

“Helpful or Harmful? Phylogenetic Trees in Public Education About Evolution”

An Honors Thesis

by

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We hereby approve the Honors Thesis of

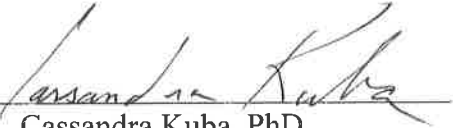
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Abstract

Phylogenetic trees are fundamental to teaching evolution and are defined as, “a graphic representation of the evolutionary relations among living and extinct organisms” (Cela-Conde & Ayala, 2007, p. 374). Their place in the classroom is unquestionable. However, the classroom is only one of many settings in which evolution can be taught. Other non-school public education forums, such as museums, often use phylogenetic trees to illustrate complex evolutionary relationships that are not nearly as simple as they seem. These visual tools often oversimplify evolutionary relationships to the point that they can create misconceptions. This paper seeks to understand the common misunderstandings inherent in phylogenetic trees when used in various public forums. Additionally, the main goal of this paper is to discover which method of visual representations (phylogenetic tree, cladogram, chronologies, etc.) can be used to minimize confusion. This will be accomplished through an extensive review of the literature surrounding the creation of phylogenetic trees, as well as the literature studying the way these trees are interpreted. Ideally, this research will provide guidance on methods of creating and presenting phylogenetic trees and cladograms that avoid bias, and can prevent misconception.

Background

*What's in name? That which we call a rose
By any other name would smell as sweet.
- William Shakespeare, Romeo and Juliet*

Human evolution is not a simple topic. The field itself is divided into a wide variety of different disciplines, with misunderstanding and inconsistencies abounding. Paleoanthropologists are those that choose to explore the wilderness for the fossil remains *in situ*. They often work between the field and the lab; they discover new fossils, interpret their place in the history of human and prehuman¹ ancestry, and ultimately communicate that information to the public. However, much as with many other disciplines, paleoanthropology is not a purely objective field. While all fossils have objective attributes (i.e.- length, width, weight, etc.), these attributes are often viewed subjectively. Classification is often defined by the eye of the beholder. Whereas one professional may see a morphological anomaly, another may see a feature well within the normal range of variation. It is with these subjective viewpoints that the issues with identification, interpretation, and classification arise. To compound the issue, while professionals may bicker over the classifications of individuals, they then have to create or illustrate relationships between multiple individuals, both synchronically and diachronically. Furthermore, what is the best way to *illustrate* the relationship after the relationship is established? This question - which includes various fields like systematics, classification, biological illustration, etc. - has not reached a definitive answer, although there are some obvious easy choices. Cladograms, phylogenetic trees, trees of life...they all attempt to

¹ For the sake of simplicity, the term "prehuman" will be used to refer to all species ancestral to *Homo sapiens*.

visually present the relationships of a variety of species throughout millions of years. However, none of them do it perfectly. Phylogenetic trees, while extremely valuable, are prone to misinterpretation and can do just as much harm as good if they are improperly installed.

Background and Terminology

According to Cela-Conde and Ayala (2007), taxonomy is the field of naming, identifying, and classifying organisms based on similarities and differences. However, while it may be simple to define what a taxonomy is, creating one classification is much more difficult. In order to create a taxonomy there are two different processes that must occur. First, the researcher has to decide which features, attributes, etc. will be classified as “similar or different.” Next, the researcher has to actually sort those features and create a taxonomy. Finally, if the researcher so chooses, he or she can create a visual interpretation of that taxonomy, such as a phylogeny (defined below), as an alternative method of conveying the information that it contains.

Systematics, the study of biological diversity, its evolution, and the way it is classified, is governed by a few basic tenets. These tenets are used to classify individuals into species, genera, etc. In order to separate one species from another, each set of individuals in a species should be internally homogeneous such that there must be more variation between species than within any one species and each species must have distinct characteristics that identify it in order for those species to be valid. Similarly, a species can be defined as an empirical unit comprising one or more individuals (thus, a species cannot exist without any members) (Nass, personal communication, 16, Feb. 2017).

It is important to note the differences between using systematics to create a taxonomy of living organisms and using it to create a taxonomy of extinct organisms. While a biological species might be defined by its geographical distribution or its genes, oftentimes extinct species can only be identified through fossil remains (Cameron & Groves, 2004). The alternative as Ezard et al. (2013) puts it is, “a (more or less) literal reading of the fossil record to assign specimens to morphospecies, that is, species-level taxa identified from morphology” (p. 746). In most cases of paleoanthropological specimens, DNA is not preserved, so assignments to species must be done on the basis of morphology alone. This is made particularly difficult by the old age and poor preservation of many of the fossils. By the far the most common fossils recovered are the teeth and parts of the cranium, which while important, do not always paint a large enough picture to create definitive hominin taxonomies.

Systematics can produce a visual representation of species and their evolutionary context known as a phylogenetic tree. Specifically, a phylogenetic tree is a “graphic representation of the evolutionary relations among living and extinct organisms” (Cela-Conde & Ayala, 2007, p. 374),

When considering evolution, it is important to consider homology and analogy. Homology refers to a trait that is present in two individual species that was derived from a single ancestor species. Homologous traits are similar because they are inherited, and, therefore, may change as the individual species evolve further (Cela-Conde & Ayala, 2007, p. 35). Analogous traits are similar in function, but not necessarily similar in form (Cela-Conde & Ayala, 2007, p. 35) and, unlike homologous characters, are not the result of common ancestry. Homologous and analogous traits are sometimes difficult to tell

apart in living individuals, but, upon further inspection, can be differentiated. Celsa-Conde and Ayala (2007) give examples of both homologous and analogous traits. A homologous trait might be something like the hand bones of many mammals (Fig. 1). Analogous traits may appear similar externally, but upon closer inspection are not. These might include wings, like those on any animal or insect that can fly (Celsa-Conde & Ayala, 2007, p. 36). The mechanisms behind homologous and analogous traits are divergent and convergent evolution respectively. Divergent evolution occurs when one species splits into two. Conversely, convergent evolution creates traits that appear similar in species that may be extremely distantly related.

Furthermore, when analyzing similarities and differences, it is important to recognize the difference between subjective classifications. For example, if a fossil were to be considered irregular, is that because it is actually is, or because the excavator merely believes it to be? For example, one commonly discussed variable in human evolution is cranial capacity. If a paleoanthropologist discovers two fossils, one with a 1,100 cubic centimeters (cc)

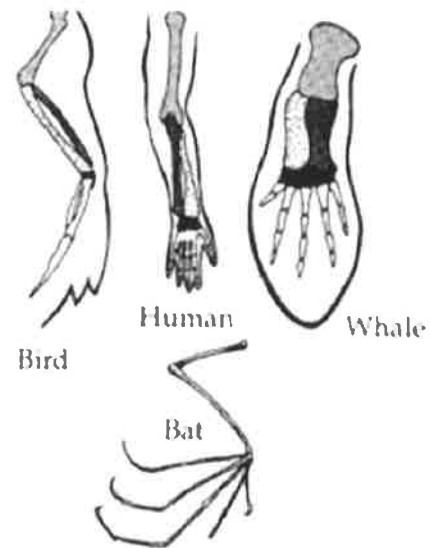


Fig. 1

volume and one with a 950 cc, can they be classified as the same species with a wide variety of cranial capacity, or are they necessarily two different species?

Another important consideration, especially in the context of the way paleoanthropologists classify different species, is the debate of lumping versus splitting. This debate involves the way a new species will be classified when it is added to all of

phylogeny. For example, one of the best-known examples of splitting and lumping is the placement of the genus *Paranthropus*. While some paleoanthropologists choose to classify the genus as a separate one because of its heavy robust chewing muscles and large teeth, others have chosen to include them with *Australopithecus*, which are more gracile.

Charles Darwin

As is with most discussions on evolution, one of the most important historical



Fig. 2

figures to recognize is Charles Darwin. While Darwin is widely known for his popularization of the theories of evolution, he is also well known for his illustration in “Notebook B” from 1837 (Fig. 2). This illustration, while well known, is not the end-all-be-all of phylogenies nor was it the first. In fact, while it conveys some information about the visual representation of evolution, it is also kept deliberately vague as to avoid making large claims that Darwin would not easily have been able to support at the

time (Shtulman; Torrens & Barahona, 2012). Darwin’s use

of a branching “tree” was meant only to be an abstract example; it was not meant to become the rule (Torrens & Black, 2012). However, as with many things, this is not how the “tree of life” was perceived. While Darwin illustrated this early cladogram, he was not the first to create a true phylogenetic tree of life. That distinction belongs to Ernst Haeckel (Hoßfeld, Watts, & Levit, 2017).

Ernst Haeckel

As is to be expected, though, the tree of life in the form of branching lines quickly became popular very soon after Darwin. Perhaps the most influential person to be influenced themselves was Ernst Haeckel. Born in 1834 and originally trained as a physician, Haeckel was so stricken by Darwin's writings that he quickly abandoned his own practice, started studying biology, and practically became one disciple of Darwin (Nicholson & Margett, 2007, p. 32). In fact:

...when Haeckel and Darwin met at the Englishman's home in Kent in October 1866, the German was reportedly so enthusiastic in his support of Darwin's theory that his host was initially rather disorientated by this devoted disciple who had extrapolated his own theory further than he would himself have dared. (Nicholson & Margett, 2007, p. 32)

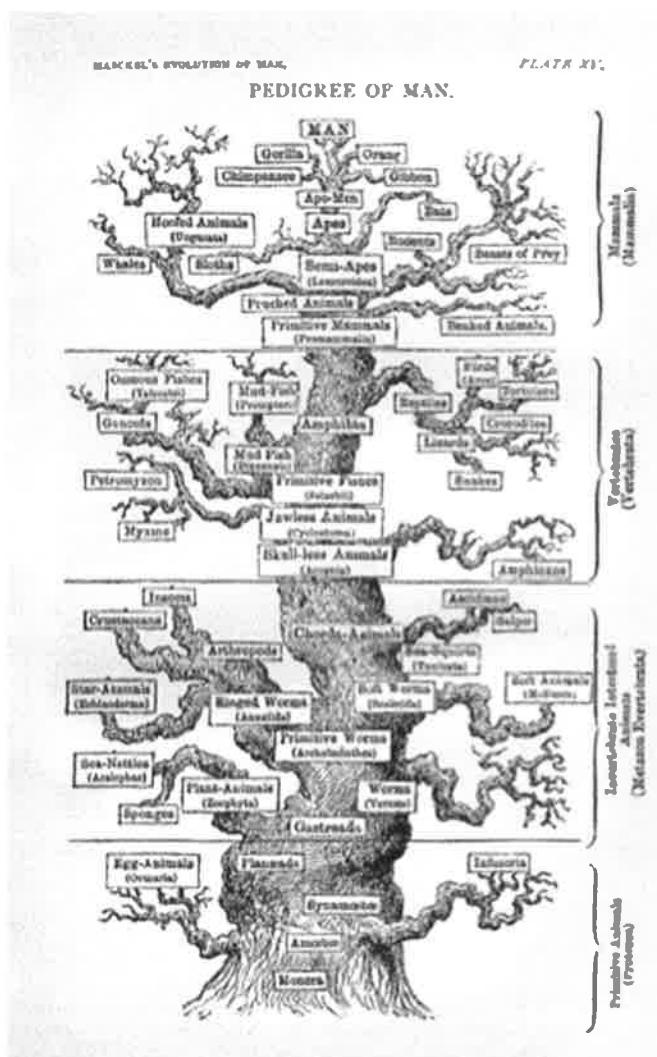


Fig. 3

Interestingly, Haeckel believed so strongly in Darwin's writings that he began to use them as a way to combat organized religion on the whole, and eventually used his own warped version of evolution to proclaim that certain races of humans were superior, a theory that can be traced to the organization and foundation of the German Nazi Party (Nicholson & Margett, 2007). Haeckel's work with trees is extremely relevant to the issue of their use because he was, by and large, the man who popularized their use.

Haeckel's "Pedigree of Man" (Fig. 3) from his 1874 *Anthropogenie oder Entwicklungsgeschichte des Menschen* (Evolution of Man) was one of the first and most "complete" phylogenetic trees, accuracy aside (Hoßfeld, Watts, & Levit, 2017). While Haeckel was a huge proponent of Darwin's ideas, he lacked Darwin's conservatism, which meant that he was not afraid to make large claims, while sometimes lacking evidence to truly justify them. For example, "in contrast to Darwin himself, Haeckel's objective was not only to visualize the principle of divergence but also to suggest phylogenetic trees illustrating the real phylogenetic relationships between different organismic groups" (Hoßfeld, Watts & Levit, 2017, p.101). So, while Haeckel contributed greatly to the use and proliferation of phylogenetic trees, he may have done so overzealously, and without the restraint and peer review that is typically used today.

Willi Hennig

While Willi Hennig (1913-1976) came later than either Darwin or Haeckel, he was no less important. Hennig created the field of cladistics, which classifies living species based on their evolutionary relationships (Reader, 2011). Eventually, Hennig's methods were applied to fossil specimens as well, and are most simply defined as using similar morphological features to infer close relationships (Reader, 2011). However,

cladistics often creates relationships that are dichotomous in nature. This means that one “mother species” would split into two “sister species” (Rieppel, 2011). This model also proposes, by its very nature, that the mother species would then always go extinct. For example, if it were decided that *Homo habilis* split into *Homo erectus* and *Homo ergaster*, then *Homo habilis* would cease to exist. This dichotomous nature is what has led some members of the biological community to question both Hennig’s work and the nature of cladistics as a whole (Rieppel, 2011). However, while the application of these methods to a phylogenetic framework has been called into question, there is no question that they are still used at least as a methodological principle (Rieppel, 2011).

The Problem

Phylogenetic trees are used commonly as a method of illustrating and teaching evolution. However, they can sometimes be misconstrued. While these trees might be thoroughly explained in a classroom where evolution is being taught, they are also used in public outreach, such as in museums and other public displays. It is here, in these public forums, that phylogenetic trees are potentially harmful to interpretation and education.

The Teleological Fallacy

Probably the main issue with illustrating phylogenetic trees is a teleological one. Many trees include humans, oftentimes either at the top or at the furthest right, which often leads to the misconception that humans are the product of evolution, and that it ends with them. This thought is most thoroughly explained by Sandvik (2009). While she explicitly uses the term “anthropocentrism,” it does not pertain specifically to humans; it can refer to *Homo sapiens*, or really any other group of hominins in which *Homo sapiens*

might be included. Cela-Conde and Ayala (2007) add, “A relevant consideration is the urgent need to avoid anthropocentrism. Often in the past, an anthropocentric bias has imposed mistaken concepts, such as hierarchical relation among living beings with humans in the role of masters of nature” (p. 52).

Throughout the literature, there is a broad emphasis on misconceptions brought about by poor implementation of phylogenetic trees (specifically in museums)

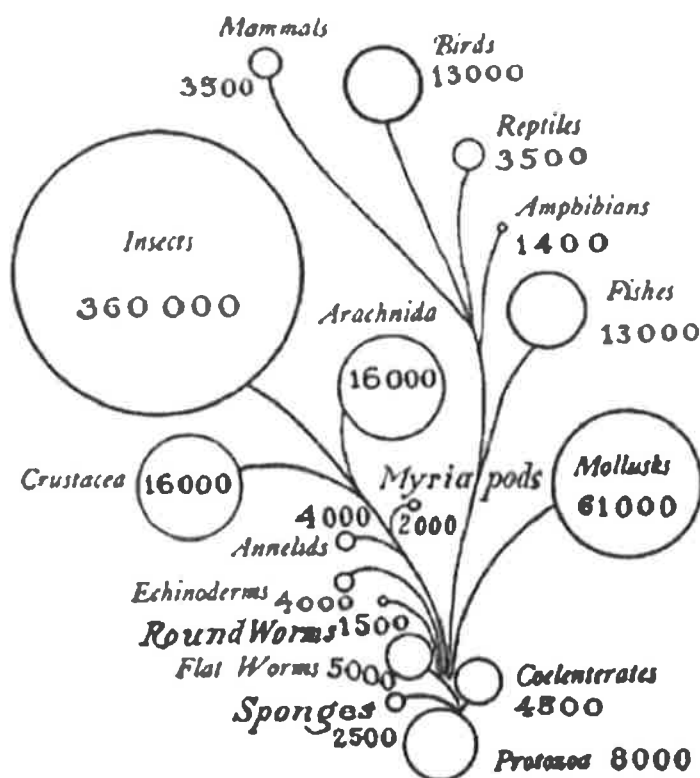


Fig. 4

(MacDonald & Wiley, 2012; Torrens & Barahona, 2012). There is also much research upon when it is appropriate to teach children to read evolutionary trees (Ainsworth & Saffer, 2013), whether or not college students can interpret them (Phillips, Novick, Catley & Funk, 2012), and about problems inherent in tree drawing in general

(Shtulman; Sandvik, 2009; Ricou & Pollock, 2012). However, another consideration to make, as extreme as it may sound, are the consequences of allowing these trees and other evolutionary representations to be misconstrued. The most extreme example of misunderstanding of evolution is the 1925 Scopes Trial (Clark, 2001).

Many of the issues that arose from the Scopes Trial stemmed from fundamental misunderstandings, not only in the way evolution functions, but also in the way it is depicted. The trial was brought about when a high school teacher taught his class about evolution using a simple phylogeny (Fig. 4) (Clark, 2001).

The main opponent to the use of this image was William Jennings Bryan, who at one point in the case declared that, “he was not a mammal” (Clark, 2001, p. 1275). The reason behind this outburst was not only because of a misunderstanding, but was also hugely anthropocentric. While Bryan clearly understood that he was a mammal, his main point was that “man” should have its own circle in this representation. He later claimed, “No circle is reserved for man alone. . . .What shall we say of the intelligence, not to say religion, of those who . . . put a man with an immortal soul in the same circle with the wolf, the hyena, and the skunk?” (Clark, 2001, p. 1279). Not only is this outrightly anthropocentric, it is also insulting to the illustrator who only intended to create an easy to understand diagram which might be used to teach a complex topic to elementary school children.

Anagenesis v. Cladogenesis

Anagenesis and cladogenesis are two important concepts that are typically poorly represented in phylogenetic trees. Figure 4.5 shows various ways in which *Homo sapiens* and *Homo neanderthalensis* may have interacted in the evolutionary timeline.

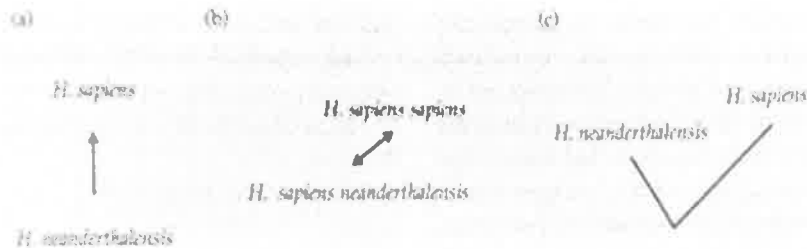


Fig. 4.5

(a) represents anagenesis in which Neanderthals evolved directly into modern humans over the course of time. (b) represents a situation in which humans and Neanderthals were contemporaneous subspecies that exchanged genes. (c) represents what is commonly known as cladogenesis. Cladogenesis indicates a common ancestor between the two species, and is commonly used in cladograms to show the relationship between two or more species. One of the most common complaints of people who do not understand evolution is that “they did not evolve from monkeys.” This belief requires an anagenetic view of evolution, which, ironically, is usually absent from most phylogenies. However, this anagenetic fallacy is not only used by laypeople, but also by many paleoanthropologists as well. As Groves (2007) states in his paper on *Homo floresiensis*, “Until about 20 years ago, many people assumed an almost straight line of human evolution: *Australopithecus afarensis*—*Australopithecus africanus*—*H. habilis*—*H. erectus*—*H. Sapiens*” (p. 123).

Tree Design

The way in which phylogenetic trees are designed is an important part of the way they are received. However, is it the case that these trees are designed in a way that is simple enough for a museumgoer to understand? Most likely, the answer is no. Tree design is done through a wide variety of methods, most of which necessitate the use of

some type of algorithm or computer program. The first and most important aspect to consider is what the source of the data for the tree will be. While most phylogenies today are built using genomic data, they were originally created using morphological data (Wiley et al., 2005, p. 431).

With that being said, what are some ways in which phylogenetic trees are made? In consideration of the data available for many of these fossil species that would be covered in the realm of human evolution, it is more likely that there will be an emphasis on morphological data. This emphasis, the focus on shape, is called “geometric morphometrics” (Wiley et al., 2005, p. 432). In this specific case, Wiley et al. (2005) created a phylogeny based of Old World Monkeys, relying entirely on casts of the crania of nine different species. Their method includes a 3D scanner, which takes measurements of various landmarks on the crania and subsequently compares them against each other. This technology, in combination with a series of numerical algorithms and the overriding computer program, was able to create a phylogeny based entirely on morphology. Additionally, this program was able to place some of the individual species as nodes on the tree, which makes them an important point at which cladogenesis could have occurred (Wiley et al., 2005).

When genetic data is available, especially in the form of a specific nucleotide sequences, there are other programs specifically built to analyze these data. For example, one program that is designed for exactly such a purpose is MEGA4 (Molecular Evolutionary Genetics Analysis version 4.0) (Tamura, Dudley, Nei, & Kumar, 2007). Most simply put, this software is made for, “mining web databases, performing automatic and manual sequence alignment, analyzing sequence alignments to estimate evolutionary

distances, inferring phylogenetic trees, and testing evolutionary hypotheses” (Tamura et al., 2007, p. 2). Specifically, in this new version of MEGA, the designers included the ability to consider Maximum Composite Likelihood (MCL) as a way of “estimating evolutionary distances between all pairs of sequences simultaneously” (Tamura et al., 2007, p. 2). This program cannot only interpret the data that it is given, but can automatically return hypotheses based on that data about the evolutionary processes at work, while also creating a phylogeny to match (Tamura et al., 2007). While this may seem to be a miraculous and simple solution to the problem of how to create a phylogeny of human evolution, genomic data is often hard to come by in many of the fossil specimens recovered because of the extreme antiquity and degradation of genetic material, which largely precludes the use of this methodology. However, it is possible, and has been done, usually in more recent ancestors such as the Neanderthals.

The Solution

Surely there is not an easily solution to this problem, and there is likely no one single answer, but in order to best address the issue, this analysis will be as narrow as possible to satisfy the needs of a museum. In a way, the purpose of this solution is to cater to the lowest denominator. As museums are places of wide and varied education, they do not typically focus on any one specific topic, with some exceptions. As such, evolutionary education is likely better suited as being presented simply to reduce confusion

Occam’s Razor

Occam’s Razor is a very simple, yet extremely important, philosophical and scientific principal. When interviewing over 40 different scientists about the importance

of Occam's Razor, Riesch (2010) asked, "When you are faced with two theories (hypotheses, statements etc) that, other things being equal, both describe the available evidence equally well, is it sensible to choose the simpler one?" (p. 77). Simply put, when faced with two possibilities that are otherwise equal, to use Occam's Razor is to choose the simplest explanation. It is important to make a distinction though, as Riesch does, between making something simple and simplistic. Here, the distinction means that while it may be prudent to present something simply, it is important that it retains its validity. It goes without saying that phylogenetic trees can be used for a wide variety of

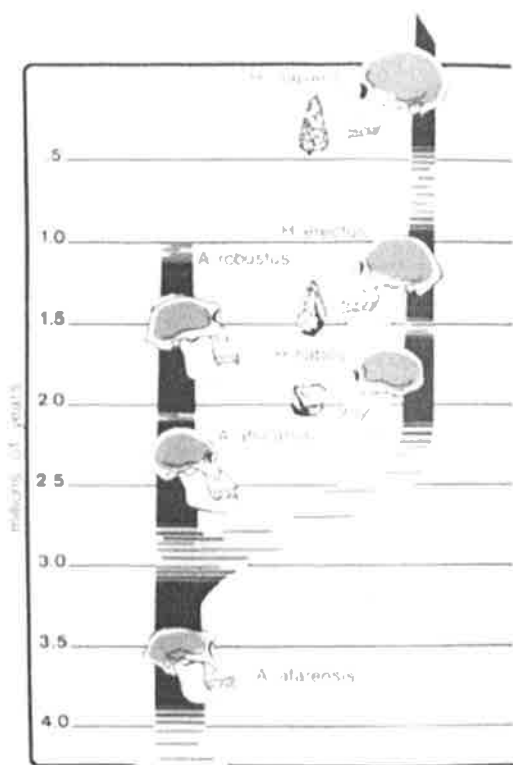


Fig. 5

purposes. As Shtulman explains, they can be used to illustrate "patterns of speciation and extinction across time, patterns of speciation and extinction across geography, changes in the complexity of existing lifeforms, or changes in the frequency of different anatomical plans" ("Missing Links..."). Furthermore, they could be used for any combination of these purposes. Of course, with each purpose added to a single tree, the complexity will increase. As a general rule, it seems simple to say that as

complexity increases, the possibility of misconceptions and misunderstanding also does. This is where Occam's Razor comes into play. While it might seem to the layperson that all scientists are out to make their work sound as complex and confusing as possible, that

is not always the case. One excellent example of the use of Occam's Razor is given by Dr. Johanson in his explanation of where to place his new australopithecine find on the tree of human evolution. He states, "The diagram that resulted represented, in our opinion, the simplest - or, to use a word favored by scientists, the most parsimonious - ways of arranging all the existing fossils and at the same time being respectful of their differences" (Fig. 5) (Johanson & Edey, 1981, p. 283). Here Johanson makes two points that have been previously addressed. The first addresses Occam's Razor (here called parsimony), in which he states that effort was made to keep the diagram as simple as possible by using the simplest explanation. Second, he makes a point of illustrating that their tree is respectful of both the similarities and differences of the various species included. The main difference between Fig. 5 and Fig. 6, however, is the inclusion of an entirely new predecessor to any of the trees.

Present Options

There exists a variety of different ways that phylogenetic trees can be presented,

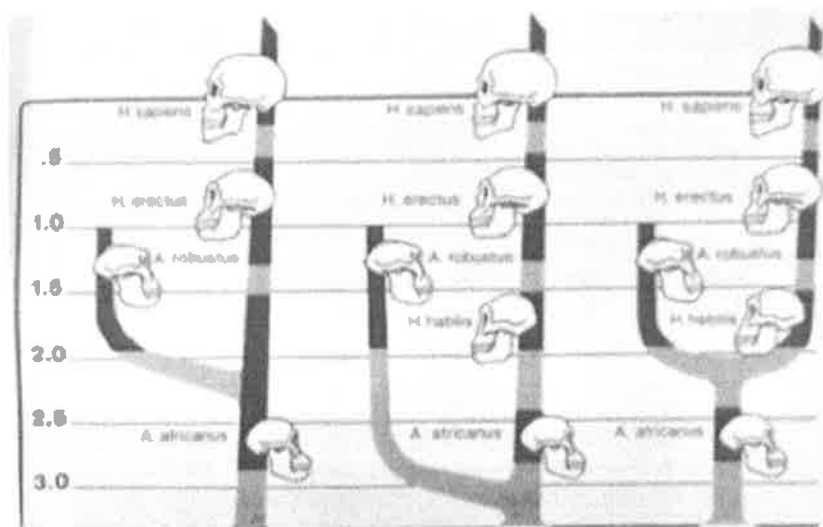


Fig. 6

all with their own strengths and weaknesses. These include: branching trees, spirals, bracketed trees, and clumped trees.

Branching. Branching trees are possibly the most common forms of phylogenetic trees, at least in terms of pure numbers. These diagrams most closely resemble the aforementioned “tree of life,” often originating at a single point and branching off at a series of nodes from there. Figure 6 (Johanson & Edey, 1981) shows a simplistic series of branching trees, which represented the three main hypotheses for how human evolution had occurred as understood in the 1970s.

Spiral. Of all of the types of trees, spirals are likely the least common. However, they can often dispel some of the biases that are inherent with the other types. Although spirals may seem to minimize the possible problems, they are definitely more complex to interpret from the beginning. Ricou and Pollock (2012) were concerned with how to best display the evolution of all life, while including as much detail as possible and reducing bias simultaneously. When asked if their creation portrayed this information in a manner that was not confusing, Dr. Pollock had this to say:

So the simplest answer to your question is that many people had some level of confusion. However, when we first created the image, the multiple levels of goals [were] that murals were going to be representative of the ~4 billion years of life, and that the diversity be represented. We also had the goal and plan that as the murals were exhibited in museums, that we would have docents trained to help guide the patrons. We also changed the signage to help guide their viewing. In general, with just a little bit of guidance, most people ‘got it’ and could track through time, lineage and could find when traits first emerged. (Pollock, personal communication, 28 March 2017)

Figures 7, 8, and 9 all depict different variations of the Spiral that Ricou and Pollock created. They emphasized the ability to manipulate their creation and use it to fit a specific niche, but they do also recognize that this flexibility inherently introduces bias as well (Ricou & Pollock, 2012, p. 24).

Fig. 7. *Spiral of Life II: Plant and Animal Co-Evolution*, digital art on canvas, 30 x 40 in, 2009. This piece was installed at Phipps Conservatory & Botanical Gardens and identifies major steps in the evolution of plants and their co-evolution with vertebrates and arthropods. In this piece, and in *Spirals I and III*, we made use of perspective to distort the spiral shape and focus on the most relevant set of branches. In this case, we focus on the plant branches and show key evolutionary milestones such as the appearance of vessels, seeds and flowers. (© Joana Ricou and John Pollock)

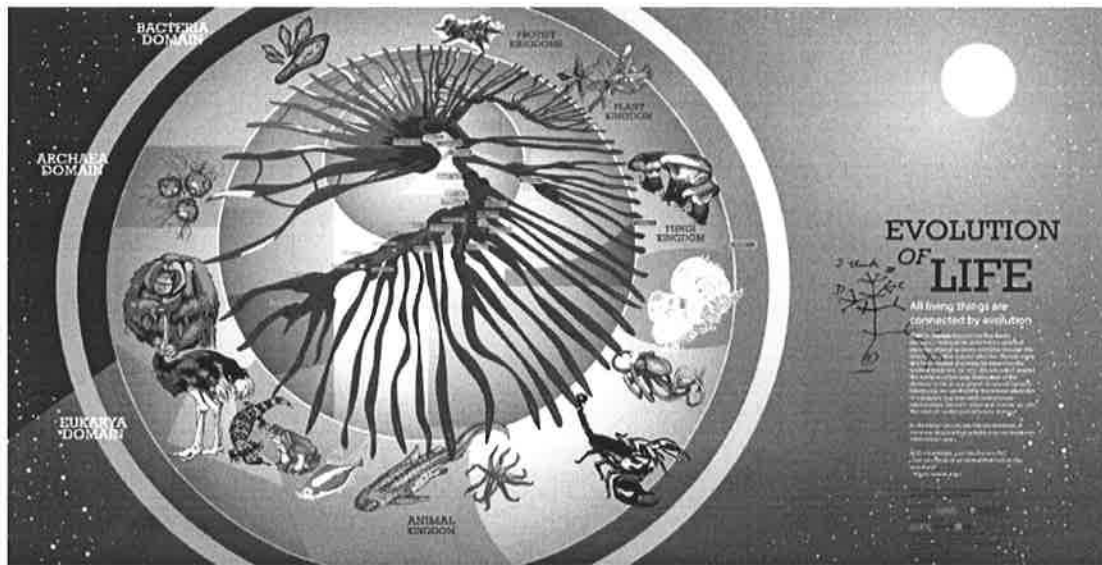


Fig. 8. *Spiral of Life III*, detail. Evolutionary milestones in the evolution of animals were explicitly labeled and illustrated. (© Joana Ricou and John Pollock)

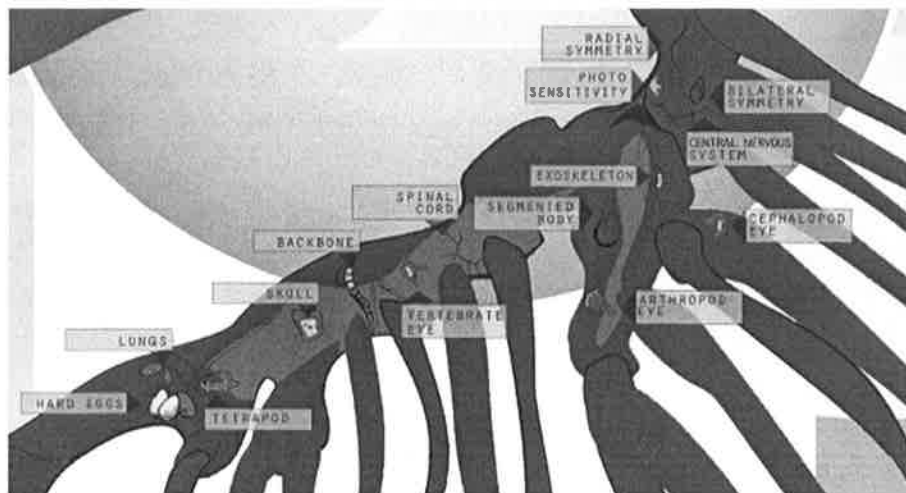


Fig. 9. *Spiral of Life V: Bird Evolution*, digital art on cintra, 6 x 5 ft, 2009, National Aviary, Pittsburgh PA. This piece contextualizes the evolution of modern birds. The main spiral is depicted in the lower center and the "dinosaur" branch is exploded to show the demise of the dinosaurs and the relatively recent evolution of birds and their diversification. (© Joana Ricou and John Pollock)



Bracketed. Bracketed trees are also quite popular, and use brackets to create monophyletic groups. These types of diagrams are usually easy to trace descent through, and make the node at each split very obvious. However, it should also be noted that bracketed trees, as well

as branching ones, could be displayed in multiple ways while still conveying the exact same information. For example, in Figure 10, if letters E and D

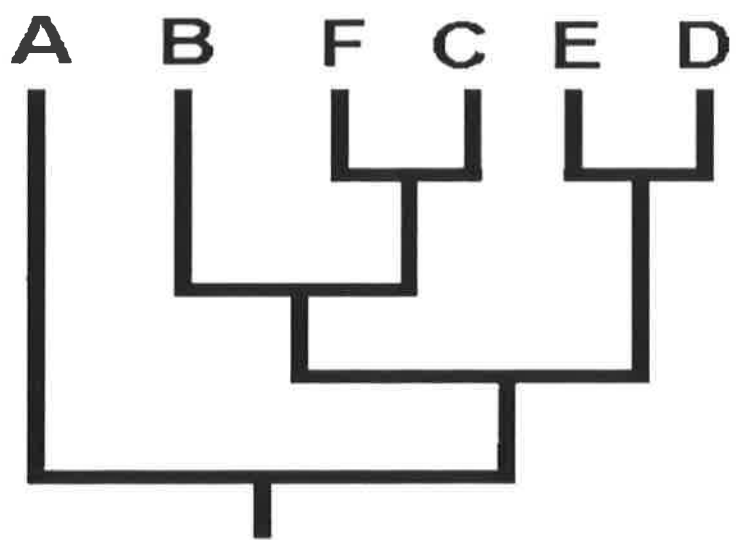


Fig. 10

represented *Homo sapiens* and *Homo neanderthalensis* respectively, they could switch spots and retain their phylogenetic relationships perfectly.

Clumping. Clumping is different from the other three types mentioned above in

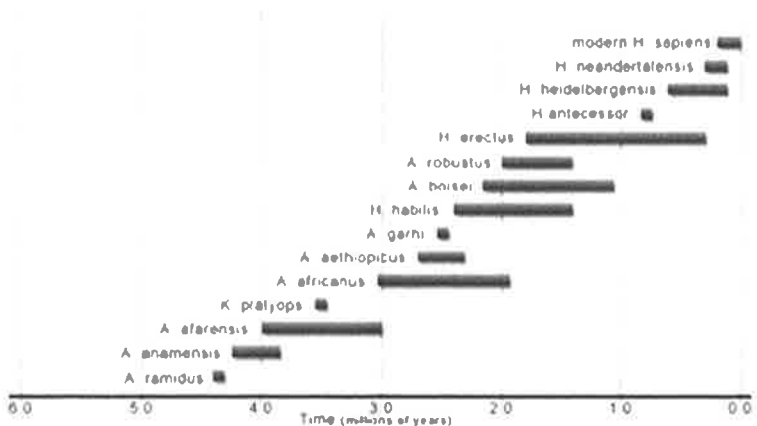


Fig. 11

aspect than most other types though. Figure 11 depicts a chronology, and not a

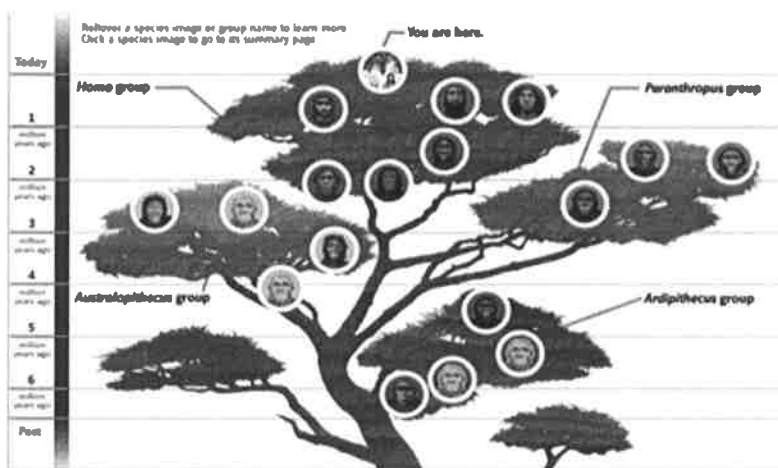


Fig. 12

but does not organize them in a way that implies teleology.

A Possible Solution

Because the focus of this paper is to understand and accommodate the average museum goer, I will use my own experience as a museum patron as my basis for

that it does not necessarily include distinct phylogenetic relationships in the form of lines connecting the different species. They can and typically do include a much stronger temporal

phylogeny. It organizes the species in a chronological order, but does not depict any phylogenetic relationships. Figure 12, on the other hand, organizes the individuals into groups,

interpretation. I have chosen to approach the solutions to the issues mentioned above this way in order to ground my thesis in reality. I have experienced plenty of museums that discuss evolution at some point, and I have seen every one of these types of trees displayed in them. Even though I hope to someday study human evolution much more closely, I understand, and suffer from, much of the confusion that various authors have mentioned in respect to the shortcomings of some of these diagrams. I believe I can speak to the needs and wants of the average museum goer, so I will attempt to do just that.

In general, my strategy to reform the way that museums depict evolution graphically favors a simple rather than a complex approach. While I have never liked the phrase “ignorance is bliss,” I believe it is applicable here. In my opinion, I believe it is better to take a simple approach to teaching and leave people with a basic understanding, rather than to overwhelm them with information and leave them questioning what it is that they just heard. In the case of evolution and its visual representation, I believe it is better to use a timeline much like Figure 12. A tree such as this loosely implies relationships between the various groups in the tree, but does not make them explicit. This has the benefit of simplifying evolutionary concepts to the point that, I believe, anyone can understand them. Furthermore, it allows for the easy addition of new or rearrangement of existing species as well. For example, if paleoanthropologists decided that one of the *Paranthropus* group would now be considered an *Australopithecus*, that species’ image could easily be moved without disrupting any established phylogenetic relationships.

Overall, I believe that the purpose of a museum is similar to that of general education courses throughout college. While some students are not interested in some of

the courses they are forced to take, a good professor can easily change their opinion and help them enjoy the course even if they do not plan to pursue that particular field. Museums are much the same. While most museums have a theme (i.e. - natural history, American history, contemporary art, etc.) they typically illustrate the theme through a wide variety of displays. Human evolution (given the examples listed above) would typically be restrained to a Natural History museum. However, it will likely not be the focus. So, it is likely that many patrons will come to the museum uninterested in learning about evolution, and if it is not portrayed in a way that is simple and comprehensible, then it is likely they will come away either ignorant or apathetic of any evolutionary lessons they might have otherwise learned.

Ironically, the example I most prefer (Fig. 12) comes from a museum (The Smithsonian National Museum of Natural History). Within the same museum, however, there are many examples of cladograms with exactly the same issues discussed above

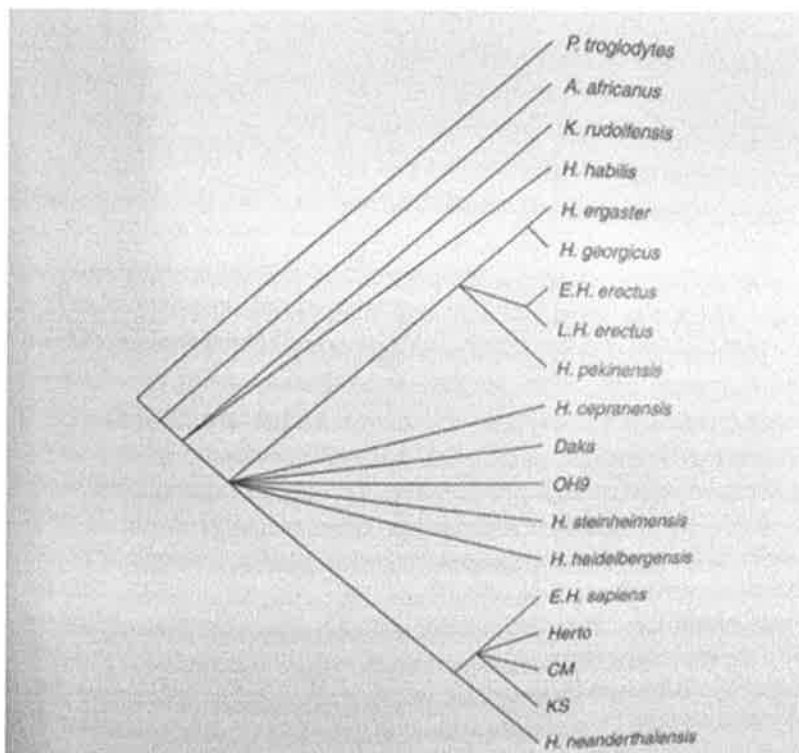


Fig. 13

(teleology and anthropocentrism). When I first began this project I wanted to focus on specific morphological characteristics of the various fossil species as I believed that this would lead to a purely

unbiased representation of human evolution. Here, in Figure 13, Cameron and Groves (2004) have done just that. This tree shows a wide variety of species and individuals all organized by 27 cranial traits. However, as you can see, this is probably the most complex tree of any shown in this paper (with the exception of the spirals). Additionally, it lacks a chronological control, which implies that all of the individual species in the tree are contemporaneous when some would likely have been ancestral to others. So, when I eventually decided to focus more greatly on the implications behind public outreach, I moved my priorities from being unbiased to being simple and easy to understand. I do think, though, that simplicity sometimes works to diminish bias as well.

Conclusions

With all of the issues considered above, I believe that Occam's Razor is, by far, the most important factor to consider when implementing phylogenetic trees in museums where the average visitor may not have extensive background knowledge of evolutionary theories. My ultimate conclusion is that simple grouped phylogenies, such as in Figure 12, work best in this setting. Figure 12 contains both phylogenetic information as well as chronological information, while remaining simple. While Figure 12 may seem anthropocentric, *Homo sapiens'* place at the top of the tree can be explained by its place on the timeline. Seeing as all other species are extinct, it makes sense that *Homo sapiens* is at the top, and therefore the present. Additionally, I believe this resolves some of the main issues found in both bracketed and branching trees as well. Oftentimes, these types of diagrams do not include temporal aspects at all, and as such, the inclusion of the species within the diagram on a single plane may imply to some viewers that they all exist simultaneously.

Figure 12 is nearly the ideal form of phylogeny that I was looking for, but there are two possible additions that I do not think would introduce too much confusion. The first addition that might improve it would be a simple geographic element. Overall, all four groups are found in Africa to some extent, and only parts of the *Homo* group ever left. With that in mind, it should be easy to indicate that the other three groups were constrained to Africa, while perhaps illustrating where the rogue elements of the *Homo* groups might have wandered off to. This could include a small representation of the continents that these species might have been found upon next to the depiction of the species itself. The second addition is very similar to the first, but focuses on the fossils themselves, rather than where they were found. With this in mind, the tree could be a flip board of sorts, with which the patron can flip the image of each species to see the bones most commonly discovered in association with each fossil. Most commonly this would be restrained to the teeth and cranial bones, with some exceptions like in the case of Lucy, an australopithecine with about 40% of the bones intact. These two changes, which add extra data without complicating the image any more, would likely be able to enhance the knowledge that the patrons would be able to glean from such a display.

In paleoanthropology, at least in reference to the big picture, there is very little debate about the overarching themes of evolution. There is no question that *Homo sapiens* evolved from some earlier *Homo* and likely from one of the australopithecines before that. However, the debate begins when individuals begin to explain which individual species are ancestral and which are not. Whereas one paleoanthropologist may believe that *Australopithecus africanus* may be directly ancestral to the *Homo* genus, another may disagree and argue that it is not. Figure 12 resolves this issue by grouping

highly similar individuals together, in this case by genus, and leaving the relationships between the genera more ambiguous. Additionally, the groups are arranged in a way that relies on chronology more than phylogeny.

As I stated from the very beginning, human evolution is not a simple topic. Therefore, my ultimate goal became to make it as simple as possible so that it can be understood. At the end of the day, my goal is to make this field accessible to as many as possible, and in order to do that, the basic concepts, those concepts likely to be found in museums, have to be simple.

Afterword

In a reassuring discovery via Dr. Tebbitt, I was informed that the Natural History Museum in London might have had an exhibit on human origins that might interest me. I can say that he was correct, and I was happy to see the image on their homepage (Fig. 14). I was very happy to see this image because it is exactly the type of diagram I was hoping would be implemented in a situation such as this, which certainly made me feel as though this research is worthwhile.

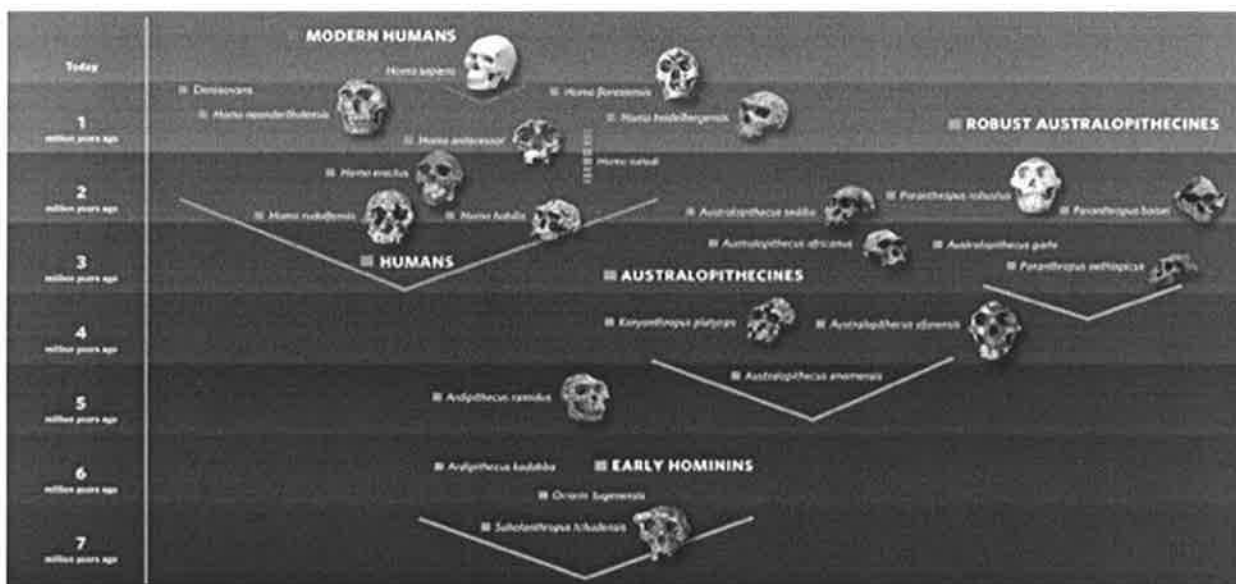


Fig. 14

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Image Credits

Fig. 1 - Cela-Conde, C. J., & Ayala, F. J. (2007). *Human evolution: Trails from the past*. New York, NY: Oxford University Press.

Fig. 2 - Darwin, C. (1837). *Notebook "B"* (public domain)

Fig. 3 - Haeckel, E. (1879) *Evolution of Man—Pedigree of Man Plate XV* (public domain)

Fig. 4 - Clark, C. A. (2001). Evolution for John Doe: Pictures, the public, and the Scopes trial debate. *The Journal of American History*, 87(4), 1275-1303.

Fig. 4.5- Cela-Conde, C. J., & Ayala, F. J. (2007). *Human evolution: Trails from the past*. New York, NY: Oxford University Press.

Fig. 5 - Johanson, D., & Edey, M. (1981). *Lucy: The beginnings of humankind*. New York, NY: Simon and Schuster.

Fig. 6 - Johanson, D., & Edey, M. (1981). *Lucy: The beginnings of humankind*. New York, NY: Simon and Schuster.

Fig. 7 - Ricou, J., & Pollock, J. A. (2012). The tree, the spiral and the web of life: A visual exploration of biological evolution for public murals. *Leonardo*, 45(1), 18-25.

Fig. 8 - Ricou, J., & Pollock, J. A. (2012). The tree, the spiral and the web of life: A visual exploration of biological evolution for public murals. *Leonardo*, 45(1), 18-25.

Fig. 9 - Ricou, J., & Pollock, J. A. (2012). The tree, the spiral and the web of life: A visual exploration of biological evolution for public murals. *Leonardo*, 45(1), 18-25.

Fig. 10 - Shtulman, A. (n.d.). *Missing links: How cladograms reify common evolutionary misconceptions*. (Unpublished doctoral dissertation). Occidental College, Los Angeles.

Fig. 11 - <http://darwiniana.org/trees.htm>

Fig. 12 - <http://humanorigins.si.edu/evidence/human-family-tree>

Fig. 13 - Cameron, D. W., & Groves, C. P. (2004). *Bones, stones and molecules: "Out of Africa" and human origins*. Burlington, MA: Elsevier Academic Press.

Fig. 14 - <http://www.nhm.ac.uk/discover/the-origin-of-our-species.html>