationship and they do not change the way the organisms might be classified.

Nearness of relationship equates to recency of common ancestry. In all cases, species 3 and 4 share a more recent common ancestor with each other than either does with species 2.
Closely related taxa are called “sister taxa.”

An “outgroup” is a taxon that is distantly related to the group being studied.

Outgroups allow the direction of evolution of characters to be estimated. This will be covered later.
Alternate states of a character may represent evolutionary changes. For any two states of a character one may have originated earlier in the evolutionary history of the group and one may have originated later.

Character states that originated earlier in the evolutionary history of a group can be called **primitive** or **ancestral** or **plesiomorphic**.

Character states that originated later are called **advanced** or **derived** or **apomorphic**.

Derived states of a character provide information about the degree of relatedness of two or more species. A derived state that is shared by two or more species is called a **synapomorphy**.

Synapomorphies allow species to be grouped and organized into a phylogeny.
In this example

0 = ancestral state
1 = derived state

Lungs are a synapomorphy that allow all vertebrates with four legs to be grouped together - descendants of the first lunged vertebrate.

A synapomorphy can identify a **monophyletic group** or **clade** - all the descendants of the single common ancestor.

The hypothetical common ancestor of each monophyletic group possessed the derived state of the character.
Synapomorphies are the basis for modern classifications. Organisms that share the derived state of a characteristic that evolved only once can be classified as belonging to the same group because they are all descended from the same common ancestor.

Ancestral states do not provide information about evolutionary relatedness and are usually not used for classifying organisms.
A **paraphyletic** group includes some but not all descendants of a common ancestor. The group called “fish” is paraphyletic because not all the descendants of the common ancestor of “fish” are called “fish”. The group called “tetrapods” is monophyletic.

Modern systematists create classifications using monophyletic groups.
A **polyphyletic** group is not based on evolutionary relationship. It includes organisms that are members of more than one monophyletic group and excludes some members of those groups. The group “pachyderms” is polyphyletic.

“Pachyderms” are members of more than one monophyletic group. Other relatives, like hyraxes and pigs are not pachyderms.
A tree of relationships can be presented as a rooted tree, with the direction of evolution implied from the base of the tree to the tips.

A tree of relationships can also be presented as unrooted. Some methods for estimating phylogenetic relationships start by constructing an unrooted tree and then use one or more outgroups to decide how the tree should be rooted. (covered later)

Different roots create very different estimates of relationship.
A **cladogram** shows the pattern of relationship but does not convey the amount of evolution on each branch or the amount of time that transpired along each branch.
A phylogram shows the pattern of relationship and the amount of evolution along each branch.
A chronogram gives estimates of the time when branching or other evolutionarily important events occurred.
(C) - represents another way of presenting a cladogram that is more efficient for presentation of large phylogenies.

Read: Smith and Donoghue’s test of the “generation time hypothesis.”
Important inferences are made from analysis of phylogenies.

Features of an organism almost always evolve from a pre-existing feature present in their ancestors - complex characters don’t evolve *de novo*.

Wings evolved from forelimbs at least 3 times in vertebrates (birds, bats, pterodactyls).
Homology vs Analogy vs Parallel Evolution vs Convergent Evolution

Wings and forelimbs are **homologous characters** - they arise from the same embryonic structures and their development is controlled by the same genes.

Homology is established by

• correspondence of position
• correspondence of structure
• correspondence in development
• continuity from an inferred ancestor in a phylogeny

**Analogous structures** violate one or more of the criteria for homology.
Analogous structures violate one or more of the criteria for homology.
Independent evolution of similar characteristics in homologous structures is called parallel evolution.
Independent evolution of similar characteristics in non-homologous structures is called convergent evolution.
Similar characteristics that have evolved independently, as parallel evolution or as convergent evolution, are called homoplasies.

**Homoplasies** can be misleading if they are not identified as such because they may be interpreted as synapomorphies and result in unrelated groups being interpreted as closely related.

Convergent and parallel evolution are often due to independent adaptation to similar environments.
Another kind of homoplasy is an **evolutionary reversal**. The ancestral state of a character can re-evolve.

The jawless fishes were the first to evolve bone - as protective armor over the outside of their body. Ancestors of fishes, like cephalochordates, lacked bone.

Modern descendants of the early jawless fishes have bodies lacking bone entirely.
Read -- The Evolutionary Origins of Snake Venom

Read -- Deep Homology: Lipid Droplets
Vestigial Traits - traits that have no known current function in modern species but appear to have had an function in ancestors of modern species.

Examples:

The appendix of humans and close relatives is a remnant of a former digestive pouch called the caecum. The caecum is still an important digestive organ in mammals that have large amounts of vegetable matter in their diet.

The nictitating membrane (inner eyelid) of birds and reptiles serves to protect the eye and moderate light levels. Mammals have a rudimentary inner eyelid called the plica semilunaris with little or no function.
Rudimentary hindlimbs in snakes

Mosasauroidea
- Forelimbs, hind limbs, regionalized axial skeleton

Pachyrhachis
- Complete hind limbs only

Scolecopilids
- Pelvic rudiments only

Loss of forelimbs

Booidea
- Hind limb rudiments only

Alethinophidians

Loss of hind limbs

Colubroidea
- Limbless

Loss of vestigial hind limbs

(Extinct)
Rudimentary limb skeleton in cetaceans

Figure 14.16. Evolution of whales from land creatures, showing the numerous transitional fossils now documented from the Eocene beds of Africa and Pakistan. (Drawing by Carl Buell)