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Use cladograms to find hypothetical evolutionary relationships between different organisms. Trace evolutionary changes by following the main line of a cladogram from the beginning to the end. Discover similarities between different animals by identifying their common ancestor as a node on a cladogram. Make your own cladogram by choosing 3-4 animals and showing their evolutionary relationship based on specific characteristics. A cladogram is a diagram that shows the evolutionary relationship between organisms. It does this with reference to specific traits that the organisms have in common. The features of a cladogram help you make sense of these relationships: The main line of a cladogram represents the passage of time. The start of the line is the furthest back in the past, typically millions of years ago. The nodes of a cladogram represent common ancestors that evolved a particular physical trait or characteristic. All of the animals that branch off at or after a node share that trait or characteristic (and that common ancestor). The branches of a cladogram show when each animal split off from the main line. The node where an animal branches off is the last characteristic that animal has in common with the animals that branch off further up the line. Advertisement 1 A cladogram is based on characteristics while a phylogenetic tree is based on genetics. The relationships cladograms show are hypothetical, meaning they haven't been proven genetically. In contrast, the relationships shown on a phylogenetic tree are backed by molecular evidence, usually from DNA.[1] You read cladograms and phylogenetic trees the same way, but phylogenetic trees are often more complex than cladograms. While you can easily make a cladogram on your own, you couldn't make a phylogenetic tree without access to DNA or other molecular data for the animals you're studying. To make things somewhat confusing, many biologists use these two terms interchangeably, or refer to both types of diagrams as "evolutionary trees." 2 A cladogram shows the passage of time while a phylogenetic tree shows genetic difference. The main line on a cladogram isn't drawn to any specific scale, but you can infer that nodes closer to the start of the main line happened longer ago than nodes closer to the end. With a phylogenetic tree, the main line shows the degree to which organisms change genetically. While this might be over time, the time itself is less important than the amount of genetic difference.[2] On a phylogenetic tree, animals that are closer together are also more genetically similar. This isn't necessarily true on a cladogram that doesn't use any molecular evidence. Advertisement 1 Locate the starting point of the cladogram. Every cladogram has a main line that represents time. The line starts at one end before there are any branches. The starting point is usually the bottom-left, but it might be a different spot depending on the orientation of the cladogram you're looking at. Orientation doesn't matter with cladograms—they still convey the same information regardless of how they're turned. 2 Move up the main line of the cladogram to move forward through time. That starting point you identified is the earliest point in time represented on the cladogram you're looking at. The opposite end of the cladogram is the most recent point in time. The position of a node on the line indicates the relative point in time when that particular characteristic or trait evolved. Lines on a cladogram aren't drawn to scale. In other words, the main line doesn't start or end on any particular year and the distance between nodes doesn't correspond to any particular range of years. Since the lines aren't drawn to scale, you can't infer how long ago any particular characteristic evolved. You can only infer whether a characteristic evolved before or after another characteristic represented on the cladogram. 3 Use the position of the nodes to determine which characteristics evolved first. The node closest to the start represents the characteristic that evolved first relative to the other characteristics represented by the cladogram. The next one up from that was the next characteristic to evolve, and so on until the last node, which represents the most recent evolutionary development. For example, if the node closest to the starting point of the main line represents "teeth" and the node halfway up the main line from the starting point represents "lungs," you can infer from the cladogram that animals evolved teeth before they evolved lungs. Remember that since the lines don't represent specific dates or ranges of dates, you can't say exactly how long it took for these evolutionary developments to happen—only the general order in which they happened. 4 Determine differences in animals based on where they branch off from the main line. An animal branches off the main line at the point that its evolution diverges from the other animals depicted on the cladogram. It doesn't have any of the characteristics beyond the node where it branched off. For example, imagine a simple cladogram that includes the characteristics "backbone" and "four limbs." Two of the animals are sharks and humans. Both sharks and humans have backbones, but sharks don't have four limbs. Sharks would branch out from the main line at the backbone node. 5 Relate the animals to each other based on the characteristics they share. Larger groups of animals have a common ancestor further back in time. If you start at the first node of a cladogram, all of the animals that branch off after that node have the characteristic indicated by the first node in common.[3] For example, suppose you're looking at a cladogram with nodes for four limbs, hair, and retractable claws. The animals represented on the cladogram include reptiles, kangaroos, dogs, and cats. Of these animals, you could say that kangaroos, dogs, and cats all share 2 of the characteristics (four limbs and hair). In this example, reptiles would be considered an outgroup—they only have 1 characteristic in common with the other groups, and likely have significantly more differences. On a cladogram, they're the first animal that branches off the main line.[4] Advertisement 1 Choose 3 or 4 animals for the endpoints of your cladogram. The largest cladograms analyze hundreds, or even thousands, of organisms and use computers to compile the data and generate the resulting diagram. But if you narrow that down to just a few animals, you can pretty easily make a cladogram yourself.[5] For example, you might choose dogs, cats, horses, and turtles. 2 Find a characteristic that all of your animals have in common. The first node on your cladogram represents a common ancestor that evolved one characteristic that all of your animals have in common. This characteristic is also the first characteristic to evolve out of all the characteristics that will eventually be included on your cladogram.[6] For example, dogs, cats, horses, and turtles all have a backbone, so that could be the first node on the main line of your cladogram—the common ancestor all of these animals have in common that developed a backbone. 3 Brainstorm other characteristics the animals have. Try to come up with around twice the number of characteristics as you have animals. Make a table and run your list of characteristics down the left side. Along the top line of the table, make a column for each animal you want to include in your cladogram. Then, you can simply place a checkmark in the row for the characteristic if the animal in that column has it.[7] For example, you might list backbone, hooves, walks on 4 legs, carnivorous, hair/fur, warm-blooded, mammary glands, and retractable claws. Then, you would place checkmarks in the "horse" column for all of those traits except for retractable claws. 4 Narrow down your list so one animal branches off at each node. Look at your table to find 1 trait that all of the animals have, 1 trait that all but one animal has, another trait that all but 2 animals have, and so on. If you hit a block here, brainstorm more characteristics until you find one that fits.[8] To return to the previous example, you can see that only horses have hooves, so you can eliminate that characteristic—since no other animals have it, you have nothing to compare them to. Cats, on the other hand, are a strong contender for the final slot because they have all of the traits (except hooves, which you've eliminated). Since all animals have 4 legs and all animals have a backbone, you only need one of these characteristics for your first node—you can eliminate the other one. 5 Draw concentric circles to illustrate which animals have which characteristics in common. The largest circle represents the characteristic that all of your animals have in common. Then, draw a smaller circle inside it that represents a characteristic some, but not all, of the animals have.[9] For the example with dogs, cats, horses, and turtles, your largest circle would be the "backbone" circle, because all of your animals have one of those. Inside that circle, you'd draw a circle for warm-blooded, which captures all of your animals except turtles. Then, you'd have a smaller circle for "carnivorous," with the smallest circle going to "retractable claws." Label each of your animals in the circle that represents the last characteristic it has in common with the other animals before it diverges. In the above example, turtles would go in the largest circle, then horses in the next-largest, then dogs, with cats in the smallest circle. 6 Create a cladogram from your concentric circles. Draw the main line of your cladogram diagonally from the bottom-left corner to the top-right corner. Create a branch a little way up from the starting point at the bottom-left corner. Then create the rest of the branches at intervals up the line until you get to the end.[10] In the example, turtles would branch off first, from the node that represents "backbone." Your next node would be "warm-blooded, " with horses branching off from it. Then you would branch of dogs from the "carnivorous" node, leaving only cats after the "retractable claws" node. Advertisement Cladograms give you a better understanding of how animals are related than the traditional system of classification. You might have previously learned about the traditional (or Linnaean) system of classification, which organizes plants and animals into ranked groupings of kingdoms, phyla, orders, and so on. The phylogenetic system of classification is more biologically accurate than the traditional system.[11] For example, since both cats (Felidae) and orchids (Orchidae) are family-level groups, you might think the members of each group have similar things in common. But, in fact, orchids are tens of millions of years older than cats and are more similar to one another biologically. Switching from the Linneaean system to the phylogenetic system doesn't actually change biological names you might be used to all that much. For example, humans are still known as Homo sapiens. Modern biologists classify plants and animals according to clades, the groupings depicted on cladograms. Some traditional classifications don't make the cut. For example, reptiles don't form a clade. Ask a Question Advertisement Thanks Advertisement Co-authored by: Registered Professional Biologist This article was co-authored by Michael Simpson, PhD and by wikiHow staff writer, Jennifer Mueller, JD. Dr. Michael Simpson (Mike) is a Registered Professional Biologist in British Columbia, Canada. He has over 20 years of experience in ecology research and professional practice in Britain and North America, with an emphasis on plants and biological diversity. Mike also specializes in science communication and providing education and technical support for ecology projects. Mike received a BSc with honors in Ecology and an MA in Society, Science, and Nature from The University of Lancaster in England as well as a Ph.D. from the University of Alberta. He has worked in British, North American, and South American ecosystems, and with First Nations communities, non-profits, government, academia, and industry. This article has been viewed 71,773 times. Co-authors: 6 Updated: March 24, 2025 Views: 71,773 Categories: Biology Print Send fan mail to authors Thanks to all authors for creating a page that has been read 71,773 times. Home » Biology A cladogram is the graphical representation of the hypothetical relationship (phylogenetic relationship) between different groups of organisms. It is used in the phylogenetic analysis of organisms to determine the evolutionary relationship between them. The cladogram is derived from Greek words clados and gramma where 'clados' means branch and 'gramma' means characters. It is an unscaled representation of a phylogenetic analysis where only the topography of the diagram matters. However, it doesn't have any time axis and is instead a simple diagram that summarises a pattern of characters among different organisms. Although a cladogram includes hypothetical ancestors to derive a relationship, it is the starting point for further analysis. The trees that result from the cladistic analysis are relative statements of relationship and do not indicate ancestors or descendants. E.g., it hypothesizes that Birds and Mammals are related but not that Mammals evolved from Birds or that Birds evolved from Mammals. In a cladogram, branch lengths are not proportional to the number of evolutionary changes and thus have no phylogenetic meaning. The external taxa of a cladogram line up neatly in a row or a column. Cladograms are generated by the analysis of morphological characters of the organisms and DNA or RNA sequencing data. Recently, however, computational phylogenetics is also used in the combination of the existing characters for the generation of cladograms. Cladograms are the assumptions for the preparation of phylogenetic trees. Even though cladograms are of different shapes, they all consist of lines that branch off of other lines representing the hypothetical ancestors of different organisms. A cladogram is a diagram consisting of the following parts: Image Source: BioNinja. A root is the initial common ancestors of all the organisms in a cladogram. A root is the starting point for any given cladogram. However, the root might also indicate that it comes from some other larger clades. Each node is a hypothetical ancestor that gives rise to two or more daughter taxa. Nodes indicate the bifurcating branch point of divergence in all cladograms. Thus, a node exists in each point where a group of organisms divides or separate into further different groups. Clades are groups of organisms or genes that include the most recent common ancestor of all of its members and all of the descendants of that most recent common ancestor. A clade is made up of an ancestor and all its descendants. It includes a particular node and all of its connected branches. A taxon or an outgroup is the most distantly related group of animals that isn't necessarily a clade. This functions as a point of reference or comparison for the rest of the cladogram. A branch in a cladogram is a line that connects all the other parts of the cladogram. The branch length in some cases represents the extent of divergence or the extent of the relationship among different taxa. As discussed, cladograms can be generated either based on the morphological characteristics or molecular evidence like DNA, RNA or protein sequencing. Therefore, on the basis of the characters used in the cladograms, these can be made in two different ways: The first step in phylogenetic analysis is to determine whether a character is derived or primitive (innate). In this case, the characters that are not influenced by environmental factors are to be selected. The outgroup comparison method is the primary method in use for the construction of cladograms or other trees. In the outgroup method, a character of an organism is selected where the organisms is not a member of the group of animals to be classified, but the selected character is the same as some of the organisms in the group, then such a character can be used as a defined character. Here, the outside organism is called the outgroup, and the organisms being classified are the ingroup. Now, within the group, other characters are selected to separate the organisms in the ingroup further. Characters SharkBullfrogKangarooHumanVertebraeXXXXTwo pairs of limbs XXXMammary glands XXPlacenta   X Here, the organism with the least common characters represents the outgroup. In this table above, Shark is the outgroup. For the grouping of the organisms, a Venn diagram can be constructed prior to developing a cladogram. In the Venn diagram, begin with the character that is common in all groups and place it on the outside. Image Source: Now, convert the Venn diagram into a cladogram. Image Source: The first step in phylogenetic construction using molecular evidence is to decide whether to use DNA sequences or protein sequences. Protein sequences are preferable in most cases. However, for studying very recent evolution, DNA is the marker of choice. Some examples of proteins that are common in many organisms are hemoglobin and cytochrome c. Multiple sequence alignment software like Clustal Omega can be used to align multiple DNA or amino acid sequences to determine similarities and dissimilarities. The closely related organisms will have a higher degree of similarity in the sequences compared to the organisms that are distantly related. The next step is to select a proper substitution model that provides estimates of the relationship between the organisms by taking into account the results of multiple sequence alignment. The commonly used nucleotide substitution models are the Jukes-Cantor and Kimura models. The commonly used amino acid substitution models are the PAM and JTT models. Even if a cladogram doesn't provide a complete explanation of the relationship between different organisms, it does, however, give a basic plot in establishing a relationship. For the interpretation of a cladogram, let us consider the following example of a cladogram. Image Source: In the cladogram above, four phylogenetic characters are studied. This represents that humans and kangaroo are more closely related than humans and bullfrogs. The extent of the relationship cannot be determined by this cladogram as it is an unscaled diagram. The orientation of the lines and the order of the animals also don't matter. Similarly, in the cladogram, as we move towards the right of the diagram, the organisms become less related to each other. Sharks and humans are more distantly related than bulldog and humans. Characteristic to all cladograms, the ancestors of the organisms are hypothetical and thus are not indicated. In the above diagram, the shark is the outgroup, whereas human and kangaroo form a clade. There are different styles of cladograms based on the shapes of the branches and the orientation of the branches. However, because a cladogram is an unscaled representation of phylogenetic analysis, the shape, length, and orientation of the branches don't matter. The following are some styles of drawing cladograms: In both of the given diagrams, two phylogenetic characters are studied and represent the same relationship between the three organisms. Cladograms can be used to differentiate different organisms based on some specific shared characteristics. The following are some examples of cladogram that can be used to distinguish organisms into further different groups based on their morphological characters: Figure: Cladogram of primates. Image Source: Biology Dictionary. Primates can be distinguished into separate taxa based on some specific characters. In the cladogram above, the branch towards lemurs and lorises is considered the outgroup while the rest are in the ingroup. Lemurs and Lorises also form a separate clade with a common node. The internal nodes present within the cladogram present hypothetical ancestors between different groups. Similarly, the closer the groups are to each other, the more closely related to each other they are. Figure: Cladogram of vertebrates. Vertebrates can also be further divided into groups based on various characteristics. Among the characters, the above cladogram represents the differentiation of vertebrates based on the ventrolateral muscle layers. In the given cladogram, all the groups share a common of at least two muscle layers. As we move further up towards the top, the taxa are separated based on the presence of four layers on the ventrolateral body wall. Here, the bony fish form the outgroup while the rest of the taxa are resent in the ingroup. Similarly, crocodiles and birds form a clade with the commonest ancestor. As in all other cladograms, the closer the organisms in the cladogram, the more closely related they are based on their morphological characteristics. Both the cladogram and phylogenetic tree are the diagrammatic representation of phylogenetic analysis. Both of these provide a relationship between different groups of organisms. The characters used in both cladogram and phylogenetic tree are the same and involve a similar process of construction. However, the cladogram is often considered an initial step towards the construction of a phylogenetic tree. CharacteristicsCladogramPhylogenetic tree (phylogram)NatureCladograms are mostly simple and can be used for the general classification of organisms.Phylogenetic trees are more complex and are mostly used to determine the evolutionary relationship between different groups of organisms.RepresentationCladograms do not represent the evolutionary relationships between different groups of the organism and thus is not an evolutionary tree.A phylogenetic tree is an evolutionary tree that shows the evolutionary relationships between different groups of animals.UseCladograms give a hypothetical picture of the actual evolutionary history of the organisms.Phylogenetic trees give an actual representation of the evolutionary history of the organisms.Length of the branchesAll the branches in a cladogram are of equal length as they do not represent any evolutionary distance between different groups.The branches in a phylogenetic tree usually are of different lengths as they represent the evolutionary distance between the groups.Evolutionary timeThe separation of the organism in a cladogram is solely based on the defined characters. Thus, the distance doesn't indicate the evolutionary time of the groups.A phylogenetic tree indicates the duration of evolution and the relative divergence time of the branches based on the distance between the groups.Position of external taxaThe external taxa of a cladogram line up neatly in a row or a column.The external taxa of a phylogenetic tree might or might not line up in a row or a column. Verma HN et al. (2013). Bioinformatics. First Edition. Universal Training Solutions, Pvt. Ltd. Baxevanis AD and Ouellete BF (2001). Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. Second Edition. Wiley Interscience. Xiong J (2006). Essential Bioinformatics. First Edition. Cambridge University Press. Hall, Margaret & Rodriguez-Sosa, Jose & Plochocki, Jeffrey. (2017). Reorganization of mammalian body wall patterning with cloacal septation. Scientific Reports. 7. 10.1038/s41598-017-09359-y. 1% – clade/faculty/lipscomb/Cladistics.pdf 1% – 1% – 1% –