

- To trace ***phylogeny*** or the evolutionary history of life, biologists use evidence from areas such as paleontology, molecular data, and comparative anatomy.
 - Tracing phylogeny is one of the main goals of ***systematics***, *the study of biological diversity in an evolutionary context*.
 - Systematists have studied morphological and biochemical similarities among organisms as a basis for determining evolutionary relationships.
 - Recently, molecular systematics, comparisons of DNA, RNA, and other molecules has been utilized to infer evolutionary relationships between individual genes and even between entire genomes.
 - Systematics includes ***taxonomy***, which is *the naming and classification of species and groups of species*.
 - Taxonomy uses a hierarchical system of classification.
- The Linnean system, first formally proposed by Carlos Linneaus in the 18th century, has two main characteristics.
 - Each species has a two-part name (binomial).
 - Species are organized hierarchically into broader and broader groups of organisms.
- Under the binomial system, each species is assigned a two-part latinized name, a **binomial**.
 - The first part, the **genus**, is the closest group to which a species belongs.
 - The second part, the ***specific epithet***, refers to one species within each genus.
 - The first letter of the genus is capitalized and both names are italicized and latinized.
 - For example, Linnaeus assigned to humans the scientific name *Homo sapiens*, which means “wise man,” perhaps in a show of optimism.
- A **hierachical classification** will group species into broader taxonomic categories.
- Species that appear to be closely related are grouped into the same genus.
 - For example, the leopard, *Panthera pardus*, belongs to a genus that includes the African lion (*Panthera leo*) and the tiger (*Panthera tigris*).
 - Biology’s taxonomic scheme formalizes our tendency to group related objects.

- Each taxonomic level is more comprehensive than the previous one.
 - As an example, all species of cats are mammals, but not all mammals are cats.
- The named taxonomic unit at any level is called a **taxon**.
 - Example: *Pinus* is a taxon at the genus level, the generic name for various species of pine trees.
 - Mammalia, a taxon at the class level, includes all the many orders of mammals.
- Phylogenetic trees reflect the hierarchical classification of taxonomic groups nested within more inclusive (more broad) groups.

Modern phylogenetic systematics is based on cladistic analysis

- A phylogeny is determined by a variety of evidence including fossils, molecular data, anatomy, and other features.
- Most scientists use cladistic analysis to analyze the data.
- A phylogenetic diagram or **cladogram** is constructed from a series of dichotomies.
- These dichotomous branching diagrams can include more taxa.
- The sequence of branching symbolizes historical chronology.
 - The last ancestor common to both the cat and dog families lived longer ago than the last common ancestor shared by leopards and domestic cats.
- Each branch or **clade** can be nested within larger clades.
- A clade consists of an ancestral species and all its descendants. This is called a monophyletic group.
- Groups that do not fit this definition are unacceptable in cladistics.
 - Monophyletic (meaning single tribe) signifies that the group consists of the ancestor species and all its descendants – there are no species in any other taxon
 - Paraphyletic – members do not include all of the ancestor's descendants
 - Polyphyletic – members of group descended from 2 or more ancestral forms not common to all

- The Fossil Record
 - Help establish relationships between living organisms
 - Reveal ancestral characteristics that may have been lost over time in certain lineages
 - Limited, however, because it is not complete – only a fraction of existing fossils have been discovered
 - Consequently, biased in favor of species that existed a long time ago, were abundant and widespread, and had hard shells, skeletons, or other hard parts that facilitated their fossilization
- Morphological homologies

Similarities due to shared ancestry are called homologies

Example: number and arrangement of bones in the forelimbs of mammals – a **morphological** homology
- Molecular homologies
 - Comparison of amino acid sequences in proteins
 - Comparison of DNA or RNA sequences
 - Nuclear/mitochondrial DNA (change rapidly)
 - Ribosomal RNA (change slowly)

Homology vs. Analogy

- Determining which similarities between species are relevant to grouping the species in a clade is a challenge.
- It is especially important to distinguish similarities that are based on shared ancestry or **homology** from those that are based on **convergent evolution** or **analogy**.
 - Analogous adaptations can be described as similarities between two species that are due to convergent evolution – **independent development of similar traits between unrelated species as a result of adaptations to similar environments** instead of descent from a common ancestor.
 - These two desert plants are not closely related but owe their resemblance to analogous adaptations.
- As a general rule, the more homologous parts that two species share, the more closely related they are.
 - Adaptation can obscure homology and convergence can create misleading analogies.
- Also, the more complex two structures are, the less likely that they evolved independently.
 - For example, the skulls of a human and chimpanzee are composed not of a single bone, but a fusion of multiple bones that match almost perfectly.
 - It is highly improbable that such complex structures matching in so many details could have separate origins.