Chapter 26

26.1 Investigating the tree of life

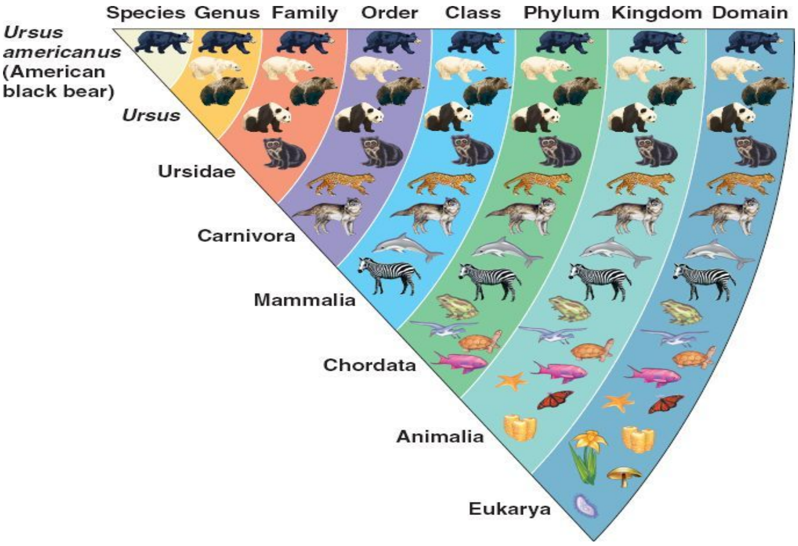
Organisms have shared many characteristics due to our common ancestry. The way that it is used to organized and understand the information about the biological world is called taxonomy. Taxonomy is used to identify names and species, and placing it into hierarchical classifications by their morphological (phenotype) relatedness to each other.

Binomial

Binomial is a two part form of a scientific name, this is a way that biologist communicate their research. The first part of the binomial is the genus which is the specifics they belong to and the second part is the specific epithet which is unique for each species that are within the genus.

Hierarchical Classification

Linnaean Classification is the name of the taxonomic system. The units at any level of the hierarchy is called a taxon. Classifying species is the way we structure our human view of the world. The characteristics used to classify used differs from group to group.



Linking Classification and Phylogeny

- The phylogenetic tree is a branched diagram which represents a hypothesized evolutionary history and relationships of the group. Sometimes taxonomists have classified species within a genus that are not mostly related. MIsclassification is due to the lost of key features shared by close relatives. Also issue with linnaean system is that they group mammals, reptiles, bird and vertebrates together but they don't tell us about the evolutionary relationship with each other.
- This is why it has led to a new method of classifying system called PhyloCode. PhyloCode is a system where spiece are classified by their evolutionary relationship. This includes the common ancestor and all the descendents.
- This system only changes the way taxa are defined and recognized but not the taxonomic names. There would not be ranks or classes with this system an some

commonly recognized groups would be part of other groups that was prvoused in the same ranking.
    - (Ex. birds -Aves- which was a subgroup of reptiles but now would be its own group).
- The general patterns of the branching (phylogenetic tree) is the tree topology, this is the shows the relationship as a dichotomies or a two way branch points. Which represents the divergence lineage.
    - Sister taxa are groups of organism that share immediate common ancestor(close relatives). The phenotypic trees are rooted meaning that branch points represent that most recent ancestor.
- Basal taxon refers to the lineage that averages early in the history group.
- Polygamy is a branch point from which more than two descendent groups emerge

26.2 Phylogenies are inferred from morphological and molecular data

Morphological and molecular Homologies

Homologies is a phenotypic and genetic similarities due to shared ancestry.

Sorting homology from Analogy

Analogy is the phylogenetic similarities do to convergent evolution. (happens to environmental pressure and natural selection). Distinguishing between the homology and analogy is critical in reconstructing phylogenies.

Homoplasies is the analogous structures that arose independent.

Evaluating molecular Homologies

- Aligning comparable sequences from the species being in studied which is hard to find.
- Species that are similar differ in a few sequences
- 2 sequences that resembles each other at many points along their length are most likely homologous
- Molecular Homoplasies: organisms that do not appear to be closely related but their sequence base is similar.
- Molecular systematics: the use of data form the DNA and other molecules to determine evolutionary relationships

26.3 Shared character are used to construct phylogenetic trees

First differentiation homologous features and analogous ones. Second choose a method of inferring phylogeny from homologous characters, this would be through cladistics

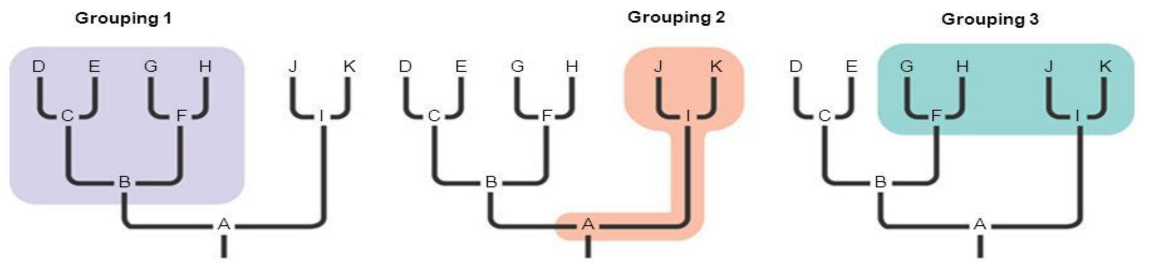
Cladistics

Common ancestry is the primary criterion used to classify organism

- Clades: groups of species that include the ancestral species and its descendant

Taxon is equivalent to a clade only if it is monophyletic

- **Monophyletic:** consist of ancestral species and all of its descendants
- **Paraphyletic:** consist of an ancestiacm specie and some decedent
- **Polyphyletic:** includes taxa with different ancestors



(a) Monophyletic. In this tree, grouping 1, consisting of the seven species B–H, is a monophyletic group, or clade. A monophyletic group is made up of an ancestral species (species B in this case) and *all* of its descendant species. Only monophyletic groups qualify as legitimate taxa derived from cladistics.

(b) Paraphyletic. Grouping 2 does not meet the cladistic criterion: It is paraphyletic, which means that it consists of an ancestor (A in this case) and *some*, but not all, of that ancestor's descendants. (Grouping 2 includes the descendants I, J, and K, but excludes B–H, which also descended from A.)

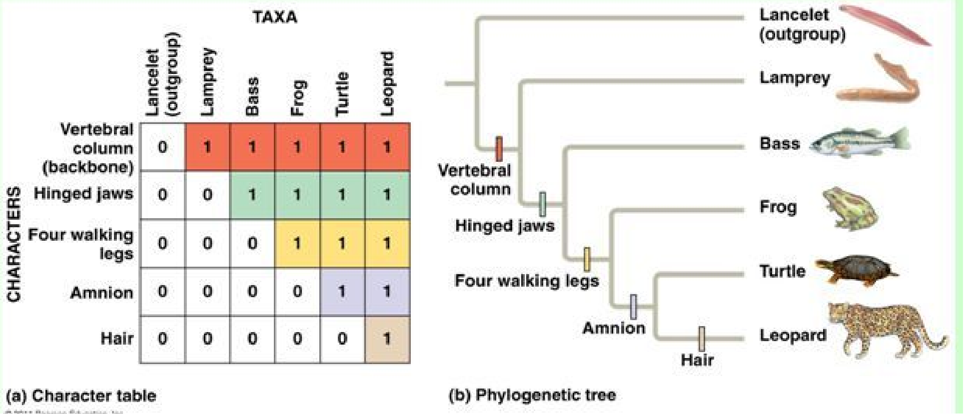
(c) Polyphyletic. Grouping 3 also fails the cladistic test. It is polyphyletic, which means that it lacks the common ancestor of (A) the species in the group. Furthermore, a valid taxon that includes the extant species G, H, J, and K would necessarily also contain D and E, which are also descended from A.

Shared ancestral and shared derived characters:

- **Shared ancestral character:** a character that originated in an ancestor of the taxon
- **Shared derived character:** an evolutionary novelty unique to a clade
- Need the context of the history of the species to identify whether it is an ancestral or derived

Inferring phylogenies using derived characters:

- **Outgroup:** is a species or group of species from an evolutionary lineage that is known to have diverged
- **Ingroup:** before the lineage that includes the species that are being studied



CHARACTERS	Lancelet (outgroup)	Lamprey	Bass	Frog	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amnion	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

(b) Phylogenetic tree

Maximum parsimony and maximum likelihood :

- **Maximum parsimony:** the principle of shaving off the unnecessary characteristics/explanations
- **Maximum likelihood:** identifies the tree most likely to have produced a given set of DNA data.

Interpreting Phylogenetic trees

The phylogenetic trees are used to show pattern of descent, not similarity

There are 2 main trees

- Cladogram - depicts branch order

- Phylogram- shows evolutionary relationship; branch length depends to evolutionary change

A taxons are not on a phylogenetic tree
Phylograms branch lengths depends on a genetic difference and to evolutionary time

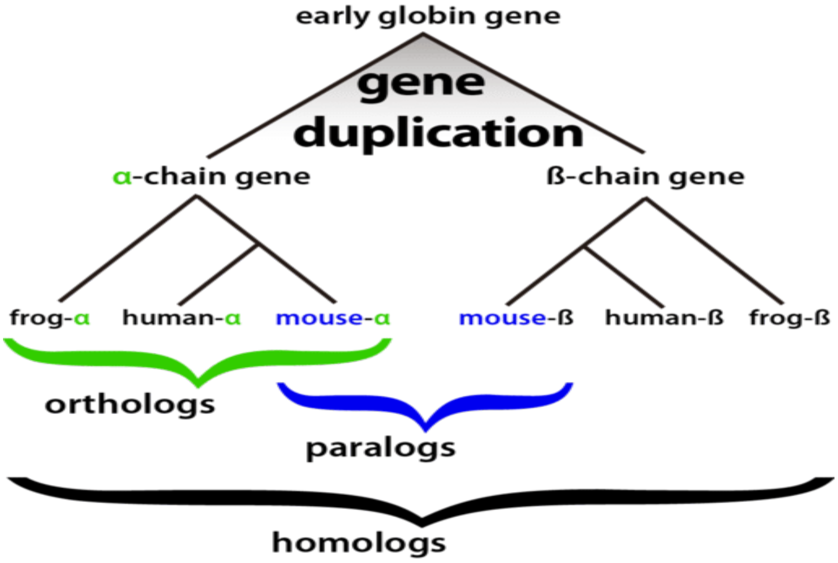
26.4 Evolution history is in its genome

Comparison of DNA sequence are useful for investigating relationships between taxons

Gene Duplications and Gene Families

Gene families are group of related genes within an organism's genome. There are 2 types of homologous genes

- **Orthologous genes:** they are genes found in different species and their divergence traces back to the speciation events that produced the species
- **Paralogous genes**: it is the homology results from gene duplications; hence, multiple copies of these genes have diverged from one another within a species



Genome Evolution

Comparing the entire genomes of different organism, including our own. Two patterns have emerged form is

- Lineages that diveraghed long ago can share orthologous genes
- Numbers on genes a species has doesn't seem to increase through duplication at the same rate as perceived phenotypic complexity

26.5 Molecular clocks help track evolutionary

This is used to understand the relationship among all organism, including those who have no fossil records.

Molecular Clocks

- Molecular clock is a yardstick for measuring the absolute time of evolutionary changes based on the observation that some genes and other regions of genomes appear to evolve at constant rates.
- The assumption underlying The molecular clock is that the number of nucleotide Substitution in the orthologous genes is the proportional To the time that has elapsed since the species branched from their common ancestors(divergent time).
- But for paralogous genes, the number of substitution is proportional to the time since the ancestral Gene was duplicated

The Molecular clock can be calibrated through the gene that has a reliable average rate of evolution by graphing the number of genetic differences.Breeds of clock may vary greatly from one gene to another. Some portions genes can evolve and irregular burst that is not at all clock like.

Neutral Theory

- This theory states that much evolutionary change in genes and proteins has no effect on fitness and therefore is not influenced by natural selection. Resulting in a slow rate of gene changing
  - Difference in clock rate for different genes are a function of how important a gene is.

Problems with the Molecular clocks

It does not run as smoothly as a neutral theory predicts. Problems can be avoided by Calibrating molecular clocks within many genes rather than just one or a few genes (as often done)

Applying a molecular clock: the origin of HIV

Researchers have used a molecular clock to date the origin of HIV Infections in human Their phylogenetic analysis shows that HIV, the virus that causes Aid is descended from virus says that infect chimpanzees and other primates.

26.6 New information continues to revise our understanding of the tree of life

Horizontal Gene transfer is a process in which genes are transferred from one genome to another through mechanisms such as exchange of transportable elements and plasmid viral infections and perhaps fusions of organisms

Some argue that the horizontal gene transfer was common in the early history of life that it should be presented as a tangled network of connected branches not as simple dichotomously branching tree, others think that it should be a ring of life and not a tree.