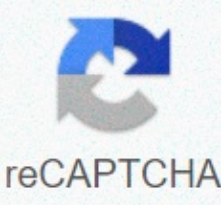




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## What is a cladogram

Skill:• Analysis of cladograms to derive evolutionary relationships Constructed cladograms, all of which typically have specific key features:Root – The original ancestor common to all organisms within the cladogram (incoming line shows that it originates from a larger clade)Nodes — Each node corresponds to a hypothetical common ancestor, which is supposed to result in two (or more) daughter taxaOutgroup – The furthest species in the Cladogram , which acts as a point of comparison and referenceKlades – A common ancestor and all its descendants (i.e. one node and all its associated branches)Key characteristics of a cladogram constructing CladogramsCladograms can be constructed either on the basis of a comparison of morphological (structural) characteristics or molecular evidenceHistorically, structural features were used to construct cladograms, but molecular evidence is now used more frequently1. Using Structural EvidenceStep 1: Organizing Selected Organisms by Defined CharacteristicsUse Characteristics That Are Determined (i.e. Congenital) And Not Affected by Environmental Impacts Step 2: Sequential Order of Organisms by Common Characteristics to Construct a CladogramGroup of Organisms Can be Facilitated by Creating a Venn Diagram Before Developing a Cladogram , with more common characteristics that represent earlier nodesThe species with the least number of characteristics together will represent the outgroup (notes base properties) 2. With Molecular EvidenceStep 1: Choose a gene or protein common to a number of selected organismsExamples of molecules that are ubiquitous in many animals are hemoglobin and cytochrome cStep 2: Copy the molecular sequence (DNA or amino acid) for each of the selected organismsUse online databases such as gene bank or ensembl to identify relevant DNA or amino acid sequences .txt. Sequence, denote a species name preceded by a forward arrow (e.B. ' &gt;Human' or ' &gt;Chimpanzee')Step 3: Performing a multiple alignment to compare molecular sequences (DNA or amino acid)Multiple Alignment Software compares DNA or protein sequences for similarities and differences. : Generate a phylogeny tree (cladogram) from multiple alignment dataClustal Omega can generate branched phylograms after a sequence alignment is complete (choose 'Phylogenetic Tree')Below is a plaintext file that can be uploaded to of different species to compare:HBA – hemoglobin alpha chain alpha chain Acid Sequence) of different typesMultiple Alignment of a Protein Sequence from Various Species A cladogram is a diagram used to represent a hypothetical relationship between animal groups called phylogeny. A cladogram is used by a scientist who studies phylogenetic systematics to visualize the groups of organisms that are compared as they are related, and their most common ancestors. A cladogram can be simple if you compare only two or three groups of organisms, or it can be enormously complex and contain all known life forms. Cladogram design is universal, if simple. A cladogram consists of the organisms, lines and nodes studied, on which these lines intersect. The lines represent the evolutionary time or a series of organisms that lead to the population with which it connects. Nodes represent common ancestors between dentypes. At some point in the past, a population of common ancestral organisms was divided, leading to the various organisms being studied. Some cladograms show evolutionary time by the scale of the lines, longer lines mean more time. Some cladograms chose to show extinct species, while others omit them. Each particular cladogram is specifically formulated for use. A cladogram gets its name from the clindes or groups of organisms that are displayed. A clade is a group of living organisms and the common ancestor from which they are derived. Scientists use synapomophes or released derived characters to define these groups. For example, mammary glands are a common feature of mammals. All mammals and their oldest common ancestors had or have mammary glands. So if we look at an unidentified animal and try to put it in a cladogram if it has mammary glands, we know it belongs in that branch. Symplesiomorphia, on the other hand, are signs that all organisms have in the cladogram. If the cladogram, including the mammals, was of all vertebrates, then the presence of vertebrae in our unknown animal would be a symplesiomorphy. Symplesiomorphies tell us nothing about the kinship of different groups in a cladogram, since all organisms have (or had) this characteristic. A very simple cladogram of vertebrates can be seen below. Scientists use cladograms to suggest and ask questions about evolutionary relationships between different species. By weighing derived characters and detecting suspect properties, scientists can identify different phylogenies of the same groups of organisms Some will be very complex, as characters must be created independently in multiple lines. Others are simple or economical and contain fewer changes between groups. Each set of characters can be used to create a cladogram. DNA is the preferred method because it is incredibly accurate. Before the days of DNA, however, the scientists created accurate cladograms using Characteristics. While the evolutionary relationships between organisms cannot be determined on a characteristic, the combination of the frugal results of many different traits will lead to the most probable phylogeny. The cladogram that describes this phylogeny will probably be the simplest and have the fewest nodes. In the above cladogram of primates, the different groups of primates that are compared are listed above. The different nodes in the diagram represent the different common ancestors between the groups. The monkeys, the group that contains humans, and all common ancestors (nodes) to the lowest monkey are considered a clad or a group of organisms with similar characteristics due to their common ancestry. The clad could be extended by anything except the lemurs, Loris and the lowest knot. If this were the case, the line that leads to lemurs would be considered an outgroup, while the rest of the primates would be considered the ingroup. These terms are simply used to describe different groups when they are discussed in scientific writing. Below is a much more complicated cladogram of whales and the animals they are related to. Many other groups are represented, up to genera and species in some cases. In this cladogram, bold lines represent living species, while narrow lines represent

extinct species from the fossil record. The numbers above each line represent the number of evolutionary changes that had to be made in this branch by the ancestral form. Overlooking the upper box of Cetaceamorpha, this branch represents whales (whales and dolphins) and their related ancestors. Until the discovery of the various fossils that bridge the gap between hippos and whales, the phylogeny of this tree was in question. However, these fossils have begun to close the gap between hippos and whales, forming a series of small steps. Near the top of the chart, the number of evolutionary changes jumps from 1 or 2 to 9 or 10 in each step. This represents an evolutionary gap that is still not understood. The ancestral forms of whales and dolphins presented on this cladogram would have been shallow aquatic animals, as their functional limbs show. As the whales' ancestors moved further out into the sea, it became increasingly unlikely that their fossilized remains would be found. Many characteristics were taken into account when creating this cladogram. For example, The Outgroup Ferae is the only group that does not have hooves or large toes. In addition, the Ferae have specialized carnivorous teeth. The rest of the groups are different various derived characters, such as humps in the camel, the presence of a ruminantiaphorpha and others. Whales are a particularly difficult group to suspect because there is a lack of fossil evidence and the great physiological difference between whales and their closest relatives. Without limbs, it is e.B. z.B. knowing that whales are related to limbed animals, unless evidence is found. Fortunately, new methods of DNA analysis allow the scientist to compare DNA directly, leading to a better understanding of the relationship between organisms and the way changes occur between populations. In the following cladograms it looks as if two different phylogenies are presented. In the cladogram on the right, it appears that A is more closely related to C than in the cladogram on the left. This is simply a trick of presentation, but does not represent any meaning in terms of kinship. These two cladograms are indeed a single phylogeny. When creating or reading Cladogram, it is important to remember that the only important features of the cladogram are the lines and nodes. In these two cladograms, the lengths of the lines are roughly the same and, more importantly, the nodes are in the same places. In both diagrams, A and B share a node that is further from the origin of the row in the chart. This tells us that A and B are more closely related to each other than C to both groups. The order of lines A and B and the orientation of the lines do not matter. A cladogram can be drawn from left to right, from right to left, from top to bottom, or from bottom to top. Some large cladograms are even designed in a circle to include all the groups they represent. In some cladograms, the evolutionary time is represented in millions of years to give an approximation to the lengths of the lines. Phylogeny – A hypothetical relationship between organisms represented by a cladogram. Symplesiomorphy—A property that all organisms on a cladogram possess. Synapomorphics—A property that has only a specific group that is descended from a common ancestor. Homoplasny – A common character shared by convergent evolution, not mean decent. 1. Which groups are most closely related in the following cladogram? A. Beetles and Ants B. Flies and Beetles C. Moths and Flies C is correct. Of these decisions, moths and flies are the most related organisms after this cladogram. The flies and beetles are least related because they are separated by the most distant distance and the number of nodes. The beetles and ants are closer, but according to this diagram, it is the moths and flies that recently fell apart and share most of the properties. 2. You make a cladogram of fruits. They have 4 fruits: a banana and orange, a red apple and a green apple. Just when it comes to appearance, which of them is an outgroup, and two belong on the node furthest from the beginning of the diagram? A. Orange; Banana and red apple B. banana; Orange and red apple C. banana; Red Apple and Green Apple C is right. Depending on the shape and appearance, the banana is the obvious outgroup. Unlike the other three fruits, it is rural and not round. The two closest related related extend farthest from the origin from the node. Red and green apples are obviously more similar than an orange, which has a completely different skin type, let alone color. This makes the apples furthest from the origin. 3. Look at the cladogram referenced #1. Which of the following features is a symplesiomorphy of the cladogram? A. Wing B. A tongue to collect nectar C. Wings that fold under a hard shell A is correct. All organisms in this cladogram have wings. Unless DNA or fossil evidence shows otherwise, it should be assumed that the wings originated and that all groups have since adapted their wings. Wings are therefore a symplesiomorphy. However, wings that fold under a shell are a common derived character of the beetles, which makes the choice C a synapomorphic. Likewise, a tongue to collect nectar is a property derived from different groups of moths, butterflies, bees and some flies. A nectar collection tongue is therefore also a synapomorphic. Synapomorphics.

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