

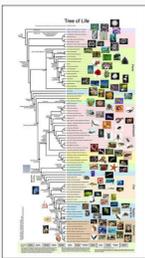


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GREAT LAKE TAUPŌ
Taupō District Council

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Taxonomy worksheet

1. Vocabulary

→ distinguish between the terms in each of the following pairs.

a) taxonomy, binomial nomenclature

b) kingdom, species

c) phylum, genus

3. Why do biologists assign each organism a universally accepted name? Give an example of this.

4. Name Linnaeus' 7 taxonomic categories from SMALLEST to LARGEST

5. Explain why each of the following characteristics of a classification system is important:

a) It assigns a single, universally accepted name to each organism.

b) It places organisms into groups that are biologically related.

c) It divides organisms into small groups.

Family Tree

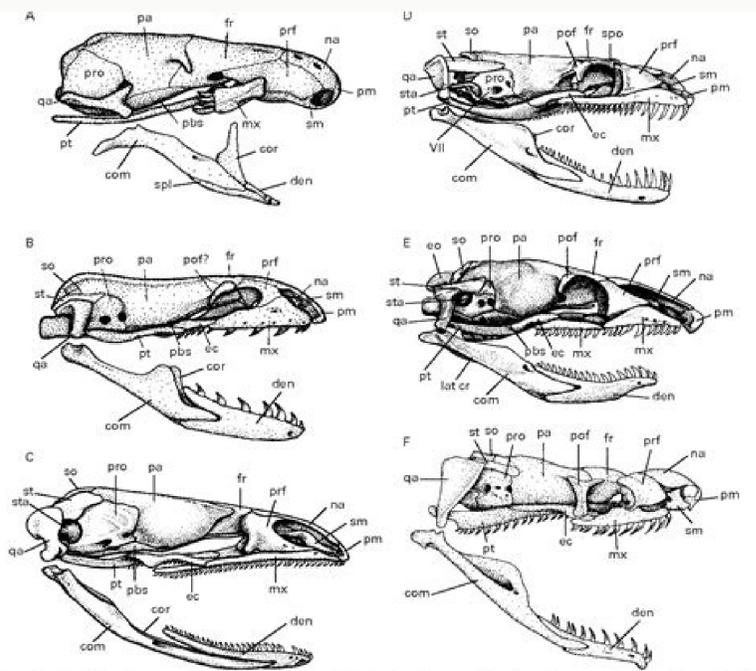
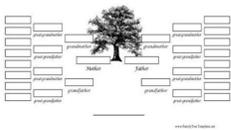


Fig. 4. Skulls of six different species of bats in side lateral view. (A) *Desmodus rotundus* (Trachilinae); (B) *C.*

Phylogenetic tree figure legend. Interpreting phylogenetic trees worksheet. Phylogenetic tree distance scale. How to interpret evolutionary trees. Phylogenetic tree a level biology.

There are reasons why we anthropomorphize trees; they stand tall like people, they sway, for torsos they have trunks and for arms, branches. If the outgroups are too divergent from the sequences of interest then the root position will be unreliable. The whole interview is poetry (hey, poetree!) but I especially love when he talks about trees and memory. Generally best avoided too. Each one was growing its branches turned away from the other rather than toward each other, as is more usually the case. They do not treat all other trees the same. For example, in the trees above, the pair of tips labelled ‘virus9’ and ‘virus10’ could be the outgroup allowing us to root the tree at the red circle. How can we work out where the root is? The numbers next to each node, in red, above, represent a measure of support for the node. So I use words of emotion to connect with people’s experience. The horizontal lines are branches and represent evolutionary lineages changing over time. But are there more similarities between trees and people than those that meet the eye? These sequences are usually referred to as the ‘outgroup’. Both these figures are representations of the same underlying tree as above: A: B: Tree A is in polar format (often called a circle tree). I have known trees that I am certain were friends, even if they don’t go out for coffee with each other. In this tree the internal nodes are labelled with the reconstructed host species based on the principle of parsimony. Peter Wohlleben is one of a number of experts who believes this to be the case. I have marked the previous rooting position with a red circle. Via Boing Boing What do we do if we don’t know? The vertical dimension is now the angle of the circle and the horizontal dimension is the distance from the centre point. Flies and insects have eyes, so they are a bit higher, but not so high as monkeys and apes and so on. The units of branch length are usually nucleotide substitutions per site – that is the number of changes or ‘substitutions’ divided by the length of the sequence (although they may be given as % change, i.e., the number of changes per 100 nucleotide sites). I say ‘approximately’ because in this tree the horizontal axis is measured as genetic change and to convert this into actual time we need to make some assumptions about the relationship between genetic change and time. We had a heavy drought here. Wohlleben has been taken to task by other scientists complaining about his tendency to anthropomorphize. But he does so very intentionally. These are our data and we usually know information about these, beyond the actual sequence, such as when they were collected, what host they were in, where that host was found, clinical features of the disease. The grey nodes are those that cannot be unambiguously reconstructed. For example, the common ancestor of the human and camel viruses could equally well be in humans, bats or camels with all three possibilities only requiring 2 host jumps: Distinguishing these three possibilities generally requires additional data perhaps with a denser sampling of viruses. In this way and others, tree friends take care of each other. The vertical lines therefore simply tell you which horizontal line connects to which and how long they are is irrelevant. The bar at the bottom of the figure provides a scale for this. A forester and best-selling author makes the case for trees and their extraordinary abilities. A high value means that there is strong evidence that the sequences to the right of the node cluster together to the exclusion of any other. We can however suggest that bats were the ultimate source of both camel and human viruses because of the much greater diversity of bat viruses. We can also say that a tree can learn, and it can remember a drought its whole life and act on that memory by being more cautious of its water usage. The internal nodes are represented by blue circles and these represent putative ancestors for the sampled viruses. This is often used when the rooting of the tree is not known (although I have marked with a red circle the equivalent position of the root in trees above). These assumptions are referred to as the ‘molecular clock’ and I will discuss this in a later article. The following comes from an exchange with Richard Schiffman at Yale e360. The vertical dimension in this figure has no meaning and is used simply to lay out the tree visually with the labels evenly spaced vertically. It may even remember that you are a friend. Here is an example (fictional) phylogeny as it may be presented in a journal article. We can start with the dimensions of the figure. Tree B is a radial format tree. Many methods of reconstructing phylogenies from gene sequences do not explicitly estimate the root of the tree. This is the reconstruction that requires the fewest jumps between host species. The root of the tree I mentioned above that if we know the root of the tree then that provides information about the order of nodes in the tree. There are two types of nodes; external nodes, also called ‘tips’ or ‘leaves’ (you can only take the tree metaphor so far and I prefer the term ‘tip’), and internal nodes. The longer the branch in the horizontal dimension, the larger the amount of change. You can read more from this wonderful interview at Yale e360 ... These can be computed by a range of statistical approaches including ‘bootstrapping’ and ‘Bayesian posterior probabilities’. For example the two viruses from humans have a closer common ancestor with each other than they do with any other virus. We say plants are the lowest caste, the pariahs because they don’t have brains, they don’t move, they don’t have big brown eyes. How do we know the the outgroup is an outgroup? Wohlleben agrees: In about one in 50 cases, we see these special friendships between trees. Now of course it would be easy to ascribe all of this to pure biological mechanics – but how egregiously species-centric that would be. The tips are shown here with green circles and these represent the actual viruses sampled and sequenced. An ancestor in this context is an infected host at sometime in the past that in turn infected 2 or more new hosts producing chains of infections that lead to the sampled viruses. In this figure the horizontal dimension gives the amount of genetic change. It is possible the outgroup has significant genomic differences suggesting they are a different group of viruses. “Humans are emotional animals,” he says. This kind of partnership is well known to foresters. Skip to Main Content Skip Nav Destination Research Article| May 01 2020 You do not currently have access to this content. Alternatively it might be possible to assume that one or more sequences are the outgroup simply because they are the most divergent (virus9 and virus10, above, might be an example of this). Phylogenetics trees contain a lot of information about the inferred evolutionary relationships between a set of viruses. However, this might also mean the outgroup viruses are extremely divergent from the ones we are interested in. There are two ways of finding the root of a phylogenetic tree. We may have created the language to describe friendship as it pertains to people, but we should also be intellectually expansive enough to broaden our horizons. Just today, I saw two old beeches standing next to each other. This tree is rooted which suggests we know where the ultimate common ancestor of all the sampled viruses was (the red circle). This can be broken down into nodes (represented in the tree, above, as circles) and branches (the lines connecting them). This is basically the same as the trees above but in polar coordinates. It may come as little surprise that we’ve written about the tree-whispering Wohlleben before. At first glance it may seem that human viruses are more closely related to bat viruses than camel viruses because they sit next to each other but remember that the vertical dimension is meaningless. In subsequent years, the trees that had suffered through the drought consumed less water in the spring so that they had more available for the summer months. These are generally numbers between 0 and 1 (but may be given as percentages) where 1 represents maximal support. Reconstructing epidemiology Here is the same tree as above but with the tips labeled by the type of host they were isolated from: You can immediately see that there is some structure there with viruses grouping by host. First there was Trees in the forest are social beings, followed by Trees can form bonds like an old couple and look after each – and thus it appears that whenever I read another interview with Wohlleben, I can’t help but to write again. Trees distinguish between one individual and another. Knowing this gives the tree an order of branching events in the horizontal dimension: Ancestor ‘A’ exists prior to ancestors ‘B’ and ‘C’ and time is approximately flowing from left to right. This means we can’t say from this tree if camels are the source of the human viruses or vice-versa, or just as likely, bats are independently the source of both human and camel outbreaks. Just because we don’t speak their language doesn’t mean trees don’t communicate – even if they do so with chemical and electrical signals, as Wohlleben explains, also noting that trees are badly misunderstood: We just see them as oxygen producers, as timber producers, as creators of shade. We have this essentially arbitrary caste system for living beings. Is life in the slow lane worth less than life on the fast track?Perhaps we create these artificial barriers between humans and animals, between animals and plants, so that we can use them indiscriminately and without care, without considering the suffering that we are subjecting them to. Click on the red circle and select Reroot on this node to switch the tree back to using this root. Wohlleben is a German forester and the best-selling author of The Hidden Life of Trees. Science often takes these words out, but then you have a language people can’t relate to, that they can’t understand.” And certainly speaking of trees as having special friendships will raise an eyebrow for some; but why does the definition of friendship have to be exclusive to humans? For example, here is the tree, above, rooted in an arbitrary place: This is exactly the same underlying tree as those above. Another way to look at this is that the common ancestors of the human and camel viruses lie within the diversity of all the bat viruses. These tree formats are often used to make a big visual impact in papers but generally have reduced readability - it is difficult to compare how far nodes are from the centre. The second approach to rooting the tree is to use a method that implicitly assumes a time scale – a molecular clock model – as described below. When scientists remove the emotion from writing, it loses its impact. How do we work out where the root is? and in the meantime, don’t forget to hug a tree. The branches then represent this chain of infections. When the tree is generated it will often have an arbitrary root. I want to remove trees from this caste system. He has spent decades working with our arboreal cohabitants and getting to know their secrets. This format tends to clump closely related sequences together making their precise relationships difficult to see. Skip to Main Content Skip Nav Destination Research Article| September 01 2016 You do not currently have access to this content. Figures that are arbitrarily rooted should mention this in the legend but they often don’t. Next, we will consider tree structure itself. Trees are sometimes drawn in other ways. This hierarchical ranking of living beings is totally unscientific. They know that if you see such a couple, they are really like a human couple; you have to chop down both if you chop one down, because the other will die anyway. They are best avoided. Trees make decisions. What is important to note is that it no longer holds that the left to right order of the internal nodes (the blue circles) can be interpreted as the order of common ancestors. I will not mention these formats again. The first is to include one or more sequences in the data set that are known to lie outside the diversity of the sequences of interest. “We feel things, we don’t just know the world intellectually. Decoding that information is not always straightforward and requires some understanding of the elements of a phylogeny and what they represent. They can decide things. Plants process information just as animals do, but for the most part they do this much more slowly. The details of what technique was used will be in the figure legend. In this case the line segment with the number ‘0.07’ shows the length of branch that represents an amount genetic change of 0.07. In fact the viruses can be swapped round at any internal node and the tree is the same: In fact the human and camel viruses are more closely related to each other and equally related to the bat viruses.

The swallows, martins, and saw-wings, or Hirundinidae, are a family of passerine birds found around the world on all continents, including occasionally in Antarctica. Highly adapted to aerial feeding, they have a distinctive appearance. The term "swallow" is used colloquially in Europe as the barn swallow.Around 90 species of Hirundinidae are known, divided into 19 ... The molecular clock is a figurative term for a technique that uses the mutation rate of biomolecules to deduce the time in prehistory when two or more life forms diverged.The biomolecular data used for such calculations are usually nucleotide sequences for DNA, RNA, or amino acid sequences for proteins.The benchmarks for determining the mutation rate are ...

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