https://www.youtube.com/watch?v=IrlSnwUbgNA

Tree-Thinking Video Transcript with Time Indications.

0:16 Phylogenetic or evolutionary trees are
0:19 diagrams that are used throughout
0:20 biology in studies ranging from
0:22 conservation to epidemiology.
0:24 They contain a great deal of information
0:26 about the evolutionary relationships and
0:28 diversification within and among
0:30 different kinds of organisms.
0:32 This video will address the following
0:33 questions about phylogenetic trees:
0:36 What are the parts?
0:37 How are they constructed?
0:40 And finally, how are they interpreted?
0:44 Although phylogenetic trees can be used for any taxonomic group,
0:47 species will be used in this video
0:49 for clarity.
0:51 To begin with, phylogenetic trees can be drawn a number of different
        ways.
0:55 Whether sloped with
0:57 angled branches or even showing a
0:59 slightly circular type of diagram,
1:02 these phylogenies all show the same
1:04 relationship among the Species A through E
1:06 because they have the same branching pattern.
1:09 You can even draw the phylogeny
1:10 with a different angle of orientation
1:12 and it still shows the same
1:14 relationships among these species.
1:16 Regardless of how the phylogeny is drawn,
1:18 they are all made of the same parts.
1:20 The ends are called the tips. The base is the
1:22 root. The lines are branches or clades.
1:25 And the points where the branches
1:27 diverge from one another called nodes.
1:30 The "out-group" is a sister species that's

1:32 used as a basis for comparison.
1:34 Species that are the focus of the study are
1:37 called the "in-group".
1:40 Another important nuts-and-bolts kind of thing to know
1:42 about phylogenetic trees is that you can
1:44 rotate them around the nodes that
1:46 doesn't change the relationship shown in them.
1:49 For example, in all three of the
1:51 trees shown here, the relationships among
1:54 species A, B and C are the same.
1:57 B and C are more closely related to one another
1:59 than either is to species A because B and C
2:02 share more recent node with one another.
2:07 Now, let's compare
2:08 the tree on the left with this
2:10 tree showing a different relationship of
2:12 branching patterns among A, B and C.
2:15 This tree shows a different relationship among the
2:17 species because A and C share a more
2:19 recent node with one another than either
2:22 one does with B.
2:23 So, while rotating around notes doesn't matter their sequence does.
2:28 Let's now focus on
2:29 interpreting trees in more detail.
2:31 In the example shown here, we have four species:
2:34 one shown by a square and then three circles.
2:37 There is a time component of
2:38 phylogenetic trees, and in them, the root
2:41 indicates the past and the tips indicate
2:43 the present.
2:46 In this tree, the three circle species
2:48 are joined at a note that indicates the
2:50 most recent common ancestor, and the
2:52 different branches represent lineages of
2:55 organisms that gave rise to the species
2:57 at the tips.
2:58 What this means is that at some point
3:00 along these lineages, new characteristics
3:02 arose and were passed on to all the

3:04 descendants in that lineage.
3:06 So, as indicated by the traits of round, blue and
3:09 stripe in this tree,
3:11 those traits arose due to some mutation that then became
3:14 established in those lineages.
3:16 Let's zoom in on the phylogeny to consider what that means.
3:20 Starting with a lineage, we
3:21 have each branch and it's composed of
3:23 many different populations, which are
3:24 indicated by these blue lines.
3:26 Populations exist independently from one
3:28 another but they are genetically united
3:31 by movement of individuals among them,
3:33 a process called gene flow.
3:34 Inside each of these populations are individuals who
3:37 mate, reproduce, and pass their DNA from
3:39 ancestors to descendants over time
3:41 as is indicated by these pedigrees.
3:44 And so, a lineage is actually a representation of
3:46 many different populations composed of
3:48 reproducing individuals over time.
3:52 Let's now consider what is represented by a node.
3:55 Now, I want you to think about
3:56 what is being drawn here as a
3:57 cross-section through the lineage just
3:59 below the node with each population
4:01 represented by a circle.
4:05 Looking inside one of these populations, we can see the
4:07 different individuals that compose it.
4:09 Suppose a mutation arises in one of these
4:11 individuals. Let's also have this
4:13 population with our new red mutation
4:15 become isolated from the other
4:17 populations of the species, so there's no
4:19 more gene flow between them.
4:21 Either due to conferring some survival advantage or
4:23 completely random processes, the red
4:25 trait becomes more common and, ultimately,
4:27 becomes the only trait found

4:29 in this population.
4:30 If other changes occur so that red individuals are reproductively
4:33 isolated and can no longer mate with
4:35 blue individuals when they come into
4:36 contact with them,
4:37 this results in genetic separation of
4:39 the blue and red individuals and leads to
4:41 the evolution of a new species, or speciation.
4:44 So, nodes represent reproductive isolation of lineages and
4:48 ultimately speciation.
4:52 These concepts about nodes and lineages are the basis
4:55 of how modern biologist group species
4:57 into larger groupings.
4:59 For example, grouping species B, C and E into
5:02 a genus that excludes D would be called
5:04 a paraphyletic group because it is
5:06 excluding one of the descendants of
5:08 these four species' most recent common ancestor.
5:12 Biologist prefer to include
5:14 all the descendants of a common ancestor
5:15 in their groupings, so by including D in
5:18 this genus we now have what biologists
5:20 call a monophyletic group, meaning
5:22 that this genus now contains all the
5:25 descendants of the four species' most
5:26 recent common ancestor.
5:28 This brings us to the question of how does one draw the
5:31 correct phylogenetic tree for a group of species?
5:34 Once again, let's return to our example with the circles and square.
5:38 There are several possible arrangements of this
5:40 "in-group" with the circles and the red
5:42 square as the comparator "out-group" species.
5:45 Two are shown here.
5:47 Now, a phylogenetic tree is a graphical
5:49 hypothesis of the relationship among species.
5:52 So, as with any scientific
5:53 hypothesis, we need to see which ones are
5:56 rejected by our data and which ones do
5:58 we fail to reject.

6:00 In a simple phylogenetic study, our data are the
6:02 traits that we collect from the different species.
6:06 So, let's make a simple
6:07 data matrix for these four species
6:09 usingy the traits: shape, color and fill.
6:12 Let's further assume that the traits are
6:14 independent of each other, and each
6:16 transition in character state represents
6:18 a unique individual change in characteristics.
6:21 In the tree on the left,
6:22 we can place these traits on the tree
6:24 showing how each trait changed or
6:26 evolved once, and there's no more than
6:28 one trait change per branch.
6:31 In the tree on the right, there are two changes on the
6:33 first branch from red square to blue circle
6:37 the change in the fill pattern
6:38 from solid stripe and a final change
6:41 from blue stripe back to solid red.
6:43 So, the arrangement of species in the tree
6:45 on the left required three trait changes
6:47 while the tree on the right required five.
6:50 Biologist would therefore consider
6:52 the tree on the left to be the most
6:53 likely pattern of relationship among
6:55 these species given these data because
6:58 it requires fewer trait changes, or it's
7:01 more parsimonious than the tree on the right.
7:04 For phylogenetic studies,
7:06 researchers will often code the data
7:08 numerically which makes analysis easier.
7:10 In this example, the ancestral traits are
7:13 coded with a 0 and derived or
7:15 traits that have changed are coded with 1.
7:24 Let's now consider a slightly more
7:25 complex tree.
7:27 In the phylogenetic tree
7:28 shown here, Species P through V
7:32 form a single monophyletic clade

7:34 Members of this clade are unified by a shared ancestral
7:37 trait called a plesiomorphy.
7:39 Each clade however is defined by a unique
7:41 derived trait called an apomorphy.
7:45 And as the lines in this diagram show,
7:46 apomorphies are found throughout the
7:48 tree defining and characterizing each
7:51 unique clade.
7:54 In this phylogeny, P and Q
7:56 share recent common ancestor and they
7:58 both share recent common ancestor with
7:59 species R.
8:01 Likewise, in the other clade,
8:02 the other species show their own
8:04 patterns of common ancestry among them.
8:07 Lines being drawn on the right show how
8:09 different groupings of these species are
8:11 united different shared common ancestors.
8:16 The ability to read phylogenetic trees
8:18 and interpret the information in them is
8:20 called tree thinking.
8:21 So let's look at some examples and test your tree thinking skills.
8:27 For the phylogeny shown here,
8:29 who is species C more closely related to?
8:32 Species D or Species F?
8:38 The correct answer is that C is equally related to both.
8:42 If you said that C was
8:44 more closely related to D because it is
8:46 closer to it on the phylogeny,
8:48 then you're likely reading across the tips
8:50 which is not a correct way to read these
8:52 types of diagrams.
8:53 What matters are the nodes, and as this
8:56 diagram shows, species C shares the same
8:59 common ancestor with D and F
9:02 and is, therefore, equally related to both of them.
9:06 Now, let's look at another example.
9:09 Who is C more closely related to A or F?
9:14 If you chose A, you may be reading across

9:16 the tips again. Although C is closer to
9:19 A in this phylogeny, it shares a more
9:21 recent common ancestor with F and is,
9:24 therefore, more closely related to that
9:26 species.
9:27 You may have also chosen A because there
9:30 are fewer nodes between C and A then
9:33 there are between C and F.
9:34 This is something called node counting,
9:36 and it is also an incorrect way to
9:39 interpret a phylogeny.
9:40 All that matters
9:41 are the pattern of most recent common ancestors.
9:45 So, to interpret trees correctly,
9:47 don't read across the tips or
9:49 use node counting to determine
9:50 relationships.
9:52 Let's look at one last example.
9:55 This phylogeny shows the hypothesized
9:57 relationships among five different
9:59 clades of animals.
10:01 Based on this tree,
10:03 who would you say that fish are more
10:05 closely related to,
10:06 snails or humans?
10:09 The correct answer is humans, because fish
10:12 share more recent common ancestor with the human clade.
10:16 Here's another tree.
10:17 Does it indicate a different relationship
10:19 among these five species?
10:28 The correct answer is no. Both trees show exactly the
10:31 same relationships despite the node rotations.
10:37 To summarize,
10:39 the ability to correctly
10:40 apply tree thinking allows one to
10:42 interpret and explain the information
10:45 about the patterns of evolutionary
10:46 relationships that are contained in
10:48 phylogenetic tree diagrams.

10:51 Biologists use these diagrams extensively to
10:53 identify monophyletic groups using
10:55 shared ancestral traits that show unity
10:58 and common ancestry among clades and
11:01 derive traits that help to differentiate
11:03 and identify unique evolutionary traits
11:06 and lineages.

Glossary of Key Terms

Apopmorphy: a novel or derived trait or character state that may be found on one taxon or shared among several members of a clade.

Character: any trait or feature of an organism that can be studied or compared among organisms of the same or different species or other taxa.

Character state: the condition of a particular character.

Clade: a "branch" in a phylogenetic tree that includes all of the members of a common ancestor.

Ingroup: the focal taxa of a phylogentic study whose evolutionary relationships to one another are being studied.

Monophyletic: a group that contains all of the members of a common ancestor.

Node: a point in a phylogeny where two clades diverge, denotes the hypothetical common ancestor.

Outgroup: a clade related to the study species that is used to determine which traits are ancestral and which are derived.

Paraphyletic: a grouping of taxa that is not monophyletic.

Phylogeny: an evolutionary tree diagram.

Plesiomorphy: Ancestral character or character state.