Phylogenetics

**Phylogeny**

The evolutionary history of a species or group of related species

Outline

- Key concepts
- Binomial
- Classification categories
- Three domains and six kingdoms
- Understanding Phylogenies
- Examples of Using Phylogenetics
- Key Terms
- Conclusions

Key Concepts:

- **Phylogeny**
  - The evolutionary history of a species or group of related species
- **Systematics**: Field of biology that deals with the diversity of life. Systematics is usually divided into the two areas of Phylogenetics and Taxonomy.
- **Taxonomy**: The science of describing, naming, and classifying organisms
- **Classification**: The arrangement of organisms by their physical similarities, which reflect historical and evolutionary relationships
Key Concepts:
- **Phylogenetics** – Field of biology that deals with the relationships between organisms. It includes the discovery of these relationships, and the study of the causes behind this pattern.

Binomial
- Millions of kinds of organisms exist
- In 18th Carolus Linneaus developed modern *binomial nomenclature*
  - Each species has *two unique names* – hence \*binomial\*
  - *Genus*
  - *Specific epithet*
  - Each is italicized or underlined
  - *Genus* name is capitalized; *species* name is not
Texas Bluebonnet
*Lupinus texensis* / *Lupinus texensis*

The Linnean system, first formally proposed by Linnaeus in *Systema naturae* in the 18th century, has two main characteristics.

- Each species has a two-part name.
- Species are organized hierarchically into broader and broader groups of organisms.

**Taxonomy employs a hierarchical system of classification**

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**Taxonomic Levels**

- **Domain**
- **Kingdom**
- **Phylum**
- **Class**
- **Order**
- **Family**
- **Genus**
- **Species**

Here, domestic cat

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**Classification Schemes Reflect Scientific Knowledge and Technology**

1. **Prior to 1970**: two-kingdom system
   - Plants and animals

2. **1969**: Roger Whittaker-five-kingdom system
   - Monera, Protista, Fungi, Plantae, Animalia

3. **Recent proposal**: Carl Woese-three-domain system
   - Bacteria, Archaea, Eukarya

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**How Many Kingdoms?**

- **Whittaker’s Five-Kingdom Scheme**
  - Monera
  - Protista
  - Fungi
  - Plantae
  - Animalia
3 Domains

- The classification Domain is above kingdoms.
  - Archaea
  - Bacteria
  - Eukarya
- 6 kingdoms are still maintained by most biologists:
  - Archaeabacteria
  - Eubacteria
  - Protista
  - Fungi
  - Plantae
  - Animalia

Representatives of Life’s Diversity

- Archaeabacteria
- Eubacteria
- Protista

Representatives of Life’s Diversity

- Fungi
- Plantae
Understanding a phylogeny is a lot like reading a family tree. The root of the tree represents the ancestral lineage, and the tips of the branches represent the descendents of that ancestor. As you move from the root to the tips, you are moving forward in time.
Understanding Phylogenies

- When a lineage splits (speciation), it is represented as branching on a phylogeny. When a speciation event occurs, a single ancestral lineage gives rise to two or more daughter lineages.

Understanding Phylogenies

- Phylogenies trace patterns of shared ancestry between lineages. Each lineage has a part of its history that is unique to it alone and parts that are shared with other lineages.

Understanding Phylogenies

- Similarly, each lineage has ancestors that are unique to that lineage and ancestors that are shared with other lineages—common ancestors.
A clade is a grouping that includes a common ancestor and all the descendants (living and extinct) of that ancestor. Using a phylogeny, it is easy to tell if a group of lineages forms a clade. Imagine clipping a single branch off the phylogeny—all of the organisms on that pruned branch make up a clade.

Clades are nested within one another—they form a nested hierarchy. A clade may include many thousands of species or just a few. Some examples of clades at different levels are marked on the phylogenies below. Notice how clades are nested within larger clades.

So far, we’ve said that the tips of a phylogeny represent descendant lineages. Depending on how many branches of the tree you are including however, the descendants at the tips might be different populations of a species, different species, or different clades, each composed of many species.

Several times in the past, biologists have committed themselves to the erroneous idea that life can be organized on a ladder of lower to higher organisms. This idea lies at the heart of Aristotle’s Great Chain of Being (see right).

Similarly, it’s easy to misinterpret phylogenies as implying that some organisms are more “advanced” than others; however, phylogenies don’t imply this at all. Phylogenies trace patterns of shared ancestry between lineages. Each lineage has a part of its history that is unique to it alone and parts that are shared with other lineages.
**Trees, Not Ladders**

* Phylogenies trace patterns of shared ancestry between lineages. Each lineage has a part of its history that is in this highly simplified phylogeny, a speciation event occurred resulting in two lineages. One led to the mosses of today; the other led to the fern, pine, and rose. Since that speciation event, both lineages have had an equal amount of time to evolve. So, although mosses branched off early on the tree of life and share many features with the ancestor of all land plants, living moss species are not ancestral to other land plants. Nor are they more primitive. Mosses are the cousins of other land plants, unique to it alone and parts that are shared with other lineages.

![Phylogenetic Tree](image)

**Understanding Phylogenies**

* So when reading a phylogeny, it is important to keep three things in mind:
  1. Evolution produces a pattern of relationships that is tree-like, not ladder-like.
  2. Just because we tend to read phylogenies from left to right, there is no correlation with level of advancement.
  3. For any speciation event on a phylogeny, the choice of which lineage goes to the right and which goes to the left is arbitrary. The following phylogenies are equivalent: 

![Phylogenetic Equivalences](image)
Examples of Using Phylogenetics

- Human
- Chimpanzee
- Gorilla
- Orangutan
- Gibbon
- Spider monkey

Substitutions occur along each branch in the tree, so closest relatives share similarities.

State of Louisiana vs. Richard P. Schmidt

The trial: Phylogenetic analysis used to convict Schmidt of attempted murder.
Schmidt was convicted of attempted murder; currently serving term of 50 years of hard labor

- First use of phylogenetic analysis in U.S. criminal case
- Phylogenetics can be used to trace infections of human pathogens among individuals

**Phylogenetic analysis**

- Forensic analysis of crimes
- Epidemiology of HIV (and other viral diseases)
- Origins of emerging diseases
- Global diversity, vaccine development
- Predicting the future course of viral epidemics (selecting strains for vaccines)

Vaccine development

Phylogenetic prediction of the future of influenza:

Which current strains will lead to the epidemics of tomorrow?

*Bush et al., 1999 (Science 286:1921–1925)*
Many other applications...

- Health applications: rapid identification of pathogens
- Rapid discovery of new species
- Rapid identification of poisonous vs. edible species
- Many applications in basic research

Key Terms

- Binomial
- Clade
- Class
- Classification
- Domain
- Family
- Order
- Phylogenetic tree
- Phylogeny
- Phylum
- Systematics
- Taxon
- Taxonomy

In Conclusion

- A major goal of evolutionary biology is to reconstruct the history of life on earth.
- Phylogeny is the evolutionary history of a group of organisms.
- To reconstruct phylogeny, scientists use an analytical approach to understanding the diversity and relationships of living and extinct organisms.
In Conclusion

- Evidence used to reconstruct phylogenies can be obtained from the fossil record and from morphological and biochemical similarities between organisms.
- In recent decades, systematists have gained a powerful new tool in molecular systematics, which uses comparisons of nucleotide sequences in DNA and RNA to help identify evolutionary relationships between individual genes or even entire genomes.