

Classification of Organisms



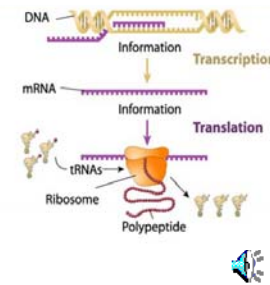
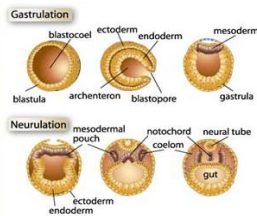
Data Used in Classification



- Classification of organisms is largely based on
 - morphology
 - anatomy / development
 - the fossil record
 - molecular data



Virtual Fossil Museum



In order to better understand the world around us, we have always attempted to classify various aspects of it, including the soils, rocks, waters, clouds, even winds, as well as the diversity of life around us. We share our planet with millions of other types of organisms – by some estimates up to 100 million other species. Some species share many similarities with us, while others appear extremely different. The classification of our biological diversity has historically been based on visible characteristics of organisms, such as morphology, anatomy and development, and the fossil record. However, molecular information, including the nucleotide sequences of DNA and RNA molecules and the amino acid sequences of proteins, has played an increasing role in classification over the past twenty to thirty years.

Classification: Placing Organisms into Groups

- All animals with hair are classified as mammals



- The Steller's jay and the blue jay

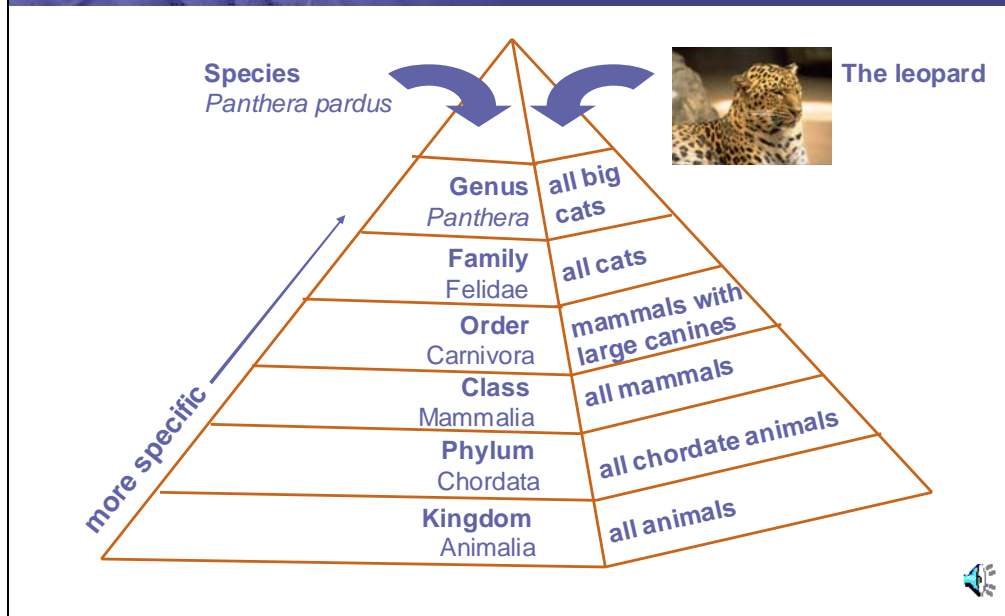


When organisms are classified, they are placed into groups based on the physical and molecular characteristics that they possess. These groups may be very broad, including many types of organisms, or very specific. For example, all organisms that have hair are grouped together in a relatively broad group called Mammalia, or the mammals; all organisms that have feathers are grouped together in a group called Aves, or the birds. Alternatively, the characteristics of organisms also play an important role in defining less inclusive groups, such as species. For example, on the slide here you can see pictures of two species of jays – the eastern blue jay and the Steller's jay. Both birds have morphological characteristics that allow them to be classified as jays, but each has other, unique characteristics, such as the plumage coloration, that leads them to be classified as different species of jays.

In addition to the physical characteristics of the adult forms of organisms, details of the developmental patterns of organisms are also used to classify organisms. For instance, it is common to use larval stages to determine how various invertebrate species should be classified. Alternatively, certain developmental characteristics also help define larger groups of organisms. For example, development of the young in an aquatic environment is common to virtually all amphibians.

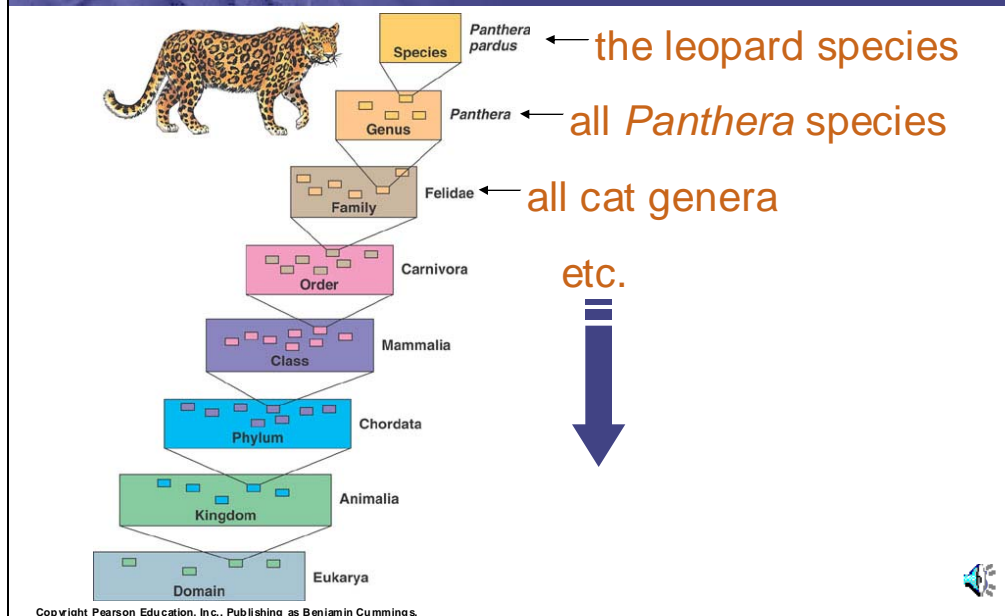
Finally, it is also important to note that morphological and developmental characteristics are not just utilized for living species, but play an essential role in interpreting the fossil record.

Linnaean System: Hierarchical Classification



The Linnaean system, put forth by the Swedish botanist Carolus Linnaeus in 1735, is a hierarchical system that has been used in classification for over 200 years. In the Linnaean system, organisms are placed into successively more inclusive groups based on similarities that they share with other organisms. These taxonomic groups are as follows, in order from least specific to most specific: kingdom, phylum, class, order, family, genus, species. In Linnaean classification, all types of organisms are given a species name, which consists of two parts: the genus name and the specific epithet. The species name is also referred to as a binomial. In all cases, the genus and specific epithet of a binomial are either italicized or underlined. In addition, genera (the plural of genus) are always capitalized, while specific epithets are not. From there, related genera are grouped into families, related families into orders, and so on. All of these groups, while not italicized or underlined, are capitalized.

Linnaean System: Hierarchical Classification

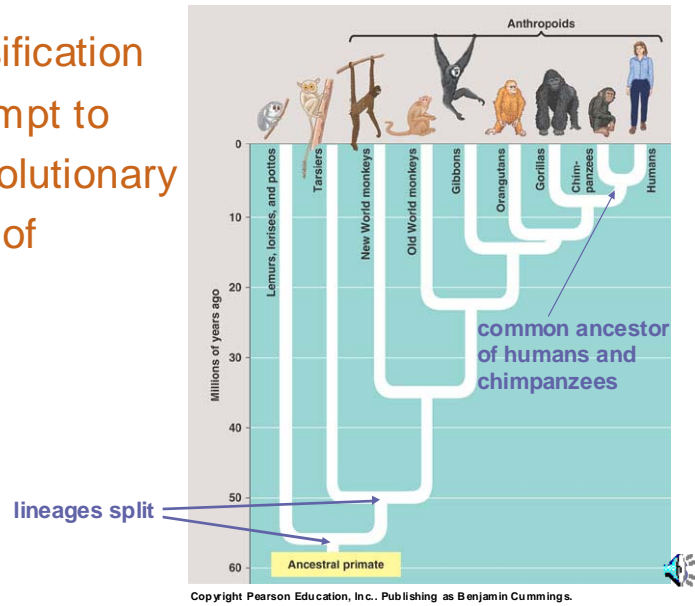


Let's use the leopard as an example to illustrate the Linnaean system. The leopard is a type of big cat found in Africa and Asia which grows to around 2 meters in length and has a specific coat pattern and other characteristics that differentiate it from all other big cats. All cats that have the specific characteristics of the leopard are labeled as the species *Panthera pardus* – again note the italics and capitalization. There are also other types of cats that are fairly similar to the leopard, yet differ in a significant number of characteristics. These cats are also classified within the genus *Panthera*, but are different species, such as *Panthera leo* (the lion) or *Panthera tigris* (the tiger). Subsequently, there are a number of types of cats that share similarities with the big cats in the genus *Panthera*, but differ from the big cats more than the big cats differ from each other. These other cats are classified as species in different genera, such as *Felis*, but we can include all of them, and all of the *Panthera* species, in the same family, the family Felidae. This pattern will continue until we reach the Animal Kingdom, which includes all of the animals in the world – the mammals, the reptiles, the insects, the sponges, and so on.

It is also worth noting that some modifications have been made to the Linnaean system since its original inception into the scientific world. Taxonomic designations have been made below the level of species, such as subspecies and variety. In addition, the designation of domain has been added to differentiate the three major lineages of life – the Bacteria, the Archaea and the Eukarya.

Evolutionary Classification

- Current classification systems attempt to reflect the evolutionary relationships of organisms

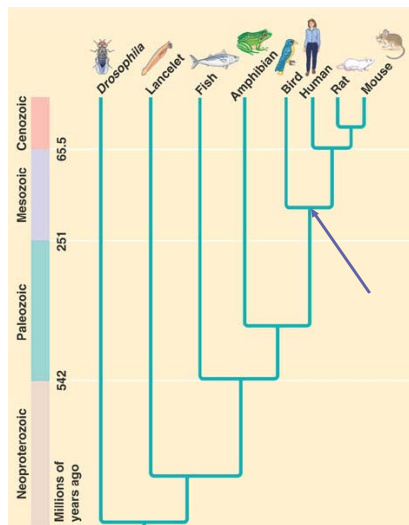


The main question, then, is ‘what do classification schemes ultimately show us?’ Originally, organisms classified using the Linnaean system were grouped together based simply on physical similarities. Today, the ultimate goal of scientific classification is to show the most accurate historical relationships between different types of organisms. In other words, organisms today are classified based on their evolutionary (genealogical) histories. The science of classifying organisms based on their evolutionary relationships is referred to as cladistics.

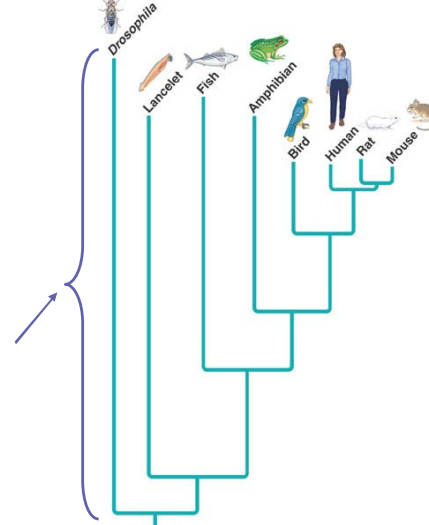
For example, let’s look at the current classification of the primates. As you can see on the diagram here, it is thought that all primates arose from a single ancestral lineage between 55 and 60 million years ago. This lineage split to give rise to two other lineages – one lineage that gave rise to the lemurs, lorises and pottos, and another lineage that gave rise to all of the other primates. The second lineage here subsequently split to give rise to two more lineages – one lineage that gave rise to the tarsiers and another lineage that gave rise to the New and Old World monkeys, the gibbons, orangutans, etc.

The primates living today are related to each other based on how recently they have shared a common ancestor. Humans and chimpanzees, as you can see, appear to have shared a common ancestor around 7 million years ago, while humans and orangutans shared a common ancestor around 13 million years ago. How is this determined? Again, such proposed relationships are based on the types of evidence mentioned previously – morphological and developmental evidence, the fossil record and molecular evidence.

Phylogenetic Trees



• An ultrametric tree



• A phylogram

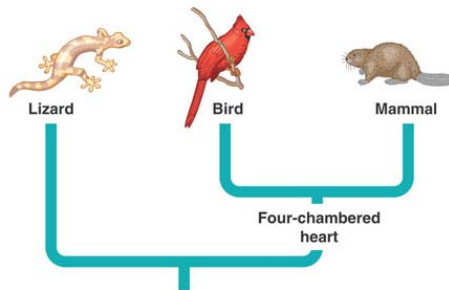
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As you saw on the previous slide, organisms are classified today based on their evolutionary histories. The proposed relationships between different types of organisms are displayed in diagrams called phylogenetic trees. Two specific types of phylogenetic trees bear mention here: ultrametric trees and phylograms.

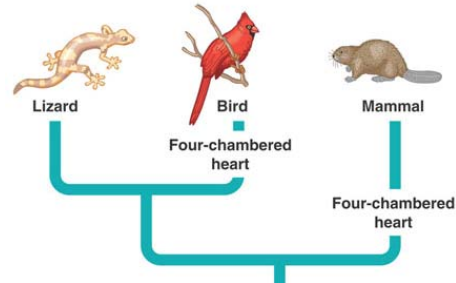
Ultrametric trees, such as the one shown on the left of the slide here and the one on the previous slide, are useful for displaying *when* important evolutionary events took place. For example, on the tree here you can see that mammals, such as humans, rats and mice, last shared a common ancestor with birds during the Mesozoic era, some 200 million years or so ago. You should also be able to find the approximate dates of other interesting lineage splits on this tree if you take a moment to examine it. Essentially, the vertical distance on an ultrametric tree is directly proportional to time.

Phylograms, on the other hand, are utilized to show the *amount of genetic divergence* that has occurred between lineages since they last shared a common ancestor. For example, on the phylogram on the right of the slide, you can see that the lineage leading to *Drosophila* is longer vertically than the lineage leading to any of the other organisms. This signifies that more genetic change has occurred in the *Drosophila* lineage than in any of the other lineages since they all shared a common ancestor. So, as opposed to ultrametric trees, vertical distance on a phylogram corresponds to the amount of genetic change, rather than time.

The Principle of Parsimony



- This tree is more parsimonious



- This tree is plausible, but less parsimonious

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In addition to understanding what different types of phylogenetic trees are telling you, it is also important to have at least a fundamental grasp of how data is used to formulate phylogenetic trees. Scientists today use two general principles in interpreting phylogenetic data – the principle of parsimony and the principle of maximum likelihood.

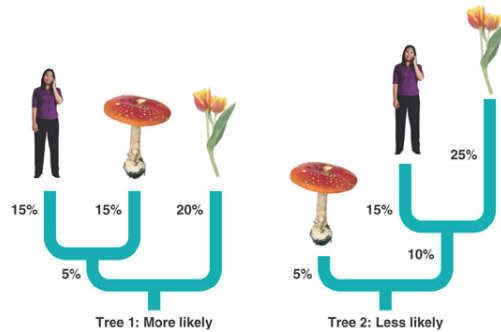
The principle of parsimony states that the simplest explanation consistent with the facts is the most likely explanation. As an example, consider the relationships among reptiles, birds, and mammals. To determine these relationships, we may focus on the fact that both birds and mammals have four-chambered hearts, while reptiles have only three-chambered hearts. According to the principle of parsimony, the simplest explanation is that four-chambered hearts evolved only once, in a common ancestor of birds and mammals, rather than twice. Based on this, we would choose the phylogenetic tree on the left, in which birds and mammals share a more recent common ancestor than either do with reptiles, as the most likely tree. Alternatively, one could hypothesize that the four-chambered heart evolved independently in each lineage. This hypothesis, however, would be less parsimonious.

The principle of parsimony is a powerful principle, in that it quickly and objectively narrows down the number of possible explanations of the relationships between organisms. As we will see in a moment, though, while parsimony is a very useful tool, it isn't always correct. First, though, let's briefly discuss the principle of maximum likelihood.

The Principle of Maximum Likelihood

	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

(a) Percentage differences between sequences



(b) Comparison of possible trees

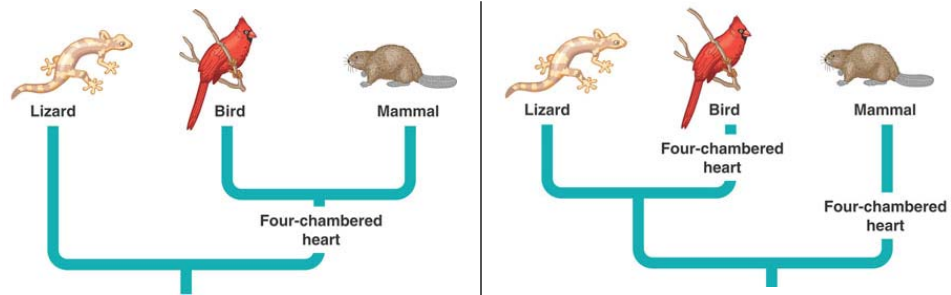
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- Tree 1 is more likely if DNA changes at constant rate

- Tree 2 is more likely if DNA changes more quickly in plants

The principle of maximum likelihood utilizes known information about how DNA changes over time to determine the most likely sequence of evolutionary changes and, hence, the most likely evolutionary relationships. Take for example the relationships between the Plant, Animal and Fungi kingdoms. Evidence to date indicates that genetically both animals and fungi differ from plants by about 40%. Animals and fungi, however, only differ from each other by about 30%. Based on this data, and based on the knowledge that DNA changes fairly regularly over time, we would categorize animals and fungi as more closely related to each other than either are to plants, as shown in the phylogenetic tree on the left. On the other hand, if evidence suggested that DNA changed very slowly in the mushroom lineage for some reason, but relatively quickly in the plant lineage, tree two would have a greater likelihood.

Difficulties in Classification



- More parsimonious, but not supported by other data

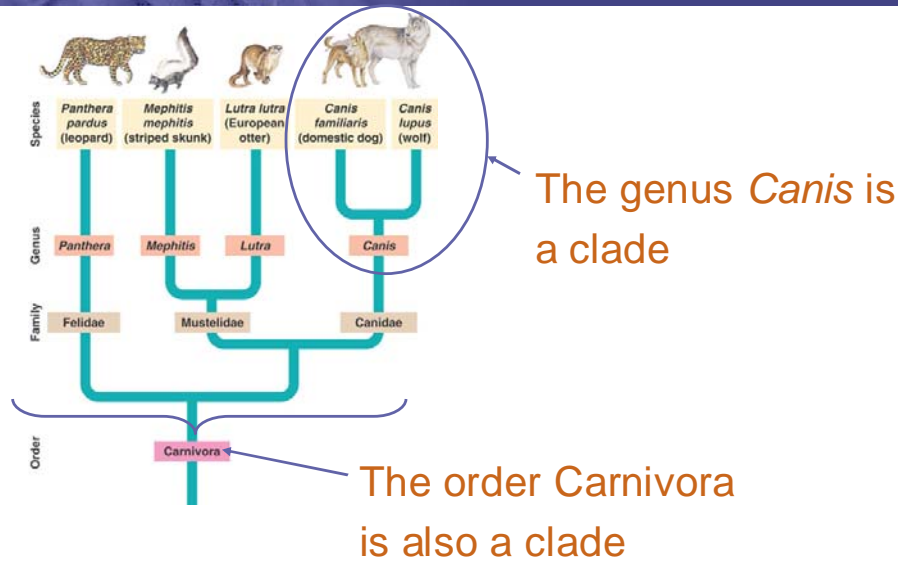
- Less parsimonious, but strongly supported by other data

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Now that we have covered the basic principles of classification, it may seem that classification is at least simple in theory – in general, the more similar organisms are, whether at the molecular or morphological level, the more closely related they are. However, it is important to realize that classification in practice is often extremely complicated. One of the most challenging problems in classification is the determination of homologous versus analogous traits. Homologous traits are physical structures or molecular sequences present in different lineages due to a shared common ancestry. Analogous traits, on the other hand, are similar but independently derived structures or molecular sequences in different types of organisms. In other words, analogous structures have evolved independently in more than one lineage and are similar due to convergent evolution. To illustrate, let's return to our example of the four-chambered heart. Recall that both birds and mammals have four-chambered hearts, while reptilian hearts have only three chambers. According to the principle of parsimony, we previously determined birds and mammals to be more closely related to each other than either is to reptiles. In addition, we could further conclude that the four-chambered heart is present in both birds and mammals because it was present in their common ancestor. The four-chambered heart would then be considered a homologous structure. However, a significant body of evidence, including molecular and fossil evidence, indicates that birds are actually more closely related to reptiles than they are to mammals. This suggests, then, that the four-chambered heart of birds evolved independently of the four-chambered heart of mammals. In other words, the four-chambered heart arose twice in evolutionary history, and so is considered an analogous structure. In turn, the tree on the right more accurately represents the true evolutionary relationships between these organisms.

Clades: Ideal Units of Classification



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Now let's consider how understanding the evolutionary relationships between organisms affects how we classify them within the Linnaean system. As mentioned before, the goal of classification today is to determine the true evolutionary histories of organisms. It follows then, that the goal of taxonomy (the science of naming organisms) today is to group organisms into the Linnaean categories in a way that accurately reflects their evolutionary histories. To do so, scientists strive to define and use what are called clades, or monophyletic groups, as units of classification. A clade includes a common ancestor and all of its descendants. As you can see on the phylogenetic tree shown here, a clade can be defined at different levels. For example, the order Carnivora, which includes many of the truly carnivorous mammals, such as the cats, mustelids, and dogs, is a clade. In other words, the order Carnivora includes all of the descendants of the original common ancestor of all of these carnivorous mammals – there are no members of the Carnivora who do not share that common ancestor. Alternatively, the genus *Canis*, which includes the dogs, wolves, foxes and jackals, among others, is also a clade, in that it contains all of the descendants of the common ancestor of all of these organisms.

Ultimately, then, all of the Linnaean categories for all types of organisms should represent clades as much as possible because this gives us the truest representation of the relationships among organisms. However, as noted before, challenges such as convergent evolution can make this very challenging in some cases.

