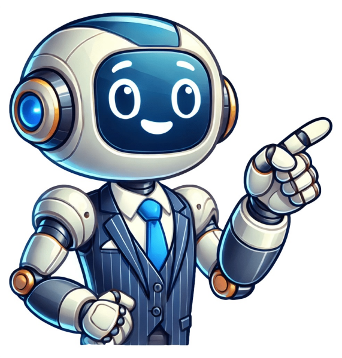

Unformatted Attachment Preview Lets Build a Cladogram!Teacher Guide and Answer KeyTips and Suggestions:1. My school does not allow color printing. The images used in this resource look best if printed incolor. I print a class set of the pictures on my computer at home and then have them laminated atschool so that I can use them year after year. The two-page picture file can be printed on thefront/back of one piece of card stock paper. Laminate the pages so that you can use them year afteryear. You can also print the image file in black/white to save ink. This will not affect the outcome ofthe lesson. 2. I allow my students to work in groups of two for this activity. However, I do require students tocomplete their own set of handouts. The student handouts consist of four pages. These can beprinted front/back to save paper. Further, you can print just one class set, and require that studentscomplete the ... Purchase document to see full attachment User generated content is uploaded by users for the purposes of learning and should be used following Studypool's honor code & terms of service. Studypool 4.7 Indeed 4.5 Sitejabber 4.4 Stuck on a study question? Our verified tutors can answer all questions, from basicmathto advanced rocket science! 67%(12)67% found this document useful (12 votes)60K views1. The document provides instructions for using a Gizmo called Cladograms to build cladograms based on morphological characteristics of different groups of organisms. 2. It guides the userAI-enhanced title and descriptionSaveSave cladogram gizmo For Later67%67% found this document useful, undefinedHow can financial brands set themselves apart through visual storytelling? Our experts explainhow.Learn MoreThe Motorsport Images Collections captures events from 1895 to todays most recentcoverage.Discover The CollectionCurated, compelling, and worth your time. 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These drawings are used in cladistics, and nowhere resembles an evolutionary tree; they are instead used for tracing out the common hypothetical ancestor that exhibits similar characteristics as the other organisms of the taxonomy. History of Cladograms The history of cladograms is vague; however, it is thought to date back to the 1950 era when Willi Hennig, a German entomologist, introduced his ideas on cladistics. Hennig wrote a book discussing the phylogeny of organisms and ways to discover the relationship between them. However, since the book was not in English, it stayed ignored till 1966, after which it was translated, and the ideas were interpreted. Hennig, in his book, had proposed the idea of classifying organisms through a branching system rather than a ladder-which was being used previously. Since then, Hennig is credited as the founder of cladistics. Parts of A Cladogram A typical cladogram will exhibit the following features: 1.Root The root is a common initial ancestor and is marked as the starting point for the diagram. An incoming line represents that the root comes from larger clades. 2.Nodes A node is a region that marks the point of divergence in cladograms and represents the hypothetical ancestor that further divides to bifurcate into two or more daughter taxa. 3.Clades A clade is a specific part of the cladogram that includes the recent ancestor and its descendants. It can be indicated by marking out a particular node and all of its associated branches. 4.Branches The branches indicate the bifurcation of the root into nodes. Links between the organisms can be deduced via tracing out the branches. 5.Taxon / Outgroup The taxon or the outgroup is the most distantly related organism in the entire chart. This group doesnt usually form a clade and instead offers a point of comparison for the rest of the cladogram. Pros and Cons of Using A Cladogram The most significant advantage of using a cladogram is the convenience and ease they provide. Cladograms are pretty important, especially in biological studies, because they offer a quick overview of the traits of ancestors. For years, they have been used by biologists and are effective at sorting out organisms based on their characteristics. However, the biggest drawback of using a cladogram is that they only provide hypothetical ancestral information. Sometimes, this information can be misleading and misguide you about the ancestral heritage of the organisms. Besides, cladograms with overabundant branching can make it difficult to understand and interpret the diagram. Types of Clades As defined previously, clades are a specific group of organisms in a cladogram that shows one ancestor and its branching descendants. They have been subdivided into three main categories: monophyly, paraphyly, and polyphyly, describing the different ways of grouping the taxa. Lets have a look. 1.Monophyletic As interpreted from the term mono, these groups refer to a single clade form the fundamental basis of taxonomy. The monophyletic group shows descendants of a single common ancestor. Any organism that descends from that specific ancestral lineage will be considered a part of this group. 2.Paraphyletic Paraphyletic clades do not include all the descendants of a specific ancestor; instead, a certain subset of organisms is deliberately ignored while forming this group. Interestingly, these clades have great practical value and are used to describe the surreal lineage of dinosaurs and birds. 3.Polyphyletic Polyphyletic groups are those taxa that do not share a common ancestral lineage and have multiple origins. They are grouped based on a common characteristic that is thought to be inherited from a common ancestor, but in fact, it isnt. Polyphyletic groups are confusing, and cladists and phylogenists rarely use them. Cladogram VS Phylogenetic Tree Cladograms are often confused with being a phylogenetic tree; however, this is not true. Both of these diagrams represent a phylogenetic analysis and aim to show the linkages between the different taxa. The constructing process is also similar, and even the characters used for describing organisms are similar. However, the cladogram is a type of phylogenetic diagram and is considered the essential step for constructing complex phylogenetic diagrams. Lets have a look at how these both are different from each other. Features Cladogram Phylogenetic Diagram Representation Cladograms only represent the linkage between different organisms. They offer a hypothetical image of the common ancestor of the organisms. Phylogenetic diagrams connect the organisms via evolutionary changes and are regarded as evolutionary trees. They provide an accurate representation of ancestors based on evolutionary history. Nature These diagrams are simple and very easy to understand. These diagrams are complex and require a good knowledge of evolution to understand them. Branching The branch length is equal and does not represent the evolutionary distance. The branch lengths are variable depending on the evolutionary distance between two organisms. Position of Taxa The external taxa link neatly in a proper row or a column. The taxa may or may not be arranged in a row or column form. Here is a phylogenetic tree of life. Here is a cladogram. Source: How to Read A Cladogram? Reading and interpreting a cladogram is super easy. Follow these steps to learn how to read a cladogram. 1.Read it Like A Family Tree The cladograms have a starting point that branches into different directions. The starting point represents the common ancestor of all species, while the branching ends indicate the descendants. 2.Know the Speciation Points The speciation is indicated at the nodes and marks the arrival of a new trait in the diagram. Trace out the intersection points and deduce the similarity between the group of animals bifurcating from the specific intersection point. 3.Study the Phylogenetic Characters While one part of the intersection line branches to show animals, the other shows the characteristics that aid in grouping the organisms. This can also be seen in the picture below. Mark out all the animals corresponding to a specific trait to interpret the classification. How To Make A Cladogram? Cladograms are made based on either their structural characteristics or molecular features like DNA and RNA. However, in recent times, cladograms constructed on molecular features have become more popular than the other type. Let us have a look at the constructing method for both of them. Structural Evidence 1.Choose a group of organisms and classify them based on their external features. Make sure to choose only developmentally fixed features instead of environmentally influenced. 2.Next, group and order your data for the cladogram. Group them by drawing a Venn diagram or a table. 3.Display each characteristic on a node, and the species that least resembles any characteristic will be placed at the end as an outgroup. Molecular Evidence 1.Choose a gene, DNA, or RNA protein that is common to all the organisms in a group. (e.g., hemoglobin, cytochrome C). Select the molecular evidence wisely, i.e., DNA or protein sequence. Even though proteins are preferred proof, DNA patterns are great for studying recent evolutions. 2. Align the genetic data by using software like Clustal Omega and deduce the similarities and differences between the protein sequences. Closely related animals will show a higher degree of similarity. 3.After the sequence alignment is done, the Clustal Omega will create branched phylograms. Examples of Cladograms Cladograms are an effective way of differentiating between organisms and tracing out a common ancestor. Following are some examples that will help you understand these charts better. Cladogram of Primates All the primates chosen for comparison are listed at the top of the chart. Different nodes in the chart represent different hypothetical ancestors. The lemurs and lorises are the outgroups, and it can be inferred that they least resemble the rest of the primates. The lemurs and lorises share a common node and form a separate clade. Apes, humans, and all the nodes are marking a common ancestor below form a clade. Cladogram of Vertebrae In this cladogram, vertebrates have been classified on the basis of their ventrolateral muscle layers. The 2 ventrolateral body wall muscle layers are common to all groups. To the top, the taxa are further classified on the basis of their 4 muscle layers on the ventrolateral body wall. The closer the organism, the higher the degree of similarity between them. Lizards, birds, and Crocodiles form a clade that ends at a common ancestor. Key Takeaways Cladograms are indeed a great way of differentiating between organisms and discovering a hypothetical common ancestor for them. With simple branching and no major complexities involved, the diagrams are easy to draw and understand. However, the whole drawing process is further simplified and made easy with EdrawMax. Offering an extensive range of tools, user-friendly interface, and beautiful templates, constructing a cladogram with Edraw is just a 5 finger process. So, what are you waiting for? Collect your data and sign up on Edraw to start creating the most beautiful cladograms in a wink of an eye! Related Articles Share copy and redistribute the material in any medium or format for any purpose, even commercially. Adapt remix, transform, and build upon the material for any purpose, even commercially. The licensor cannot revoke these freedoms as long as you follow the license terms. Attribution You must give appropriate credit , provide a link to the license, and indicate if changes were made . You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use. ShareAlike If you remix, transform, or build upon the material, you must distribute your contributions under the same license as the original. No additional restrictions You may not apply legal terms or technological measures that legally restrict others from doing anything the license permits. You do not have to comply with the license for elements of the material in the public domain or where your use is permitted by an applicable exception or limitation . No warranties are given. The license may not give you all of the permissions necessary for your intended use. For example, other rights such as publicity, privacy, or moral rights may limit how you use the material. Unlock the potential of engaging education with our comprehensive collection of Cladogram Worksheets 2025 worksheets for students and teachers. Explore a diverse range of Cladogram Worksheets 2025s topics, tailored to various grade levels. Our educational resources empower teachers and inspire students to excel academically. Access a wealth of interactive and printable Cladogram Worksheets 2025 worksheets designed to enhance learning experiences. Elevate your classroom with our user-friendly platform, fostering a dynamic and effective educational environment for all. Cladogram Practice Worksheet With Answers Circle the correct answer for the cladogram question below The cladogram shows the evolution of land plants as indicated by fossil records 21 Which discovery would challenge the validity of this cladogram A A large aquatic vascular plant about 200 million years old B A species of algae that has existed for less than one million years C What is a cladogram It is a diagram that depicts evolutionary relationships among groups It is based on PHYLOGENY which is the study of evolutionary relationships Sometimes a cladogram is called a phylogenetic tree though technically there are minor differences between the two In the past biologists would group organisms based solely Biology Cladogram Worksheets 4 18 12 You will need headphones for this set of worksheets View the movie that shows you how to construct a cladogram below You will need this set of skills to do the second and third set of worksheets Cladogram Practice Worksheet With AnswersCladogram Practice Worksheet With Answers Cladogram Worksheet Practice KEY Name Cladogram Practice Worksheet Answers Mark an X if an organism has the trait In the box below create a cladogram based off your matrix 1 According to your cladogram which two species are more closely related worms and spiders or worms and ants How do you know 2 According to your cladogram what species are dragonflies most closely related to Circle the correct answer for the cladogram question below The cladogram shows the evolution of land plants as indicated by fossil records 21 Which discovery would challenge the validity of this cladogram A A large aquatic vascular plant about 200 million years old B A species of algae that has existed for less than one million years C Examine the sample cladogram each letter on the diagram points to a derived character or something different or newer than what was seen in previous groups Match the letter to its character Note this cladogram was created for simplicity and understanding it does not represent the established phylogeny for insects and their relatives 1 B Draw a cladogram showing the relationship of these beetles Make sure it is the simplest tree invoking the fewest possible character state changes 14 Using the cladogram below the relative lengths of the frog and mouse branches in the phylogenetic tree indicate that a Frogs evolved before mice b Mice evolved before frogs c More picture related to Cladogram Practice Worksheet With Answers The Best Cladogram Worksheet Answer Key 2023 Alec Worksheet Let s Build A Cladogram Worksheet Key Live Worksheet Online A Cladogram Worksheet Best Of 5 4 Cladisticc Worksheets 1 Based on the cladogram shown we can conclude that species 2 is most closely related to species A 1 B 3 C 4 D 5 E 1 or 3 2 The cladogram shows the evolution of land plants as indicated by fossil records Which discovery would challenge the validity of this cladogram A A large aquatic vascular plant about 200 million years old 27 Which discovery would challenge the validity not be true of this cladogram Circle one A A large aquatic vascular plant about 200 million years old B A species of algae that has existed for less than one million years C A moss species that has existed for less than 380 million years D A fossil of a fern more than 425 million years Cladograms and phylogenetic trees provide a visual image of the relationships between organisms and our quiz and worksheet can help ensure that you understand all of the differences between the 1 Fill in the following table Mark an X if an organism has the trait 2 Add each of these organisms to the cladogram below worm spider ant fly 3 Explain why you put each organism where you did on the cladogram 4 On the cladogram above add traits that make the organisms different from each other Cladograms Worksheet And Practice By Brianna Jenkins TpT Worksheet Cladogram Worksheet Answer Key Sixteenth Streets Cladogram Practice Worksheet With Answers - Mark an X if an organism has the trait In the box below create a cladogram based off your matrix 1 According to your cladogram which two species are more closely related worms and spiders or worms and ants How do you know 2 According to your cladogram what species are dragonflies most closely related to What are Printable Templates?Printable templates have become an indispensable resource in today's digital age, offering a convenient and customizable way to create various documents and materials. Printable templates can save you time and effort if you're a student, professional, or simply looking to streamline your daily tasks.Printable templates are pre-designed documents you can customize and print to suit your needs. They come in various formats, including Word, Excel, PowerPoint, PDF, and more. Some popular types of printable templates include:Business templates: Resumes, cover letters, business cards, invoices, contracts, and proposals.Educational templates: Worksheets, lesson plans, quizzes, and certificates.Personal templates: Calendars, planners, organizers, labels, and party invitations.Creative templates: Flyers, posters, brochures, and social media graphics. Benefits of Using Printable TemplatesUsing printable templates can bring numerous benefits to your daily life and work. Some of the most significant advantages include:Increased Productivity: Printable templates can help you save time and effort by providing a pre-designed layout that you can fill in with your own information. This can be especially useful for tasks that require repetitive formatting, such as creating invoices or reports.Improved Organization: Printable templates can help you stay organized by providing a structured format for your information. This can be especially useful for tasks such as creating schedules, to-do lists, or budgets.Enhanced Professionalism: Printable templates can help you create professional-looking documents and materials, even if you don't have extensive design experience. This can be especially useful for small businesses or individuals who want to create a professional image.Cost-Effective: Printable templates are often free or low-cost, making them a budget-friendly option for individuals and businesses.Applications of Printable TemplatesPrintable templates can be used for a wide range of purposes, including:Business: Printable templates can be used to create business cards, brochures, invoices, reports, and other business-related documents.Education: Printable templates can be used to create lesson plans, worksheets, and other educational materials.Personal: Printable templates can be used to create schedules, to-do lists, budgets, and other personal organization tools.Creative Projects: Printable templates can be used to create art, crafts, and other creative projects.Tips for Creating and Using Printable TemplatesHere are some tips for creating and using printable templates effectively:Choose a Template that Suits Your Needs: Select a template that is specifically designed for your intended use. This will help you save time and ensure that your template is effective.Customize Your Template: Don't be afraid to customize your template to suit your individual needs. This can include adding your own logo, changing the layout, or modifying the content.Use High-Quality Images: Use high-quality images and graphics to make your template look professional and visually appealing.Proofread and Edit: Always proofread and edit your template before printing to ensure that it is error-free and looks professional.Printable templates are a powerful tool that can help you streamline your workflow, boost your productivity, and achieve your goals. By understanding the benefits and applications of printable templates, and following the tips outlined in this article, you can unlock the full potential of these versatile and customizable tools. Whether you're a business owner, student, or individual looking to stay organized, printable templates are an essential resource that can help you achieve success. Original Document: Cladogram Analysis What is a cladogram? It is a diagram that depicts evolutionary relationships among groups. It is based on PHYLOGENY, which is the study of evolutionary relationships. Sometimes a cladogram is called a phylogenetic tree (though technically, there are minor differences between the two). In the past, biologists would group organisms based solely on their physical appearance. Today, with the advances in genetics and biochemistry, biologists can look more closely at individuals to discover their pattern of evolution, and group them accordingly - this strategy is called EVOLUTIONARY CLASSIFICATION CLADISTICS is form of analysis that looks at features of organisms that are considered "innovations", or newer features that serve some kind of purpose. (Think about what the word "innovation" means in regular language.) These characteristics appear in later organisms but not earlier ones and are called DERIVED CHARACTERS. PART I - Analyze the Cladogram Examine the sample cladogram, each letter on the diagram points to a derived character, or something different (or newer) than what was seen in previous groups. Match the letter to its character. Note: this cladogram was created for simplicity and understanding, it does not represent the established phylogeny for insects and their relatives. 1. __F__ Wings 2. ___C__ 6 Legs 3. ___A___ Segmented Body 4. ___G__ Double set of wings 5. __E___ Cerci (abdomenal appendages) 6. ___D__ Crushing mouthparts 7. ___B___ Legs 8. __H__ Curly Antennae PART II - Create Your Own Cladogram To make a cladogram, you must first look at the animals you are studying and establish characteristics that they share and ones that are unique to each group. For the animals on the table, indicate whether the characteristic is present or not. Based on that chart, create a cladogram like the one pictured above. Cells Backbone Legs Hair Opposable Thumbs Slug Y Catfish Y Y Frog Y Y Y Tiger Y Y Y Y Human Y Y Y Y Y DRAWING OF YOUR CLADOGRAM Diagram used to show relations among groups of organisms with common originsA horizontal cladogram, with the root to the leftTwo vertical cladograms, the root at the bottom A cladogram (from Greek clados "branch" and gramma "character") is a diagram used in cladistics to show relations among organisms. A cladogram is not, however, an evolutionary tree because it does not show how ancestors are related to descendants, nor does it show how much they have changed, so many differing evolutionary trees can be consistent with the same cladogram.[1][2][3][4][5] A cladogram uses lines that branch off in different directions ending at a clade, a group of organisms with a last common ancestor. There are many shapes of cladograms but they all have lines that branch off from other lines. The lines can be traced back to where they branch off. These branching off points represent a hypothetical ancestor (not an actual entity) which can be inferred to exhibit the traits shared among the terminal taxa above it.[4][6] This hypothetical ancestor might then provide clues about the order of evolution of various features, adaptation, and other evolutionary narratives about ancestors. Although traditionally such cladograms were generated largely on the basis of morphological characters, DNA and RNA sequencing data and computational phylogenetics are now very commonly used in the generation of cladograms, either on their own or in combination with morphology.This section needs additional citations for verification. Please help improve this article by adding citations to reliable sources in this section. Unsourced material may be challenged and removed. (April 2016) (Learn how and when to remove this message)Cladogram of birdsThe characteristics used to create a cladogram can be roughly categorized as either morphological (synapsid skull, warm blooded, notochord, unicellular, etc.) or molecular (DNA, RNA, or other genetic information).[7] Prior to the advent of DNA sequencing, cladistic analysis primarily used morphological data. Behavioral data (for animals) may also be used.[8]As DNA sequencing has become cheaper and easier, molecular systematics has become a more and more popular way to infer phylogenetic hypotheses.[9] Using a parsimony criterion is only one of several methods to infer a phylogeny from molecular data. Approaches such as maximum likelihood, which incorporate explicit models of sequence evolution, are non-Hennigian ways to evaluate sequence data. Another powerful method of reconstructing phylogenies is the use of genomic retrotransposon markers, which are thought to be less prone to the problem of reversion that plagues sequence data. They are also generally assumed to have a low incidence of homoplasies because it was once thought that their integration into the genome was entirely random; this seems at least sometimes not to be the case, however.Apomorphy in cladistics. This diagram indicates "A" and "C" as ancestral states, and "B", "D" and "E" as states that are present in terminal taxa. Note that in practice, ancestral conditions are not known a priori (as shown in this heuristic example), but must be inferred from the pattern of shared states observed in the terminals. Given that each terminal in this example has a unique state, in reality we would not be able to infer anything conclusive about the ancestral states (other than the fact that the existence of unobserved states "A" and "C" would be unparsimonious inferences!)Researchers must decide which character states are "ancestral" (plesiomorphies) and which are derived (synapomorphies), because only synapomorphic character states provide evidence of grouping.[10] This determination is usually done by comparison to the character states of one or more outgroups. States shared between the outgroup and some members of the in-group are symplesiomorphies; states that are present only in a subset of the in-group are synapomorphies. Note that character states unique to a single terminal (autapomorphies) do not provide evidence of grouping. The choice of an outgroup is a crucial step in cladistic analysis because different outgroups can produce trees with profoundly different topologies.A homoplasy is a character state that is shared by two or more taxa due to some cause other than common ancestry.[11] The two main types of homoplasy are convergence (evolution of the "same" character in at least two distinct lineages) and reversion (the return to an ancestral character state). Characters that are obviously homoplastic, such as white fur in different lineages of Arctic mammals, should not be included as a character in a phylogenetic analysis as they do not contribute anything to our understanding of relationships. However, homoplasy is often not evident from inspection of the character itself (as in DNA sequence, for example), and is then detected by its incongruence (unparsimonious distribution) on a most-parsimonious cladogram. Note that characters that are homoplastic may still contain phylogenetic signal.[12]A well-known example of homoplasy due to convergent evolution would be the character, "presence of wings". Although the wings of birds, bats, and insects serve the same function, each evolved independently, as can be seen by their anatomy. If a bird, bat, and a winged insect were scored for the character, "presence of wings", a homoplasy would be introduced into the dataset, and this could potentially confound the analysis, possibly resulting in a false hypothesis of relationships. Of course, the only reason a homoplasy is recognizable in the first place is because there are other characters that imply a pattern of relationships that reveal its homoplastic distribution.This section needs additional citations for verification. Please help improve this article by adding citations to reliable sources in this section. Unsourced material may be challenged and removed. (January 2021) (Learn how and when to remove this message)A cladogram is the diagrammatic result of an analysis, which groups taxa on the basis of synapomorphies alone. There are many other phylogenetic algorithms that treat data somewhat differently, and result in phylogenetic trees that look like cladograms but are not cladograms. For example, phenetic algorithms, such as UPGMA and Neighbor-Joining, group by overall similarity, and treat both synapomorphies and symplesiomorphies as evidence of grouping, The resulting diagrams are phenograms, not cladograms, Similarly, the results of model-based methods (Maximum Likelihood or Bayesian approaches) that take into account both branching order and "branch length," count both synapomorphies and autapomorphies as evidence for or against grouping, The diagrams resulting from those sorts of analysis are not cladograms, either.[13]There are several algorithms available to identify the "best" cladogram.[14] Most algorithms use a metric to measure how consistent a candidate cladogram is with the data. Most cladogram algorithms use the mathematical techniques of optimization and minimization.In general, cladogram generation algorithms must be implemented as computer programs, although some algorithms can be performed manually when the data sets are modest (for example, just a few species and a couple of characteristics).Some algorithms are useful only when the characteristic data are molecular (DNA, RNA); other algorithms are useful only when the characteristic data are morphological. Other algorithms can be used when the characteristic data includes both molecular and morphological data.Algorithms for cladograms or phylogenetic trees include least squares, neighbor-joining, parsimony, maximum likelihood, and Bayesian inference.Biologists sometimes use the term parsimony for a specific kind of cladogram generation algorithm and sometimes as an umbrella term for all phylogenetic algorithms.[15]Algorithms that perform optimization tasks (such as building cladograms) can be sensitive to the order in which the input data (the list of species and their characteristics) is presented. Inputting the data in various orders can cause the same algorithm to produce different "best" cladograms. In these situations, the user should input the data in various orders and compare the results.Using different algorithms on a single data set can sometimes yield different "best" cladograms, because each algorithm may have a unique definition of what is "best".Because of the astronomical number of possible cladograms, algorithms cannot guarantee that the solution is the overall best solution. A nonoptimal cladogram will be selected if the program settles on a local minimum rather than the desired global minimum.[16] To help solve this problem, many cladogram algorithms use a simulated annealing approach to increase the likelihood that the selected cladogram is the optimal one.[17]The basal position is the direction of the base (or root) of a rooted phylogenetic tree or cladogram. A basal clade is the earliest clade (of a given taxonomic rank[a]) to branch within a larger clade.The incongruence length difference test (ILD) is a measurement of how the combination of different datasets (e.g. morphological and molecular, plastid and nuclear genes) contributes to a longer tree. It is measured by first calculating the total tree length of each partition and summing them. Then replicates are made by making randomly assembled partitions consisting of the original partitions. The lengths are summed. A p value of 0.01 is obtained for 100 replicates if 99 replicates have longer combined tree lengths.Further information: Convergent evolutionSome measures attempt to measure the amount of homoplasy in a dataset with reference to a tree,[18] though it is not necessarily clear precisely what property these measures aim to quantify.[19]The consistency index (CI) measures the consistency of a tree to a set of data a measure of the minimum amount of homoplasy implied by the tree.[20] It is calculated by counting the minimum number of changes in a dataset and dividing it by the actual number of changes needed for the cladogram.[20] A consistency index can also be calculated for an individual character i, denoted ci.Besides reflecting the amount of homoplasy, the metric also reflects the number of taxa in the dataset,[21] (to a lesser extent) the number of characters in a dataset,[22] the degree to which each character carries phylogenetic information,[23] and the fashion in which additive characters are coded, rendering it unfit for purpose.[24]ci occupies a range from 1 to 1/[n.taxa/2] in binary characters with an even state distribution; its minimum value is larger when states are not evenly spread.[23][18] In general, for a binary or non-binary character with n . s t a t e s {\displaystyle n.states} , ci occupies a range from 1 to ( n . s t a t e s 1 ) / ( n . t a x a n . t a x a / n . s t a t e s ) {\displaystyle (n.states-1)/(n.taxa-\lceil n.taxa/n.states\rceil )} .[23]The retention index (RI) was proposed as an improvement of the CI "for certain applications"[25] This metric also purports to measure of the amount of homoplasy, but also measures how well synapomorphies explain the tree. It is calculated taking the (maximum number of changes on a tree minus the number of changes on the tree), and dividing by the (maximum number of changes on the tree minus the minimum number of changes in the dataset).The rescaled consistency index (RC) is obtained by multiplying the CI by the RI; in effect this stretches the range of the CI such that its minimum theoretically attainable value is rescaled to 0, with its maximum remaining at 1.[18][25] The homoplasy index (HI) is simply 1 CI.This measures the amount of homoplasy observed on a tree relative to the maximum amount of homoplasy that could theoretically be present 1 (observed homoplasy excess) / (maximum homoplasy excess).[22] A value of 1 indicates no homoplasy; 0 represents as much homoplasy as there would be in a fully random dataset, and negative values indicate more homoplasy still (and tend only to occur in contrived examples).[22] The HER is presented as the best measure of homoplasy currently available.[18][26]PhylogeneticsDendrogramBasal (phylogenetics)^ Mayr, Ernst (2009). 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