

RUNNING HEAD: Evolutionary Trees in Museums

Communicating Phylogeny: Evolutionary tree diagrams in museums

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Abstract

Tree of life diagrams are a graphic representation of phylogeny—the evolutionary history and relationships of lineages—and as such these graphics have the potential to play a significant role in conveying evolutionary ideas and principles. The interpretation and understanding of evolutionary trees involves a complex interaction between prior knowledge, a grasp of underlying concepts such as similarity, common ancestry and relatedness, and an ability to read the relationships depicted in a schematic tree diagram. This study explored the use of tree diagrams in exhibits across 207 informal science institutions, and analyzed the form and content of 185 trees used in these settings. The findings indicate that evolutionary trees form a common graphic element in many museums, and are broadly similar to those in biology textbooks. The ambiguity of some graphic elements makes interpretation difficult, which may be ameliorated by labeling and explicit references to the diagram in interpretative text. In addition, some aspects of how trees are presented may hinder their use by visitors, and several diagrammatic aspects have the potential to reinforce misconceptions. Informal science institutions play an important role in teaching evolution, and further research is needed to explore how visitors understand these diagrams to help inform effective strategies for communicating about the tree of life.

Introduction

The tree of life represents a core concept in the teaching of biology – phylogeny. Phylogeny charts the evolutionary history of life, and represents the relationships between lineages as they change through time. Tree diagrams have the potential to play a significant role in conveying evolutionary ideas and principles. Informal education environments such as museums are a critical part of how the public accesses science information, including evolution (Diamond & Evans, 2007; National Science Board, 2008); therefore, an understanding of how, and in what form, tree diagrams are used in museums is an important part of supporting the development of evolutionary thinking in museum visitors. How people interpret and understand evolutionary trees is a complex interaction between their prior knowledge and understanding of underlying evolutionary ideas such as similarity, ancestry and relatedness, and their ability to read the relationships depicted in a schematic tree diagram.

Few museums use phylogeny as an organizing principle in their galleries; however, evolutionary diagrams form a major graphic element in many museums (Diamond & Scotchmoor, 2006). In natural history museums, visitors can see a wide range of historical depictions of the tree of life depending on when an exhibit was developed and the research emphasis of the scientific curators. Each new exhibit updates the graphic representation of the tree in accordance with current usage or discipline preferences, but the older depictions often are kept on display, so one can view a range of different presentations of tree diagrams even within a single institution.

Given the diversity of depictions of the tree of life, one might ask what people understand from these different graphic representations. While work has been, and continues to be done into the use of trees for teaching about phylogenies with students in a structured learning environment (Baum, DeWitt-Smith, & Donovan, 2005; Novick & Catley, 2007), there is a gap in our knowledge about how trees are used and understood outside of a formal instructional framework.

This study begins to address the issue of how to effectively present the tree of life to visitors by: (1) exploring the use of evolutionary trees in informal science institutions; and (2) analyzing the tree diagrams currently used in these settings to assess their potential educational efficacy in light of existing research on teaching about the tree of life.

Methods

Data was collected on the use and forms of evolutionary tree diagrams from informal science education institutions including museums, science centers, zoos & aquariums. This was done by directly contacting institutions by email and through an online survey of informal organizations asking whether they use tree graphics as part of their exhibits. This provided some general information about the overall prevalence and distribution of phylogenetic diagrams in informal settings. Examples of trees were solicited from respondent institutions.

Graphics were collected, coded and analyzed according to tree type, topology (e.g. geometry, orientation), content included in the tree, and aspects of presentation (e.g. graphic panel, kiosk, etc.). In addition to copies of the graphics themselves, the following information was collected: name of exhibition; year it was developed; source or origin of the tree (e.g. published research paper, website, etc.), if known; and contact details for obtaining permission to reproduce the image.

Audience

The sample population represented science education institutions—including natural history museums, science centers, zoos and aquaria, etc.—that were surveyed with regard to their use of tree of life diagrams in their exhibits; examples of tree graphics were solicited from organizations that indicated their willingness to provide them. Appendix B lists all respondent institutions that use trees as part of their exhibits and shared them for this study.

Data Collection

Preliminary image collection began in May 2008 as part of the NSF-funded *Understanding the Tree of Life* grant project (award #0715287), and a more focused effort was undertaken in February 2009, which continued through the fall of that year. Institutions were asked whether or not they used evolutionary tree diagrams in their exhibitions, and if they were willing to share examples; example graphics and associated information were requested from those that did.

Information was solicited in two ways:

(1) Through a general posting on informal education listservs in early spring 2009 with a link to an online questionnaire at <http://www.surveymonkey.com> (see Appendix A): Association of Science-Technology Centers (ASTC) listserv (ISEN-ASTC-L@community.lsoft.com); a general purpose, cross-disciplinary museum listserv (MUSEUM-L@home.ease.lsoft.com); Association of Zoos & Aquariums exhibits and graphics advisory group (groupgag@lists.aza.org) and education listserv (education@lists.aza.org); College and University Museums & Galleries (ACUMG-L@yahoogroups.com);

(2) Directly contacting institutions by email and/or phone. Since natural history museums are more likely to have trees, based on personal experience and survey responses, these institutions were specifically targeted. Natural history museums were identified using lists on Wikipedia, as well as American Association of Museums (AAM) and Association of Science-Technology Centers (ASTC) member lists. Museums from the United States, Canada, United Kingdom and Oceania were the focus of data collection for ease of coding since all labels would be in English. However, a few institutions from outside these regions responded to the survey and so are included in the study. Several trees were shared by colleagues or found through web searches, source institutions were contacted, and in all but one case permission was granted to use them.

Digital images were either sent to me directly via email, on DVD or through a web page set up on the University of Kansas Biodiversity Institute website for institutions to upload files (<http://bifilenav.nhm.ku.edu/>). High quality images were requested along with the following information: institution name; exhibit title; date associated with the graphic; exhibit location and type (panel/kiosk/etc.); source/origin of graphic, if known (e.g. from a specific research paper); and permission preferences (who to contact for permission to reproduce an image, if necessary). Each tree was given a file name using a format of an institutional abbreviation, date of exhibit, and a short descriptor.

Coding and Analysis

Use of trees

Responses regarding the use of trees in science institutions were classified as natural history museums, science centers, zoos and aquaria, or other. These categories were selected using the following reasoning:

- Natural history museums, because of their typically long history and the nature of their work (often including close collaboration with evolutionary biologists), were thought likely to have a range of tree diagrams representing different time periods; and
- Organizations such as science centers and zoos, although not traditionally associated with evolution exhibits, increasingly have recognized the importance of their role in teaching evolution (Weiss, 2006).

Data was collected for a total of 207 informal science organizations. Only 75 of the 207 responses were collected from the online survey distributed via listservs. Three hundred and twenty-nine institutions were contacted directly by email and/or phone—176 responses were obtained through this route resulting in a response rate of just over 53%.

Respondents to the online survey were self-coding as their identification into one of these categories was included in the survey questions. Duplicate responses were removed, and instances where conflicting data was provided—e.g. when there were multiple inconsistent responses from the same institution – the institution was contacted directly to confirm the correct information. Those contacted directly were coded using criteria such as institution name, and what category they are classified in through organizational membership lists. Online data was exported and merged with responses obtained through other routes into an Excel file with a record of the institution, their response on the use of trees, the source of data (e.g. survey, email), whether they shared trees for the study, and contact details.

Tree diagrams

A total of 185 tree diagrams from 52 informal science institutions were collected. The most trees representing any one organization in the sample is 24, with most sharing one to three trees (see Appendix B). The American Museum of Natural History uses trees extensively in onsite and online exhibits, and a representative sample of 24 was taken from the more than 200 trees shared to reduce the potential for bias from one institution's particular usage of tree forms—e.g. where the same tree format was used at the entrance of each section or gallery, one example was selected. Museums whose only trees are represented by having a copy of the *Explore Evolution* exhibition were coded as using trees but are not represented in the total number of institutions that shared example trees, and the trees themselves were coded to the University of Nebraska State Museum, which was the lead institution on the grant that developed the exhibit.

Each tree graphic was coded according to: (1) tree type; (2) topological and diagrammatic elements; (3) the content included in the tree; and (4) aspects of their presentation. The criteria and organizational scheme for this is outlined below.

1) Tree type

The categories and coding criteria for tree type was developed on a preliminary assessment of sample trees, a review of existing classification schemes used for trees in biology textbooks (See Catley & Novick, 2008; Donovan & Wilcox, 2004) and in collaboration with a University of Kansas systematist (E.O. Wiley, personal communication) and others. Diagrams were coded into three categories (outlined below): cladogram, almost-a-cladogram, and non-cladistic/other evolutionary trees. These categories were chosen to allow for comparison to prior work on textbook trees, but also to reflect the complexity and diversity in museum diagrams.

The categories are based on the overall representations used in the trees, and not any

descriptors that might be associated with the tree—e.g. whether or not it was labeled as a cladogram. Few diagrams can be tied to a particular research paper, and the data sets, assumptions and methodologies used to build the three are not available or unknown. For example, there may be insufficient information to determine if the groups represented are monophyletic (groups that contain the most recent common ancestor and all descendants), as opposed to paraphyletic (groups that do not include all descendants from an ancestor) or polyphyletic (groups that do not include their common ancestor) (Wiley, 1979, 1981)—and so unless it is obvious that they are not, the assumption is made that the groups are monophyletic.

The three tree type categories and the criteria used is as follows (Figure 1):

Cladogram (=1) – Branching diagrams that depict common ancestry and the pattern of relationships between taxa, and only include monophyletic groups, and polytomies or unresolved branches.

Criteria for inclusion as a valid cladogram follow those used by Catley & Novick (2008) such as terminal taxa end points being at the same level and not including ancestor-descendant relationships (Note: the names of terminal taxa may be labeled at the ends of or along branches). However, unlike their scheme, I have included trees in this category that have labels on branches or nodes other than characters or to define branching events, since in many cases these labels refer to classification categories that also reflect shared characteristics (e.g. amniotes).

Almost-a-cladogram (=2) – Diagrams that depict patterns of relationship through branching sequence as above, but have some diagrammatic variable that preclude it from being considered a valid cladogram in the strictest sense. Following Catley & Novick (2008), this category includes trees with different terminal end points, varying branch thickness, and side branches.

Non-cladistic/other evolutionary trees (=3) – Diagrams that depict evolutionary relationships but that do not qualify as cladograms. Reasons include:

- Includes ancestor-descendant relationships: (1) there is a specified ancestral species or named taxon (e.g. species) at a node. Note: this does not include generic references to an unknown hypothetical ancestor such as ‘early primate ancestor’; (2) there are one or more taxa in a sequence along or within a branch (e.g. named taxa, illustrations, silhouettes or specimens). It is possible that the latter may be intended to represent morphotypes—hypothetical generalized forms having all the synapomorphies of a group—or other kinds of information. However, the intention, unless specified, is unknown and so the assumption is that it violates cladistic principles by including ancestor-descendant statements.
- Portrays higher-level taxonomic groups (e.g. order or family) as ancestors to other groups, and/or indicates one group as ‘coming from’, ‘leading to’ or ‘giving rise’ other taxa. Note: this does not refer to classification labels that are overlaid onto branches or at nodes to indicate broad grouping of taxa (e.g. amniotes to denote a grouping/feature at a particular node and beyond).
- Diagrams that include hybridization.
- Trees without taxa.
- The branching pattern—therefore the statement about relationship—is not clear such as obviously unconnected branches or the use of amorphous blobs.
- Includes non-branching diagrams such as bar charts.

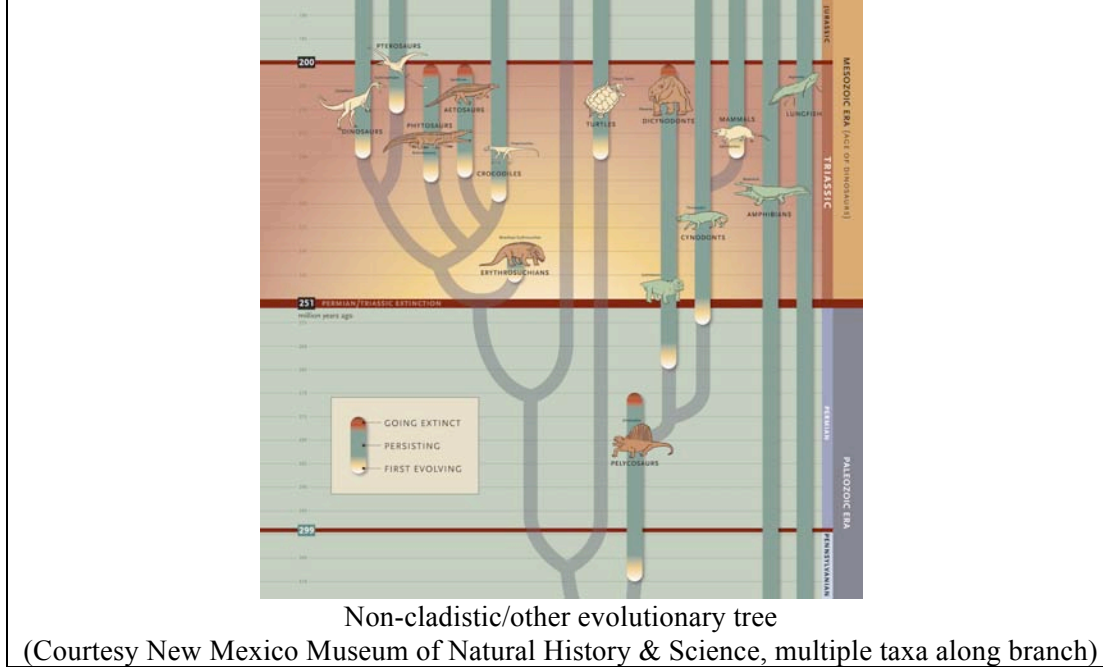
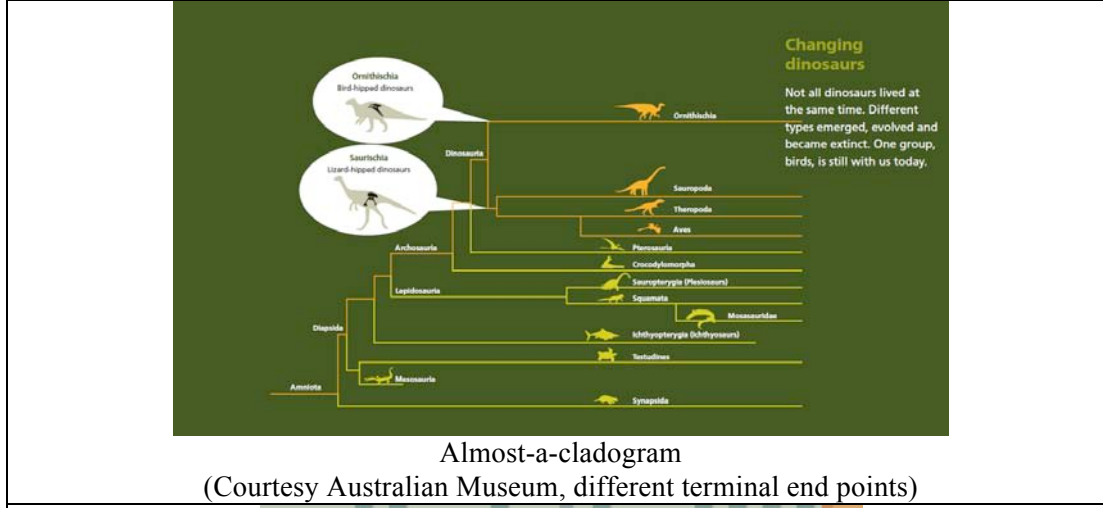
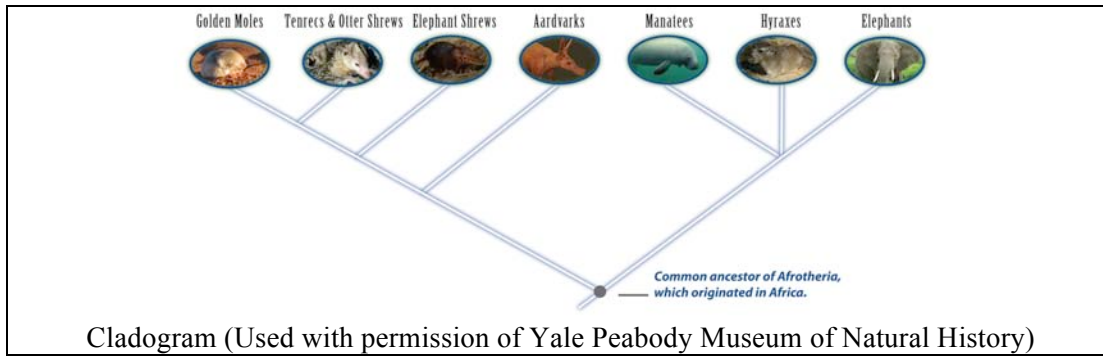


Figure 1. Examples of museum tree types.

Catley & Novick's (op cit.) classification scheme for biology textbooks used three main categories of cladograms—tree, ladder and other cladogram—with additional ‘other evolutionary diagrams’ categories for ‘almost-a-‘ cladograms, ‘Tree of Life’ and anagenic diagrams. The coding scheme used for this study differs in two ways: (1) geometry is considered separately from tree type and includes variations beyond tree and ladder formats (see Table 1); and (2) ‘almost-a-cladogram’ is its own category separate from ‘non-cladistic/other evolutionary trees’.

Cohen's Kappa statistical test assesses the agreement and consistency of category assignment of categorical variables between coders; a score of 1.0 indicates 100% agreement. Several tests were run to assess inter-coder reliability with the tree type categories. The tests were conducted with myself and another coder, who has a background in biology but not in evolutionary biology or systematics. First, we assigned the tree type categories to a set of ten diagrams collected from a web search, Kappa=1.0, $p < 0.001$, and then to a random sample of 10% ($n=9$) of trees from the data set, Kappa=1.0, $p < 0.001$. Further modifications to the tree type categories were made and refined with preliminary reliability tests. A final inter-coder reliability test was run with a random sample of 10% ($n=21$) of trees collected, Kappa=.929, $p < 0.001$.


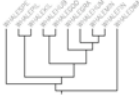



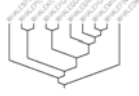
2) Topological and diagrammatic elements

Orientation – Trees were coded according to their overall orientation or the position of the root relative to branches (1=vertical or 2=horizontal). Trees which do not have a clear overall orientation such as those with circular or radial geometries were coded as 0=N/A.

Direction – Directionality of the branches were coded according to their overall direction from the root (1=up; 2=down for vertical trees; 3=l-r; or 4=r-l for horizontal trees). Circular trees were coded by the direction of the initial spiral, and trees for which a direction does not apply (e.g. radial) were coded as 0=N/A.

Geometry – Describes the varied geometrical—and informally equivalent—forms used for phylogenetic trees. Trees classified as a cladogram and ‘almost-a-cladogram’ were coded by geometry as outlined in Table 1. The name given to different geometries varies depending on the software program and researcher preference. In this study, the first name listed for each form was used (e.g. 1=angled; 2=rectangular; 3=curvogram/swoopogram; 4=circular; 5=radial; 6=eurogram). Diagrams coded as non-cladistic/other evolutionary trees, or for which a distinct geometry cannot be determined, were coded as N/A (=7).

Table 1. *Phylogenetic tree geometry (descriptions modified from tree software sites, e.g. Phylodendron, Drawgram, etc.).*

Example	Description	Names used & sources	Code
	Nodes connected to other nodes and to tips by straight lines directly from one to the other. This category includes diagrams with slightly wavy lines or curved lines, but have an overall pectinate layout.	<ul style="list-style-type: none"> • Angled (e.g. PhyloDraw, TreeView) • Slanted (e.g. PhyloDraw, TreeView) • Cladogram (e.g. Drawgram, Phylodendron) • Diagonal (e.g. Mesquite) • Ladder (Catley & Novick 2008) 	1
	Nodes connected to other nodes and other tips by a horizontal and then vertical line. This category includes diagrams with slightly curved corners and/or wavy branches.	<ul style="list-style-type: none"> • Rectangular (e.g. PhyloDraw, TreeView) • Square (e.g. Drawgram, Mesquite) • Phenogram (e.g. Drawgram, Phylodendron) • Tree (Catley & Novick 2008) 	2
	Nodes connected by curves that are 1/4 of an ellipse; curvogram starts horizontally then curves up to become vertical; first 1/3 of swoopogram starts out horizontal then vertical then follows curvogram.	<ul style="list-style-type: none"> • Curvogram/Swoopogram (e.g. Drawgram, Phylodendron) • Angular curvograms/Curved curvograms (e.g. TreeDom) 	3
	Nodes connected outwards from a central point, with tips forming a circle. Radial lines run outward from the center with the arc segments centered on them.	<ul style="list-style-type: none"> • Circular (e.g. Phylodraw, TreeView, PAUP) 	4
	Nodes connected outwards from a central point without horizontal lines.	<ul style="list-style-type: none"> • Radial (e.g. Phylodraw, TreeView) 	5
	Nodes connected to other nodes and to tips by a diagonal line that goes outwards to at most 1/3 of the way up to the next node, then turns sharply straight upwards and is vertical.	<ul style="list-style-type: none"> • Eurogram (e.g. Drawgram, Phylodendron) 	6

Variation in branch thickness – Whether the branches vary in thickness (0=no; 1=yes).

Terminal branch end points – Whether branches end at different points (0=no; 1=yes).

Images of taxa – Whether taxa in the tree are represented visually, i.e. graphically through images, silhouettes, or through the use of models and/or specimens – rather than identified by text only (0=no, 1=yes).

'Tree of Life' – Diagrams that have a central main trunk with taxa branching off of it with a clear linear progression from 'lower' to 'higher' forms (0=no; 1=yes).

Tree-like depictions – Branching diagrams represented as literal trees (0=no; 1=yes).

3) Content

Anagenesis – Whether the tree depicts ancestor-descendant relationships between named taxa (e.g. genus or species) with one or more named taxa in a sequence along a branch (0=no; 1=yes).

Taxa – The group(s) of taxa included in the tree (0=invertebrates; 1=vertebrates; 2=other; 3=broad categories).

Extinct taxa – Whether the tree includes extinct taxa (0=no; 1=yes).

Humans and their most recent extinct relatives (hominins) – Whether the tree includes one or more members of this group (0=no; 1=yes).

Geological Time – Whether the tree includes an indication of time (0=no, 1=yes, labeled on the diagram itself [includes labeled specimens within the tree]; 2=yes, time referred to in the associated text).

Classification – Whether the tree makes explicit links between parts of the diagram and more familiar classification of organisms (0=no; 1=yes).

Common ancestor – If there is a reference to one or more common ancestors (0=no, 1=yes, labeled on diagram itself; 2=yes, referred to in the associated text or supplemental document). If referred to on both the tree diagram and in other text, it was coded as 1.

Synapomorphies – Whether any specific synapomorphies or other shared characteristics are referenced in support of the relationships depicted (0=no; 1=yes, labeled on the tree; 2=yes, referred to in the associated text). If included both on the tree itself and in related text, it was coded as 1. Graphics that only refer to synapomorphies in the generic sense such as shared features being used to construct the tree are coded as 0, but as 1 for ‘nature of science’ (see Presentation and Explanation coding section).

Hybridization – Whether the diagram includes lateral transfers of genetic material (0=no, 1=yes), i.e. it represents a phylogenetic network in which hybridization or similar events are believed to have been involved, rather than a tree that only depicts branching sequence.

4) Presentation and explanation

Exhibition location – Whether the tree is part of an onsite exhibit, available online or both (1=onsite; 2=online; 3=both onsite and online versions; 4=in a supplemental document).

Exhibit component – Whether the tree is a static flat graphic panel (=1), forms a graphic backdrop for specimens, models or exhibit cases (=2), is a three dimensional representation (=3), a video or game in a kiosk or online (=4); a combination such as graphic panel and kiosk (=5); and a supplemental document (=6).

Instructional information/interpretation – Whether there is an explanation of what the tree shows (e.g. it refers to relationships between taxa, describes changes in diversity within a group, or trends over time, etc.) or attempts to instruct readers about how to interpret evolutionary diagrams such as describing trees as branching diagrams that show relatedness (0=no, 1=yes,

labeled on the diagram itself; 2=yes, in the legend or associated text; 3=yes, as part of separate supporting documents).

Explicit reference to tree – Whether the instructional or interpretative information explicitly references the specific tree in the exhibit (0=no; 1=yes). Trees coded as 0 in previous category were coded as ‘no’.

Nature of Science – Whether tree labels or associated legends include information about the data used to build the tree, refer to the tree as a hypothesis, or provide any other indication that the tree is the product of scientific reasoning (0=no; 1=yes).

Metadata – Information on the exhibition title, year (specific year if known, and coded by decade), source or origin of tree, and whether the museum is associated with a university/college or is a research institution.

Data was entered into SPSS (SPSS Inc., Version 17.0 for Mac) and statistical tests were run appropriate to the data: frequency distributions for summaries of tree topology and content; Chi-Square for testing associations between variables, and Fisher’s Exact Test for those cases with a small sample size.

Results and Discussion

This study attempts to integrate data collected about evolutionary tree diagrams used in informal science settings with what is known from the learning research about tree thinking. To facilitate this, the findings of the study are presented alongside a discussion of the potential educational implications of these elements.

Use of trees diagrams in informal science institutions

Data were collected from 207 informal science institutions on whether they used tree of life diagrams in their exhibits (Table 2). The results shows that while certain individual institutions do not use trees; evolutionary tree diagrams are represented in all types of informal science institutions. Natural history museums incorporate them to greater extent than science centers and zoos, and many organizations surveyed consider themselves to be a hybrid institution—a combination of history, natural history or art museum, science center, botanical garden, and zoo/aquarium—and incorporate trees of life to varying degrees. Overall, it appears that evolutionary trees form a common graphic element in many museums, with close to a third of informal science institutions using these diagrams in their exhibitions.

Table 2. *Summary on the use of tree of life diagrams in informal science institutions.*

Organization Type	Do your exhibits use tree of life diagrams?		
	Yes	No	Total
	32.4% (67)	67.6% (140)	
<i>Natural History Museum</i>	50.0% (41)	50.0% (41)	82
<i>Science Center</i>	21.9% (5)	78.1% (16)	21
<i>Zoo/Aquarium</i>	16.1% (5)	83.9% (26)	31
<i>Other: anthropology or combination of natural history, history, art zoo/aquarium, etc.</i>	21.9% (16)	78.1 (57)	73
	Total Responses		207

Information on whether institutions were part of (or affiliated with) a university/college or have research programs was obtained from their websites. There is no significant correlation between the use of trees at freestanding museums and those institutions affiliated with universities. However, organizations that identify themselves as being involved in research were more likely to use trees in their exhibits (Fisher's Test, $df\ 1$, $n=207$, $p<0.001$).

Evolutionary tree diagrams in museums

One hundred and eighty-five evolutionary trees were collected and analyzed for this study representing 52 different informal science institutions.

Tree type

Figure 2 shows the distribution of museum trees by tree type. Overall, most of the evolutionary trees sampled are represented by cladograms in the broadest sense (61.6%, $n=114$ of 185, 61.6%)—cladogram and almost-a-cladogram categories together. However, fewer than half of those are considered to be strict cladograms (see tree type coding categories). The other museum trees fall into the non-cladistic/other evolutionary tree category and depict common ancestry between taxa along with other elements such as anagenesis, and often portray additional information such as biogeography or temporal distribution.

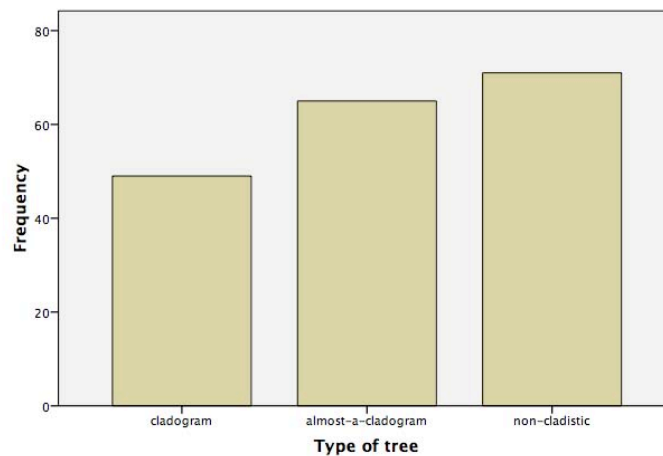


Figure 2. Frequency of museum tree diagrams by tree type.

Cladograms in the broadest sense are the most common form of tree used in museums, at over 60%. This is lower than the 72% found in a review of biology textbooks (Catley & Novick, 2008), which used a strict definition for a valid cladogram such as having all terminal branch points on the same level. If we follow a strict definition and consider the cladogram only category, the percentage of museum trees represented by cladograms falls to just over 26% ($n=49$). Catley & Novick (op cit.) expressed concern over the use of ‘almost-a’ cladogram format due their potential to create confusion about cladistic principles and misinterpretation of diagrammatic elements such as varying branch length. The percentage of other evolutionary diagrams (non-cladistic) used in museums (38.4%, $n=71$) is correspondingly higher than the 28% found in textbooks. Many of the diagrams in this category are challenging to decipher, with some

diagrammatic elements not labeled or subject to alternative interpretations.

Tree use over time

Figure 3 shows the breakdown of tree types by decade. While specific years are known for many trees, organization by decade allows for the comparison of all diagrams, since for some trees an accurate date beyond an estimated decade was not available. All but one tree collected was post-1970, with most being created post-2000 during exhibit renovations; therefore, the sample is weighted towards trees from 1990 and later.

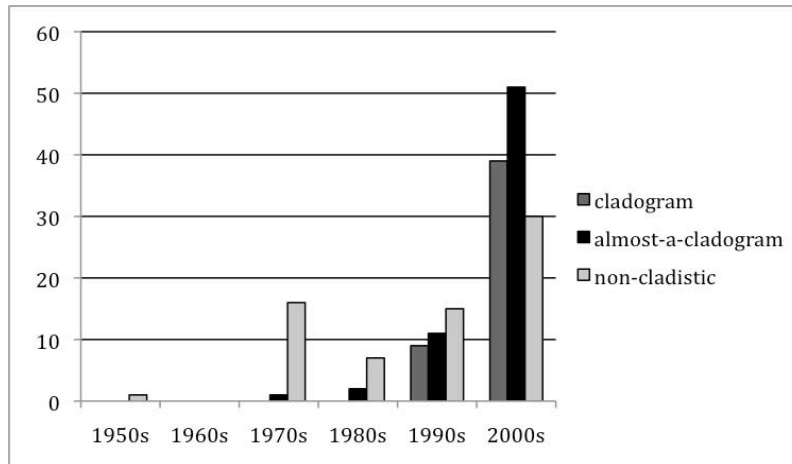


Figure 3. Frequency and distribution of tree types by decade.

Figure 4 shows the overall frequency of cladograms, in the broadest sense, over time as a percentage of the sample collected. Some trends are worth noting in these graphs: (1) many institutions have trees from across several decades in their exhibitions such as The University of Kansas Natural History Museum, which has tree diagrams from the 1950s, '70s, '90s and 2000s—therefore, visitors are often exposed to a range of evolutionary graphics during a visit; (2) cladograms (*sensu lato*) appear in museums in the '70s, but not with any frequency until the '90s; and (3) the use of non-cladistic evolutionary diagrams in museums has declined but remain a significant part of exhibits today, representing almost a third of graphics from the last decade.

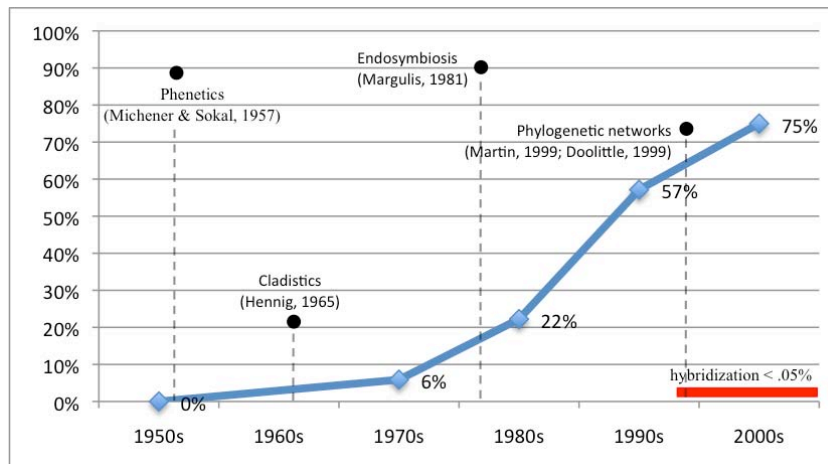


Figure 4. Percentage of museum trees that are cladograms (*sensu lato*) over time.

Tree topology and iconography

Images can be powerful tools for communicating ideas, but their interpretation and understanding are influenced by context and prior conceptions. A study of museum exhibits about human evolution (Scott, 2007) found that information about evolution is obtained from a wide range of sources including TV, films, books, family discussions and museums. Visitors’ experiences and understanding were framed within this wider cultural forum—with museums conflicting, complementing and/or providing validation for existing knowledge.

The idea of evolution as linear and progressive is a powerful cultural narrative and is reflected in popular evolutionary imagery (Clark, 2001; Green & Shapely, 2005; Matuk, 2007). Some authors suggest that many of the icons used in evolutionary diagrams—cones of increasing diversity (i.e., trees with narrow bases and wide tops), upwardly directed trees, and trees with differential resolution (emphasize some taxonomic groups)—reinforce ideas of evolution as progressive and directional (Gould, 1995, 1997; O’Hara, 1992).

In their discussions of evolutionary images, Matuk (2007) and Clark (2009) note that the simplified representations of horse evolution, first presented in 1902 (Figure 5), suggests a straightforward and linear progression that persists today. Horse evolution diagrams that depict anagenesis with taxa arranged sequentially along a time scale continue to be used in textbooks (Catley & Novick, 2008), and were found in a few museum exhibits (Figure 6).

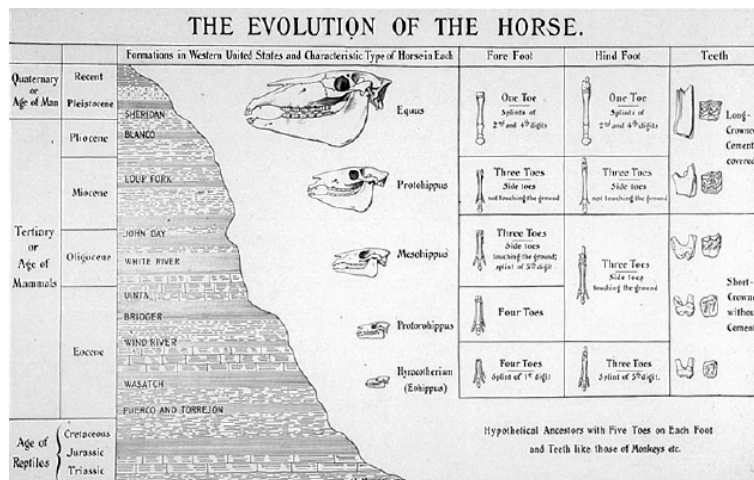


Figure 5. Horse evolution diagram (1902), Courtesy American Museum of Natural History, New York, Neg. no. 35522.

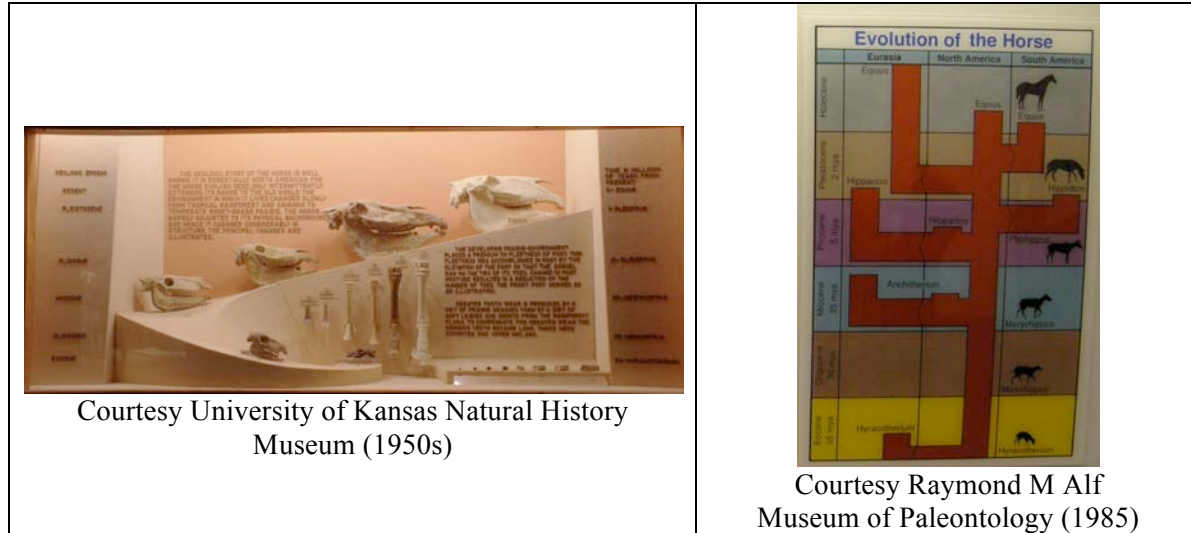
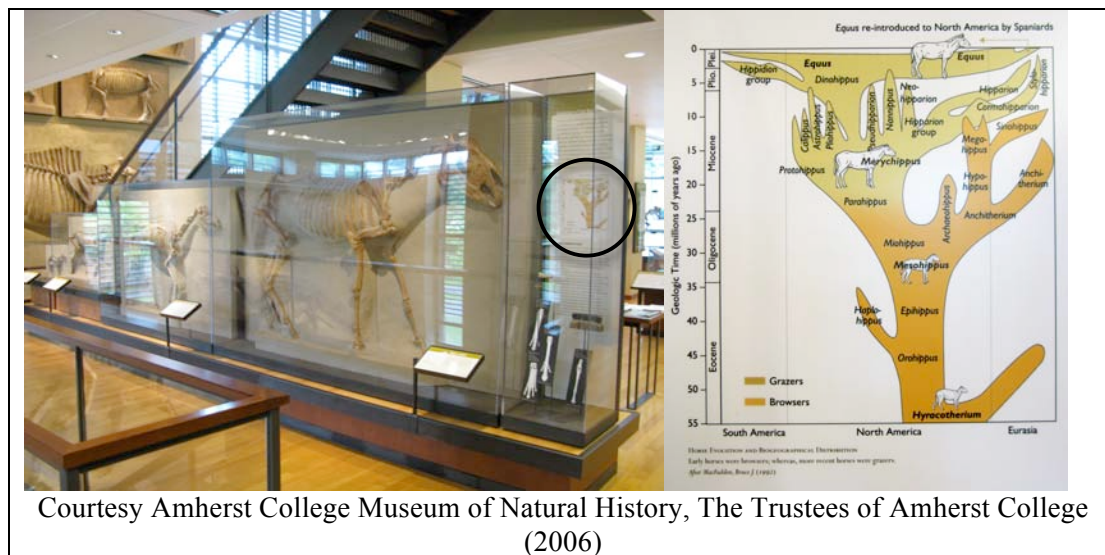


Figure 6. Examples of linear horse evolution exhibits in museums.

Of particular interest are exhibits that attempt to show the more complex (e.g. ‘bushy’) nature of horse evolutionary history in a tree diagram, but arrange the specimens associated with it in a linear fashion. For example, Figure 7 shows two exhibits that depict a more complex history in their tree graphic, but whose arrangement of specimens suggests a more simple, straightforward trend in features over time from left to right. In part this may reflect the difficulty in displaying large specimens in a more representative layout. It is possible that this mismatch in visual representation may create difficulties in interpretation; however, in one case the label explicitly describes how the evolution of horses does not follow a linear and progressive path.



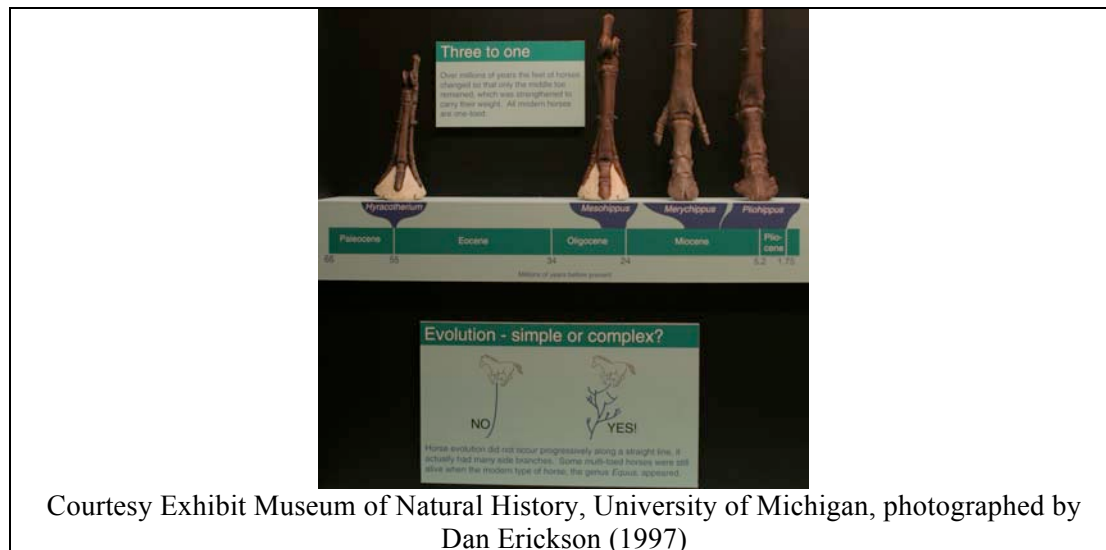
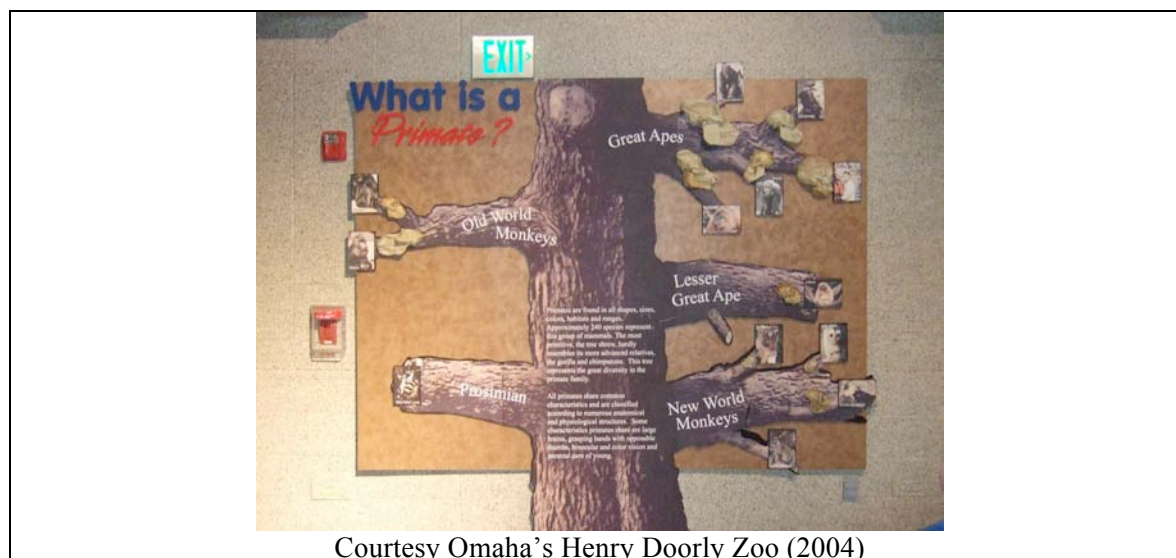
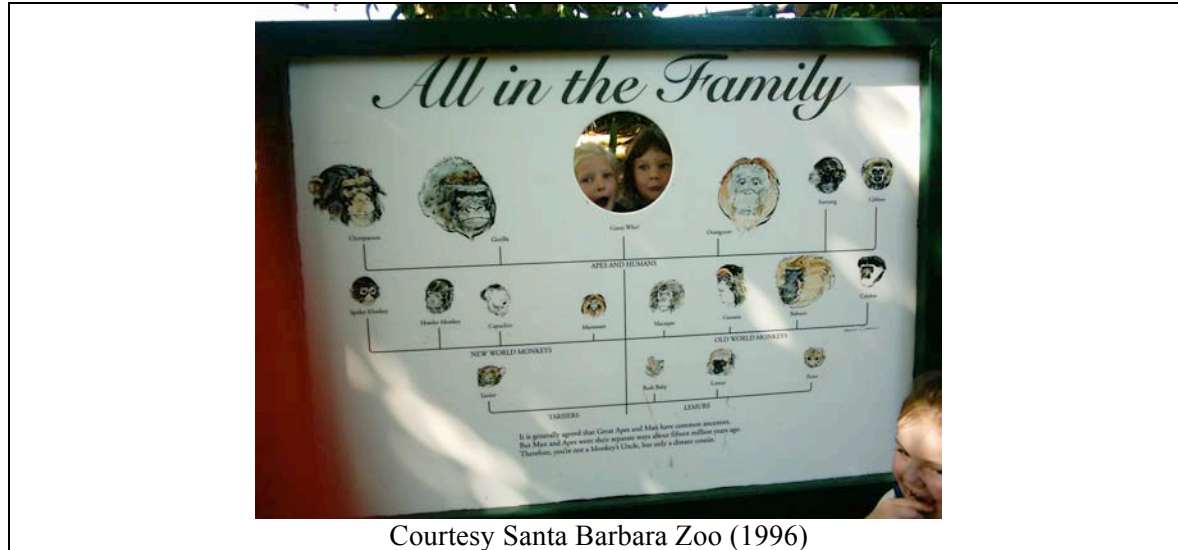


Figure 7. Horse evolution exhibits in museums

Unlike biology textbooks ‘Tree of Life’ depictions (Catley & Novick, 2008)—diagrams with a central trunk and a distinct ‘progressive’ branching sequence from ‘lower’ organisms on the bottom to ‘higher’ ones at the top—are not found in this sample of museum trees. However, two diagrams have what might be interpreted as vertical, hierarchical representations of primates with a central core and side branches with prosimians at the bottom and apes at the top (see Figure 8). What significance, if any, visitors might attribute to these particular examples is unknown, but previous work has demonstrated the potential for interpreting the layout of exhibits that include humans, their most recent extinct relatives and/or other primates as directional and progressive (Scott & Giusti, 2006).





Courtesy Santa Barbara Zoo (1996)

Figure 8. Examples of primate trees with a central trunk and side branches.

Tree orientation and direction

Most of the museum trees have a discernable orientation and direction, the majority being oriented both vertically and upward (n=124). Of the forty-nine horizontal trees represented in the sample, most are organized in a left-to right direction (n=46) (see Table 3).

Table 3. Breakdown of museum trees by orientation and direction.

Orientation	Direction				N/A	Total
	Up	Down	l-r	r-l		
Vertical	124	4	0	0	0	128
Horizontal	0	0	46	3	0	49
N/A	0	1	3	3	1	8
Total	124	5	49	6	1	185

The tendency towards using diagrams that are vertical and directed upwards has the potential to result in unintended meaning being applied to this aspect of the tree on the part of the visitor. There are biases in our perceptions of horizontal and vertical space that result from our conceptual representations of those spaces (Franklin & Tversky, 1990; Tversky, in press-a, in press-b), and vertically oriented diagrams are often associated with quantitative increases, and notably correspond to the linguistic metaphors of up and their associations with concepts of more, and better (Tversky, Kugelmass, & Winter, 1991). Furthermore, it is possible that diagrams oriented in this way have the potential to reinforce ideas of progression and direction in evolution (Gould, 1997; Matuk, 2007; O'Hara, 1992).

In addition, previous research found that both children and adults map temporal increases horizontally on diagrams, with the direction of time reflecting the direction of their written language (Tversky, 2005, in press-c; Tversky, et al., 1991). Vertically oriented diagrams then have the potential to create confusion about the direction of time, particularly when not all trees explicitly label time. In this study, more than 60% of trees (n=122 of 185) include a temporal context with many labeling time on the diagram itself (n=85) and others referring to it in associated text. Most non-cladistic evolutionary trees (n=53 of 71) include a time axis on the tree

itself. Time is an important and difficult concept in understanding evolutionary trees, and there is ongoing discussion about the interpretation of time in tree diagrams, and advantages and disadvantages of incorporating time (Catley & Novick, 2008; Dodick, 2009). Continuing research will help to clarify these issues.

In addition to vertical orientation of diagrams, the location of *Homo sapiens* and other hominin species in relation to the other taxa in the tree has the potential to reflect and reinforce ideas of teleology and progression (Matuk, 2007; Tversky, 1995). In an analysis of anthropocentrism in phylogenetic textbooks, Sandvik (2007) found the position of humans on the top-right of the left–right axis of cladograms to be significant. The common mis-reading of time across the top in a left–right direction is often interpreted as a progression from ‘old, primitive or simple’ to ‘recent and complex’, culminating in humans. This top-right bias in the placement of humans was not found in museum trees collected for this study. Of the nine vertically oriented cladograms with humans, only two positioned humans in the top-right, the others had them in middle or top-left locations.

Fewer than a third of museum trees with humans depict anagenesis (n=11 of 39). However, those that do all include humans and their most recent extinct relatives (e.g. *Homo*, *Australopithecus*, etc.) rather than only humans in relation to other living primates or other taxa. The portrayal of hominin evolution as primarily anagenic is found in biology textbook trees, and is problematic for its potential to reinforce ideas of teleology, progression and anthropocentrism (Catley & Novick, 2008).

Geometry

Of the museum trees that could be coded by geometry (n=114, cladograms and almost-a-cladograms) most use either a rectangular (45.6%, n=52) or angled format (37.7%, n=43)—referred to as tree and ladder respectively by Catley & Novick. This differs somewhat from cladograms in biology textbooks (Catley & Novick, 2008), which found a consistent preference for angled over rectangular diagrams (55%) across grade levels. However, if only strict cladograms are considered, then angled and rectangular museum trees are equal (18 each), 11 are eurograms and two are circular. This sample of museum trees shows a wide variation in geometries used including curvogram/swoopogram and eurogram (see Table 1 for descriptions).

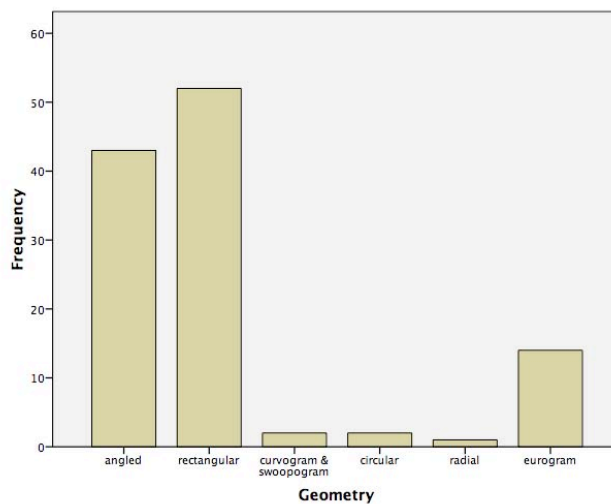


Figure 9. Frequency of museum cladograms (*sensu lato*) coded by geometry.

While different geometries show equivalent relationships, the particular form used may have implications for interpretation. In a study by Novick & Catley (2007) undergraduate students were asked to interpret and translate between three different types of diagrams—circle, tree (rectangular) and ladder (angled) formats. Students had greater difficulties extracting the hierarchical structure and relationships in ladders despite their being equivalent to the others in terms of the information they contain. Novick & Catley suggest that the difficulty in seeing the nested relationships in the ladder results from the Gestalt principle of good continuation. Good continuation implies that the sloped line at the base of the ladder/angled diagram represents a single hierarchical level rather than the multiple levels it actually represents. The principle of good continuation then acts as a cognitive constraint resulting in the straight line being seen as a unit that continues without change, making it difficult for students to understand and interpret the relationships being depicted.

Trees and time

Pictorial representations in tree diagrams elicit comments about time, common ancestry, and the relationships between species in both novices and experts (Evans, 2009), and the interpretation of time on tree is influenced by a range of factors including branch length, and naïve understanding of evolutionary processes (Dodick, 2009). It has been suggested that where temporal data is available, the inclusion of geological time on diagrams may help to support understanding (Catley & Novick, 2008), and help with the common misreading of time across the top rather than bottom-up (Meir, Perry, Herron, & Kingsolver, 2007).

Just over 46% of trees (n=85 of 183) that can be coded for time include it in some form, either as a timeline on the diagram or in labels along branches, at nodes or associated with taxa. Another 20% (n=37 of 183) refer to time in associated label text (Figure 10). This is in line with the 42% of biology textbook diagrams found to include some representation of time (Catley & Novick, 2008).

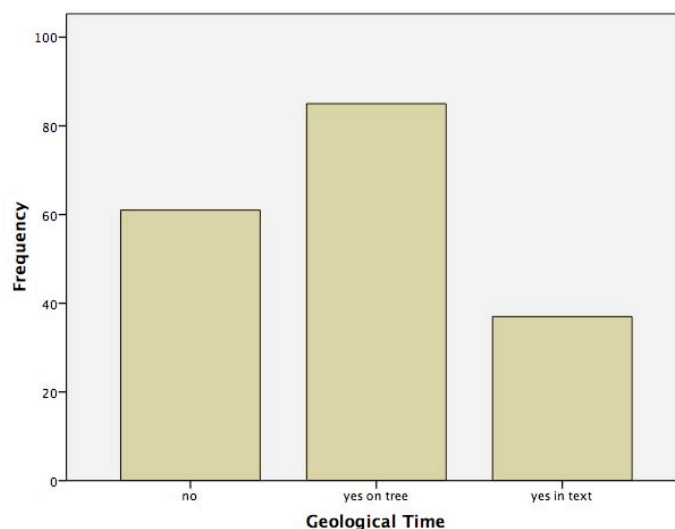


Figure 10. Frequency of geological time in museum trees.

In addition to the explicit labeling of a time axis or as data points on a diagram, time may be implied by variation in branch length between extinct and extant taxa. Variation in branch

length (differing end points for terminal taxa) and the inclusion of time on the tree diagram were significantly associated in the sample (Fisher's Test, $df = 1$, $n = 185$, $p < 0.001$). Furthermore, the inclusion of extinct taxa is significantly correlated with variation in branch length (Fisher's Test, $df = 1$, $p < 0.001$) suggesting that differing branch length is being used as a diagrammatic representation of an absolute or relative time dimension; however, in many cases extinct taxa are not labeled as such. Trees with only vertebrates are significantly more likely to include extinct taxa (Fisher's Test, $df = 1$, $n = 184$, $p < 0.001$) and so there may be an expectation that museum visitors are more familiar with extinct vertebrates (e.g. dinosaurs, mammoths) than with other organisms.

Variation in branch length is thought to have the potential to promote understanding if the earlier ending points indicate extinct taxa (Catley & Novick, 2008), and the inclusion of extinct taxa could help to avoid ideas of species persistence and progress (Donovan & Hornack, 2004)—in part because a long branch is often incorrectly interpreted as a lineage in which no change has occurred (Crisp & Cook, 2005; Novick & Catley, 2007). However, the potential value of different branch length to identify extinct groups may be hampered by the fact that the significance of this diagrammatic feature is often not made explicit.

Tree content: ancestors, classification, synapomorphies and hybridization

Many museum trees include information in addition to showing relationships between taxa. Examples include labeling nodes with specific or representative hypothetical common ancestors, highlighting the synapomorphies that support the proposed relationships, showing suggested hybridization paths or events, as well as the diversity, geographical distribution and diet of different groups. Three trees in the sample are not yet finalized and so were excluded from the analysis of some content categories.

Close to 40% of sample trees refer to ancestors or common ancestors ($n = 72$ of 182), 14.6% ($n = 27$) on the diagram itself and 24.3% ($n = 45$) in associated text. Donovan & Wilcox (2004) suggest that labeling the root or other internal node as 'common ancestor' can help to overcome the abstractness of tree representations and support the interpretation of nodes. Others argue that since the ancestor is unknown it is disingenuous to include it (Catley & Novick, 2008), and has the potential to reinforce the view of nodes as precise moment of change (Meir, et al., 2007).

Only 20% of these trees label specific synapomorphies that support the relationships depicted on the tree diagram itself ($n = 37$ of 182), and about 23% ($n = 43$) refer to particular shared characters in the text. The inclusion of synapomorphies can help visitors to understand that trees are based on shared characteristics, making their relatively uncommon use in diagrams potentially problematic.

Links to classification were found in over half of museum trees collected (55%, $n = 102$ of 182), which Donovan & Wilcox (2004) suggest may support the recognition of biological patterns. Furthermore, research suggests that teaching classification independent of phylogeny supports the development and persistence of alternative/misconceptions about animal classification (Brumby, 1984; Griffiths & Grant, 1985; O'Hara, 1992; Trowbridge & Mintzes, 1988; Wellman & Gelman, 1998; Wiley, Siegel-Causey, Brooks, & Fund, 1991; Yen, Yao, & Chiu, 2004). However, Sandvik (2007) argued that textbooks often adjust the resolution of cladograms to reflect more familiar Linnaean categories and so these taxa are overrepresented in the diagrams, creating biased and often anthropocentric samples of taxa. In addition, such classification categories are often interpreted as scientific statements of relationship.

difficult. This also appears to be the case in textbooks where branch thickness is often used to indicate diversity but the graphical significance is generally unclear and undefined (Catley & Novick, 2008). Being explicit about the significance and meaning of abstract diagrammatic elements is likely to aid in tree interpretation.

Tree content: taxa

In terms of taxonomic groups represented, most trees only include vertebrates (73%, n=135 of 185), followed by the overall relationships between broad categories across the taxonomic spectrum (15.7%, n=29); then invertebrate animals (7.6%, n=14); only a small number of trees (3.8%, n=7) show other groups such as viruses. Diamond & Evans (2007) found that reasoning about evolution differs by organism, and so the choice of taxa represented is likely to impact users' interpretation of trees. Sandvik (2007) argued that textbooks often adjust the resolution of cladograms—collapse different parts of the tree—to reflect Linnean categories. Therefore, taxa associated with such familiar categories that are the focus of the curriculum content, are overrepresented in tree diagrams, creating biased representations. Over half of the museum trees have some kind of link or reference to classification categories, but whether the distribution of taxa reflects a deliberate pruning to focus on more familiar Linnaean groups, popular taxa or institutional research focus is unknown.

Tree presentation

Of the 185 trees collected, 89.2% (n=165) are part of onsite exhibitions, the majority of which are separate flat graphic panels (73.5%, n=136), and 15.1% (n=28) incorporate specimens or models in the tree. Only two trees in the sample were represented as three-dimensional structures, and 14 were media based in the form of videos or games accessible either online, via an onsite kiosk or occasionally both.

Some visitor evaluation studies suggest that two-dimensional labels by themselves and graphics not associated with three-dimensional objects generally receive little attention from visitors (Bitgood, 2000; Peart, 1984), and that the closer the label is to the specimen that it refers to, the less effort is needed on the part of the visitor to read that label (Bitgood, Benefield, & Patterson, 1990). Furthermore, visual strategies that include three-dimensional elements such as specimens have been found to be more successful in helping visitors recall key information (Australian Museum Audience Research Unit, 2009).

More than 80% of evolutionary diagrams collected (n=151) use visual representations of the taxa in the tree either through specimens, models, illustrations or photographs, which may draw attention to the organisms and help users to recognize and identify taxa. Incorporating visuals into trees may also help visitors connect labeled synapomorphies on the tree with visible morphological characteristics. While many novices emphasize morphological features and similarity-based reasoning in their thinking about biological relationships (Gelman, 2004; Gelman & Markman, 1987; Halverson, Pires, & Abell, 2008; Sloutsky, Lo, & Fisher, 2001), explicitly labeled synapomorphies that are used to support the relationships may help highlight the evidence used to build the tree—e.g. similarity based on shared derived characters (Donovan & Wilcox, 2004).

Some of the kiosks or online trees were interactive, where the user could step through the information or navigate to different parts of the tree. Summative evaluation of Yale's *Travels in the Great Tree of Life* exhibit found that the computer game exploring relationships was effective at communicating the idea that phylogenetic relationships may not always be what you might

expect (Giusti, 2008), which suggests that perhaps interactivity and/or animation may help address some issues with reasoning using trees. In my experience, exploring the tree of life using manipulatives such as using scale models of taxa and different tree formats can be effective with museum visitors. Research on the potential role of animation in interpreting cladograms found that animations can influence the perception and interpretation of diagrams, but that it is also impacted by prior knowledge and evolution narratives (Matuk, 2008a, 2008b, 2008c; Matuk & Uttal, under contract).

Tree explanatory information

Close to 70% of trees (n=125 of 182) include some kind of description or explanation about what the particular tree shows, or refer to trees as branching diagrams that show relationships. For others the link between the tree and the exhibit or text is unclear. Of those that provide some explanation of the diagram, just over 50% make explicit reference to the tree shown (Table 4). Evaluation studies suggest that it is important to directly tie labels to what visitors can experience at that point in the exhibition (McLean, 1993; Serrell, 1996), and presenting explicit information and concrete ideas in exhibit labels help to instruct visitors about what they should look for (Bitgood, 2000; Falk, 1997; Falk & Dierking, 1992). However, the lack of explicit annotation in many museum trees is not surprising given its absence in most evolutionary diagrams used in textbooks (Catley & Novick, 2008); although its inclusion could support an understanding and interpretation of evolutionary processes (Donovan & Hornack, 2004).

In addition, more than two-thirds of these trees (n=121 of 182) do not make reference to the nature of science or tree building—e.g. indicate that it represents a hypothesis, or refers to the data used to construct trees—which could help support ideas about scientific inference (Donovan & Wilcox, 2004). The absence of explicit explanations for many trees or information about trees as products of science is likely to add to the difficulty that visitors have in reading and understanding of these diagrams.

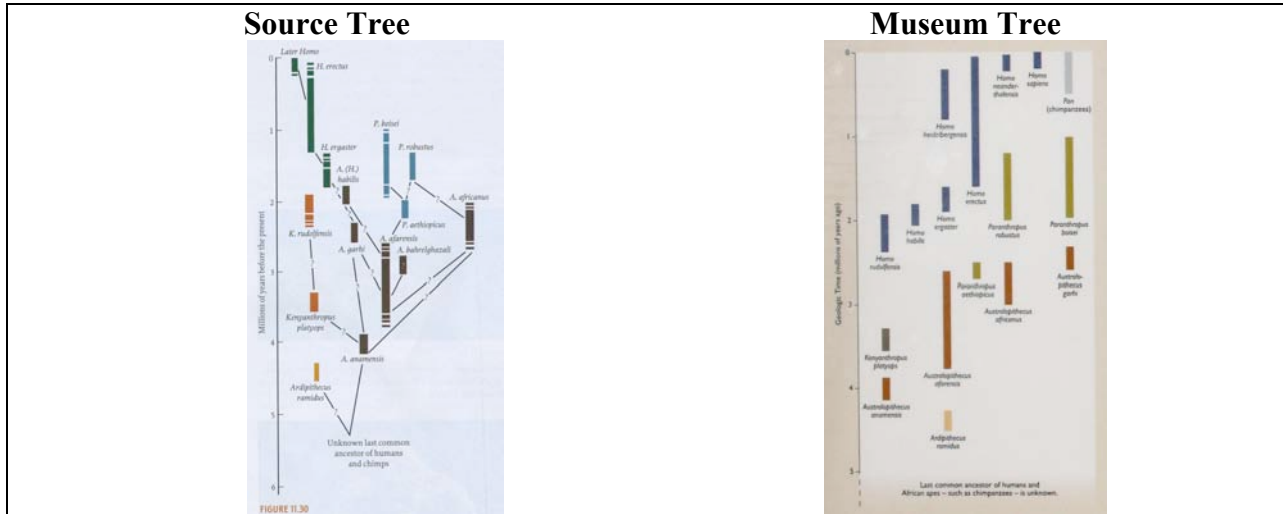
Table 4. Breakdown of trees by their reference to nature of science, and inclusion of interpretive information (*n=182 as data not available for 3 trees).

	Nature of Science*	Interpretation/ Instruction		Explicit reference to tree diagram
Yes	33.5% (61)	68.7% (125)	➔	Yes
No	66.5% (121)	31.3% (57)		No

Tree source

Few museum trees can be traced or tied to a particular source due in part to the availability of such information in exhibit development records, and many institutions indicate that their exhibit trees reflect a collaborative process between museum staff and use multiple sources. Eight trees in this study were linked to specific references. Table 5 shows four museum trees alongside their corresponding source diagrams and highlights the differences. Generally, the museum trees do not differ significantly from their source graphics in terms of overall layout. However, the museum trees reflect modified taxonomic designations, simplify some aspects (e.g. fewer taxa), and provide additional information such as images of taxa and labeling common ancestors.

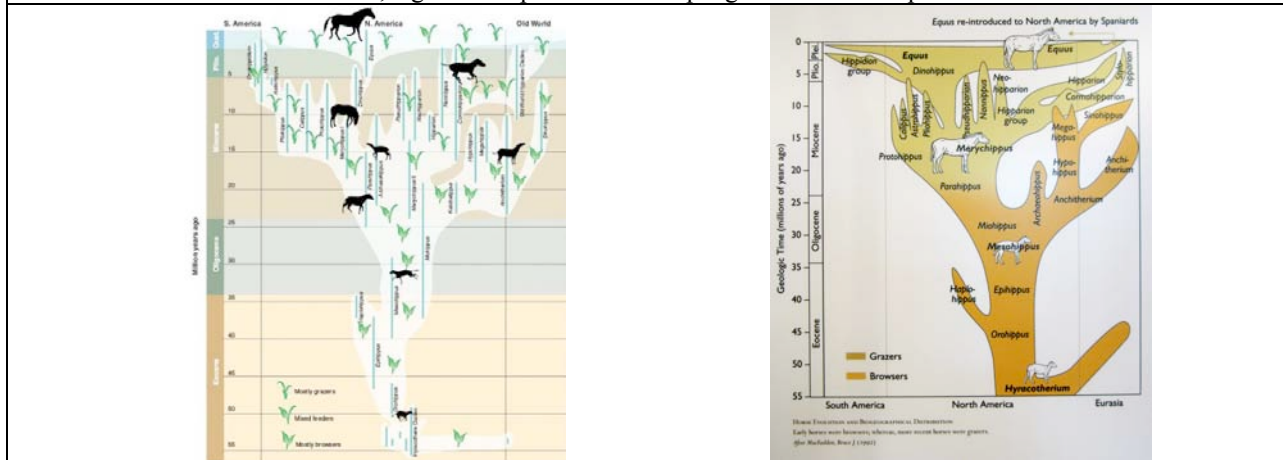
Table 5. Comparison of evolutionary tree diagrams in museums and their source trees.



Courtesy Amherst College Museum of Natural History, The Trustees of Amherst College (2006). Adapted from Boyd, R. and Silk, J.S. (2003) How Humans Evolved. WW Norton & Co Inc (Figure 11.30, from phylogeny in first published description of *Kenyanthropus platyops* in Nature).

Changes from source tree:

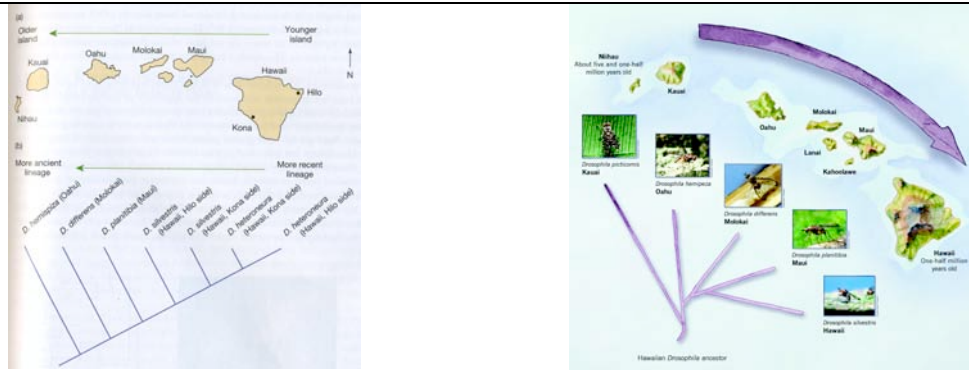
- Proposed connections between taxa absent
- Species depicted modified, e.g. *Kenyanthropus rudolfensis* = *Homo rudolfensis*, *Australopithecus bahrelghazali* absent, later *Homo* species defined, addition of *Pan* (chimpanzees)
- Position of some taxa shifted, e.g. *Homo* species on the top-right rather than top-left



Courtesy Amherst College Museum of Natural History, The Trustees of Amherst College (2006). Adapted from McFadden, B. (1992) Fossil Horses: Systematics, Paleobiology, and Evolution of the Family Equidae.

Changes from source tree:

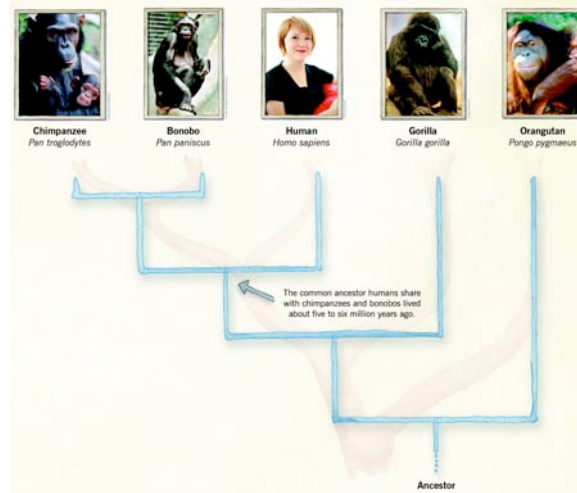
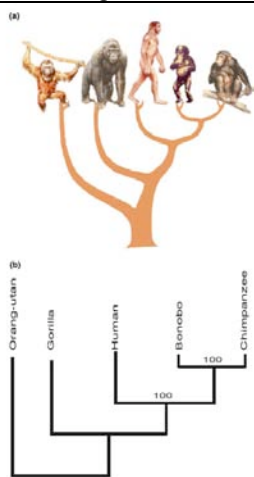
- Color coding used to distinguish browser and grazers, and white background
- Geographical distribution moved to bottom of diagram, and Old World changed to Eurasia
- Some genera renamed or absent, and fewer illustrations



Adapted from Freeman, Scott Herron, Ron Evolutionary Analysis 3rd edition 2004, modified by Kenneth Y. Kaneshiro.

Changes from source tree:

- Tree less comb-like (pectinate) and branches to the right
- More islands labeled and include topographical representation
- Ancestor labeled at root
- Millions of years added to islands
- Images of species added
- Excludes some species, and includes *Drosophila picticornis* on Kauai



Adapted from Kaessmann, H. & Paabo, S. (2002) The genetical history of humans and the great apes, Journal of Internal Medicine, 251:1-18.

Changes:

- Superimposed relatedness and molecular data diagrams (reliability values eliminated)
- Flipped horizontally
- Ancestor labeled at root
- Common ancestor of humans and chimps labeled with estimated date (mya)
- Scientific names added

Summary

Museums play an important role in communicating about evolution to the public (Diamond & Evans, 2007; National Science Board, 2008), and the organization of evolution exhibits is varied, which has implications for their understanding by diverse museum visitors (Diamond & Scotchmoor, 2006). Phylogenies represent the evolutionary history and relationships of organisms, and form a significant graphic element in museums. The long standing use of trees of life across a range of informal science institutions emphasizes the need to

assess their current use and explore strategies to increase their effectiveness as tools for communicating about evolution and the tree of life.

There is great diversity amongst tree of life diagrams used in museums, often within the same institution. In some cases this is deliberate to show alternative approaches to representing evolutionary relationships (Diamond, 2005), and in others it reflects a retention of older exhibits. As Diamond & Scotchmoor (2006) emphasized in their review of evolution exhibits, the way phylogenies are used determines their effectiveness in reinforcing fundamental concepts about evolution, and attention to the conceptual and developmental issues of how people understand evolution can make exhibits accessible to more audiences.

Overall, the findings of this study of museum trees are similar to those tree of life diagrams found in biology textbooks (Catley & Novick, 2008), but strict cladograms are less common and non-cladistic evolutionary trees are correspondingly higher in museums. In addition, obvious ‘Tree of Life’ depictions, and an anthropocentric bias towards a top-right placement of humans in vertical-upward orientated diagrams are not found in this sample of museum trees.

Many diagrams incorporate graphical elements such as variation in branch length and thickness that are not clearly defined, and therefore are difficult to interpret. It is possible that the ambiguity of diagrammatic elements in evolutionary trees may be ameliorated by labeling and making explicit references to the tree and its meaning in associated interpretative information, which was found to a varying extent in museum trees.

Some aspects of how trees are presented in museums may have the potential to hinder their use by visitors such as the absence of labeled common ancestors and synapomorphies in many trees. In addition, several topological elements common to tree diagrams such as linear depictions and vertical-upward orientation, may reinforce misconceptions about evolution, and support problems with interpreting trees such tip reading—interpreting the order of terminal nodes across the top, rather than the branching pattern, as relatedness.

How people interpret and understand evolutionary trees is a complex interaction between their prior knowledge, conceptions of underlying evolutionary concepts such as similarity, ancestry and relatedness, and their ability to read the relationships depicted in a schematic tree diagram. Further research is needed to explore how visitors interpret and understand these varied representations, the impact of prior knowledge, cognitive biases and folk narratives about evolution on understanding phylogenetic trees, as well as the influence of factors such as interactivity to help optimize the use of evolutionary trees in museums and enhance visitor understanding.

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Appendix A

As part of my doctoral research, and the NSF-funded *Understanding the Tree of Life* project, I am investigating the use of evolutionary tree diagrams in informal education settings including if and how they are used, as well as collecting examples of the graphics used for analysis.

This survey should only take a few minutes to complete and would help to assess how phylogenies are used and presented. The survey content should cause no more discomfort than you would experience in your everyday life. Your participation is solicited, although strictly voluntary. Your responses will be treated as confidential; however, it is possible with internet communications that through intent or accident someone other than the intended recipient may see your response.

Completion of the survey indicates your willingness to participate in this project and that you are at least age eighteen. If you have any additional questions about your rights as a research participant, you may call (785) 864-7429 or write the Human Subjects Committee Lawrence Campus (HSCL), University of Kansas, 2385 Irving Hill Road, Lawrence, Kansas, 66045-7563, email dhann@ku.edu.

Sincerely,

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Survey Questions

1) How would you describe your institution?

Natural History Museum
Science Center
Zoo/Aquarium
Other (please specify)

2) Please provide the name of your organization.

3) Do your exhibits use tree of life diagrams (graphics that depict evolutionary relationships) in any way?

Yes
No

3a) If you would be willing to share copies of trees graphics as part of this research study, please provide your contact information, or the most appropriate person at your institution, below.

Name

E-mail address

Phone Number

Thank you for your help!

Appendix B

List of informal science institutions that shared trees for this study. Asterisks (*) indicate partners in the *Understanding the Tree of Life* project (NSF Grant No. 0715287).

Institution	# trees shared
American Museum of Natural History	24
Amherst College Museum of Natural History	3
Australian Museum (AU)	7
Bell Museum of Natural History*	2
Booth Museum of Natural History (UK)	2
Boston Museum of Science	1
Bruce Museum	2
Canadian Museum of Nature (Canada)	3
Carnegie Museum of Natural History*	1
Central Michigan University Museum of Cultural and Natural History	2
Cincinnati Museum of Natural History & Science*	1
Cleveland Museum of Natural History*	6
Denver Museum of Nature & Science*	5
Denver Zoological Foundation	1
Duquesne University (SEPA project)	5
Elgin Museum (UK)	1
Exhibit Museum of Natural History, U. of Michigan*	8
Frank H McClung Museum, University of Tennessee	1
Harvard Museum of Natural History*	9
Hefner Zoology Museum, Miami University	1
Henry Doorly Zoo*	1
Houston Museum of Natural Science*	1
Indiana State Museum	1
International Wildlife Museum	1
Kendal Museum (UK)	1
Maxwell Museum of Anthropology	1
McWane Science Center	1
Midwest Museum of Natural History	1
Milwaukee Public Museum	1
Museum of the Earth, Paleontological Research Institute*	3
Museum of the Rockies	1
Naturalis (National Museum of Natural History, Netherlands)	4
New Mexico Museum of Natural History & Science	1
North Carolina Museum of Natural Sciences	3
Raymond M. Alf Museum of Paleontology	3
Royal Tyrrell Museum of Paleontology (Canada)	3
Sam Noble Museum Oklahoma Museum of Natural History*	15
San Diego Museum of Natural History*	2
Santa Barbara Museum of Natural History*	1
Santa Barbara Zoo	1
Science City	1
Smithsonian National Museum of Natural History	3
The Auckland Museum (NZ)	8
The Field Museum*	12
Thomas Condon Paleontology Center	1
University of California-Berkeley Museum of Paleontology*	2

University of Florida Natural History Museum*	7
University of Kansas Natural History Museum*	6
University of Nebraska State Museum* (includes 5 <i>Explore Evolution</i> trees)	8
Utah Museum of Natural History	3
Virginia Museum of Natural History*	1
Yale Peabody Museum*	2
Total	185