

The DeepTree Exhibit: Visualizing the Tree of Life to Facilitate Informal Learning

Florian Block, Michael S. Horn, Brenda Caldwell Phillips, Judy Diamond, E. Margaret Evans, and Chia Shen,
Senior Member, IEEE



Fig. 1. The DeepTree Exhibit: main view of the tree of life, image reel, and action button (left). Three kids collaboratively exploring the DeepTree (middle). Special learning activity for common descent, inheritance, and traits (right).

Abstract—In this paper, we present the DeepTree exhibit, a multi-user, multi-touch interactive visualization of the Tree of Life. We developed DeepTree to facilitate collaborative learning of evolutionary concepts. We will describe an iterative process in which a team of computer scientists, learning scientists, biologists, and museum curators worked together throughout design, development, and evaluation. We present the importance of designing the interactions and the visualization hand-in-hand in order to facilitate active learning. The outcome of this process is a fractal-based tree layout that reduces visual complexity while being able to capture all life on earth; a custom rendering and navigation engine that prioritizes visual appeal and smooth fly-through; and a multi-user interface that encourages collaborative exploration while offering guided discovery. We present an evaluation showing that the large dataset encouraged free exploration, triggers emotional responses, and facilitates visitor engagement and informal learning.

Index Terms—Informal Science Education, Collaborative Learning, Large Tree Visualizations, Multi-Touch Interaction.

1 INTRODUCTION

The design of information visualizations to support science learning in museums must strike a balance between scientific validity to educate, artistry to entice, and playfulness to engage. This form of visualization in public spaces is different from casual information visualization [46] in that museums often have specific scientific learning goals from the onset, requiring close collaboration among experts in a variety of disciplines. It also differs from visualizations designed for domain experts or analysts [24] in that the users of the visualization system are mostly novices with a diverse range of experiences and backgrounds.

In this paper, we present the DeepTree exhibit (cf. Fig. 1), an interactive visualization of the Tree of Life that illustrates the phylogenetic relationship of all life on earth. The DeepTree is part of a larger NSF-funded project called *Life on Earth* [1] with the aim of helping the public learn key concepts of biological evolution in informal science education

- Florian Block, Brenda Caldwell Phillips and Chia Shen are with Harvard University: {fblock, bcphillips, cshen}@seas.harvard.edu
- Judy Diamond is with University of Nebraska: jdiamond1@unl.edu
- Margaret Evans is with University of Michigan: evansem@umich.edu
- Michael Horn is with Northwestern University: michael-horn@northwestern.edu

Manuscript received submitted for review March, 31st.

(ISE) setting. The project is multi-disciplinary, consisting of two computer scientists, one learning scientist, two cognitive developmental psychologists, one museum curator, and five external science advisors. The DeepTree offers visitors an interactive visualization of the Tree of Life as a vehicle to grasp important evolutionary concepts including relatedness, biodiversity, common descent, and shared traits. The exhibit utilizes a multi-touch tabletop, and is designed for collaborative learning in museums. The DeepTree was tested and evaluated at the Harvard Museum of Natural History throughout the design and development process (from April 2011 to March 2012)

Our contribution in this work is three-fold: First, we present an analysis of the problem domain, deriving challenges and key questions. Second, we describe the design and implementation of a fractal tree layout algorithm based on a relative coordinate system and a custom-built rendering engine that provides seamless navigation through tree structures of unlimited size and depth. We developed this tree algorithm in conjunction with an interaction system and a multi-touch interface that allow a lay person to freely explore the tree, as well as to navigate to various points of interest enriched with learning content. The design of our exhibit is based on principles of informal science learning. Thirdly, we present insights collected from 18 months of iterative design, testing, and evaluation. We provide concrete lessons learned and guidelines for visualization and UI design for informal science education settings. We also highlight challenges faced when applying information visualization methodology to

informal learning designs, and provide indicators demonstrating that the size of the tree structure increases engagement, triggers emotional responses, and may provide a beneficial context for visitor learning.

2 THREE CHALLENGES

Four distinctive groups of stakeholders are usually involved in the development of an informal science exhibit: (1) designers and developers, (2) scientists and museum curators, (3) end users, and (4) learning researchers and evaluators. In our case the designers are information visualization and human-computer interaction specialists; the scientists are biologists; the users are museum visitors, and the evaluators are learning scientists and cognitive psychologists. This inter-disciplinary scenario gives rise to a set of design challenges to InfoVis.

2.1 Challenge 1: Users are not domain experts.

With the ubiquity of increasingly large hierarchical data sets, a significant body of research has focused on the visualization of large tree structures. A series of challenges have been addressed to optimize usage of screen real-estate [19,42,43,45,49,50,53], to provide a good global overview of the complex dataset [19,54,50], to facilitate effective navigation [34,36,43,45,50,51,52], and to support the comparison and analysis of large tree structures [21,30,40,51]. The majority of the proposed solutions have been driven by the requirements of expert audiences and professional domain tasks.

As the DeepTree is for a lay audience in informal science education, our tree visualization was subjected to different design criteria and required different solutions. First, visitors cannot be assumed to be familiar with the underlying dataset (even the phylogenetic tree representation may be foreign to visitors), thus in contrast to maximizing the amount of elements on the screen, we must prioritize aesthetics to attract visitors [25], and provide visual clarity so visitors can easily recognize the tree itself, its visual components, and its meaning in the context of evolution. Secondly, instead of navigating the tree as efficiently as possible, we want to utilize animated navigation techniques that purposefully unfolds each branching structure in the tree of life to convey the sense of scale of the tree of life and bio-diversity. Thirdly, interaction is needed to systematically and subtly guide the visitors in the learning and discovery process, in addition to afford walk-up-and-use as described in [25].

2.2 Challenge 2: Domain experts are not users.

Using information visualization for science learning also requires us to take extra care with the visual representation of the tree structure layout itself. Biologists illustrate phylogenetic trees in many different ways, ranging from a ladder or diagonal branching pattern, to a rectangular tree or a circular tree [20] depending on whether they are drawing on a blackboard, sketching on paper, making a PowerPoint slide or writing a scientific paper. For them, convenience (e.g., sketching) and space limitations (e.g., to publish a tree in a journal paper) might dictate the layout of the tree. Our biological science advisers can validate whether the phylogenetic trees we visualize are scientifically correct, but they do not have the expertise to fully judge whether certain layouts are optimal for a learner. In this case, we need to base

our visual designs on recent research on novice understanding of phylogeny [11,20].

2.3 Challenge 3: Guided free-choice interaction.

In the museum learning literature, Planned Discovery (PD) and Active Prolonged Engagement (APE) are two interactive exhibit paradigms pioneered and carefully examined by the San Francisco Exploratorium [29]. PD exhibits lead visitors through a set of prescribed scientific phenomena with directive labels, while APE exhibits are open-ended and experiential, enabling visitors to become active participants in the construction of meaning through the use of an exhibit.

In this problem space, interaction design plays a central role for information visualization in providing visitors with learning opportunities. Getting it right can give the visitor the ability to actively engage in the interactive visualization. One challenge is to not only allow visitors to interact with the encoded data, but also to enable multiple ways to move freely through the visualization in order to understand the learning content. Another challenge is to design the interaction to enable learning at user-selected levels, so that the system provides guidance for novices and depth for experts, while leading both to new inquiries and discoveries.

In the rest of this paper, we summarize how we addressed these three challenges in the design, development and evaluation of the DeepTree exhibit.

3 RITE FOR DESIGN AND EVALUATION

While information visualization [39], software engineering [15], exhibit design [29], and learning sciences [18] all advocate an iterative, or “spiral” approach to designing interactive systems, no existing methodology sufficiently addresses our three challenges. In the absence of single disciplinary experts who can continuously evaluate the efficacy of our visualization, we needed a process that could equally involve input from all four groups of stakeholders.

We utilized an adapted process of Rapid Iterative Design and Evaluation [38] – RITE – to drive the development of the DeepTree exhibit. RITE proposes rapid iterations of design driven by expert observations, in a fashion similar to formative evaluations. We were able to exhibit our interactive prototype in our partner museum, and let museum visitors interact on a walk-up-and-use basis. We obtained IRB approval to collect field notes and record video of visitor interaction for internal analysis (a sign pointed out that video recording was in progress). Our formative evaluator also obtained feedback from the visitors on their experience with our exhibit as they were leaving. Deployments between iterations varied in length, but were typically one week and involved approximately 20-40 users. A new iteration was begun when it became clear that our design goals were not yet met, or when software bugs prevented meaningful observations. Twelve iterations were conducted over the course of a year, with over 250 visitors observed in total.

RITE has a series of advantages. First, it allowed us to run all experiments in the museum setting where our exhibit would be installed with visitors who spontaneously interacted with our system – which is key to ensuring ecological validity. Secondly, in contrast to controlled experiments, the methodology is robust to (and in fact encourages) changes in design during the process, allowing us to quickly and

continually improve user experience and learning content, make remedial modifications, rather than continue throughout a study period with a possibly flawed system (as advocated by [55]). Thirdly, collected observational data (video / audio recordings) can be independently analyzed by our computer scientists regarding UI usage, by our learning psychologists to extract indicators for learning outcomes, and by our curator to judge issues related to user engagement.

RITE could also be extended by two additional assessment matrixes: 1) measures of active prolonged engagement [26,33] (APE), in which visitor engagement is derived based on dwell times and other interaction measures; and 2) discourse analyses in which conversations of selected groups were transcribed, coded and analyzed for learning indicators. While these matrixes take more time than expert observations (but less than full learning studies), they can be flexibly integrated into the RITE process.

4 DOMAIN PROBLEM AND DATA CHARACTERIZATION

The requirements for the DeepTree exhibit are to create a *collaborative* (R1) and *interactive* (R2) exhibit that uses a *visualization of the Tree of Life* (R3) as a platform to help *the wider public to learn about evolution* (R4). The specific learning goals were further specified by our learning scientists as follows:

- LG1 All life on earth is related.
- LG2 Biodiversity on earth is vast.
- LG3 Relatedness comes from common descent.
- LG4 Species inherit shared traits from common ancestors.
- LG5 Evolution is ongoing and happens over very long periods of time.

To inform our design, we translated the requirements and learning goals into a set of more specific design goals:

- G1 The tree rendering should be a) visually appealing, b) clearly show its components and minimize visual complexity, and c) have an easy to use interface.
- G2 Allow visitors to freely and seamlessly explore the tree of life.
- G3 Provide multiple entry points to engage with specific learning content.
- G4 Encourage multiple visitors to collaborate and work together when interacting with the exhibit.
- G5 The tree conveys the idea that a) its leaves represent “life”, b) that the tree includes “all” life, and c) that the tree’s branching pattern connects all leaves.
- G6 The tree conveys its enormous size.
- G7 Any two leaf nodes “meet” on an internal node that is the deepest common “parent” within the tree structure (most recent, in terms of time).
- G8 Internal nodes represent evolutionary innovations (traits) that through inheritance are passed down to all its children.
- G9 Time should be represented in the tree.

To build an interactive visualization that can achieve these learning goals requires a substantial dataset. We used data from a combination of four publicly available biological databases:

- (1) The Tree of Life Web Project (tolweb.org) [7] database is our primary phylogenetic tree dataset. It represents the

result of years of continuing collaboration by hundreds of scientists across the world. The data contains the phylogenetic tree itself, describing over 70,000 species (terminal branches) and 20,000 internal nodes with 123 levels of depth – defining the relationship amongst all species. The web portal [7] also provides about 8,000 thousand images for selected species. The database lacks many common names of species, species images, and time of divergence that are all required for our learning goals. We therefore further collected and merged data from three additional datasets.

- (2) Eol.org [2] catalogues over 1.6 million species along with imagery and common names.
- (3) NCBI [5] is a large database containing over 347,649 taxa and a large set of common names.
- (4) Timetree.org [8] provides estimates for times of divergence of any two species, from which we derive approximations of our internal nodes.

Through the respective web APIs of these databases, we walked through our base tree of tolweb.org and queried an additional 10,000 common names, 40,000 images and 250 timestamps for important internal nodes within our tree, which we selected.

5 RELATING TO PRIOR TREE VISUALIZATIONS

A list of around 230 tree visualizations can be found in [35]. The most relevant to our work are visualizations a) tailored for lay audiences, b) designed for large trees and c) visualizations of phylogenetic trees.

5.1 Tree visualization for the general public

Static phylogenetic trees are ubiquitously used in museums and schoolbooks ([37] provides a good overview). Most strikingly, educational tree visualizations make heavy use of color, rich imagery, and easy to understand labels, which are also reflected by our visualization. For the purpose of illustration, most of these examples either capture only a small selection of species (contrasting with G5 & G6), or show complexity but do not go down to the species level [10]. Another issue is that “organic”-looking tree illustrations do not map time / succession of nodes to a clear axis [10], making it hard to trace relationships between species (G7, G8), as well as to extract the direction of time (G9).

EMDialog [25] shows an interactive tree for an art museum – and thus targets the general public – but its layout and interaction techniques were not designed for large phylogenetic trees, nor multi-user interaction. Visualizations of family trees targeted at lay people [9,17] make relationships between nodes in the tree very apparent, but are not designed to scale up to thousands of nodes. Involv [33] is a interactive visualization of the Linnaean Taxonomy, which contains over 1.6 million species. The utilized Voronoi treemaps, just like all other treemaps, suffer from the fact that the underlying hierarchy is hard to discern [45,48,54]. Generally, we considered visualization based on tree-maps unsuited for our exhibit, as a central requirement was to clearly visualize the nested branching relationships between all species G6, G8 & G9.

5.2 Visualizing large trees

To a lay observer many existing visualizations of large trees do not “look like trees”. This includes radial and hyperbolic trees [12,21,36,54], treemaps [33,49,53], and other ways of depicting hierarchies that are prone to look “unconventional” to the non-expert, such as Information Pyramids [12], visualizations of hierarchical blood vessels [13], “island”-like 3D visualizations [14], point-based tree representation [50], or FlexTrees [51]. Another problematic artifact of rendering large trees is that when zoomed out large portions of the tree structure can merge into solid areas [34,40], making it hard for a lay person to recognize the tree or parse its structure. From a learning perspective, our visualization should be immediately and continuously recognizable as a tree structure, further its branching pattern and internal relationships should be easy to discern (G1a) and visual clarity (G1b). To satisfy both aesthetics (G1a) and visual clarity (G1b), we also dismissed literal “botanic” visualizations of trees [30] and settled on simple, but aesthetically pleasing Bezier curves, similar to [31].

Much work is concerned with optimizing screen usage [19,42,45,50,53]. While this is desirable from the standpoint of an expert, for a layperson it constitutes overwhelming complexity (G1b). Also, instead of optimizing the performance of navigation and node retrieval [34,45,52], we chose a fly-through algorithm that purposefully unfolds the tree branching structure in sequence in order to create a sense of the scale of the underlying dataset (G6). The stark contrast between our requirements and those of expert audiences is reflected in the layout of the DeepTree, which in prior work was discarded for its inefficiency regarding space use and navigation (cf. Space Tree [45], Fig. 9).

5.3 Visualizations of large phylogenies

Visualizations of large phylogenetic trees appear to be exclusively designed for professional audiences and domain tasks, such as those that visualize multiple traits [31], comparing large trees [40], visualizing clusters [21], and provide tree editing [34]. None of these examples seemed to provide solutions that catered for our requirements. Navigation of the tree of life has been a long standing challenge [44].

6 VISUAL ENCODING AND INTERACTION DESIGN

While presenting visual encoding and interaction design separately, both components were tightly entwined throughout the development process in order to ensure key learning steps for visitors. We will highlight these interdependencies throughout the subsections.

6.1 Rendering the Tree of Life

Our DeepTree visual design is based on recent research examining how learners comprehend phylogenetic trees that have been illustrated in textbooks [20] and museum exhibits [11], pinpointing problems leading to misconceptions and misinterpretations of the underlying scientific hypotheses.

In concurrence with related work [11,20], we found that different tree depictions may induce different conceptual interpretations of the underlying structure. First, the way we illustrated the branches had an impact on the way visitors perceived the tree. We started with a very abstract rectangular layout (Fig. 2a), which did not satisfy our need for aesthetics

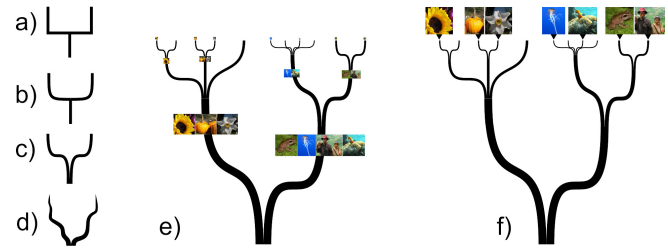


Fig. 2. Different ways of drawing branches (a-d) and positioning images (e&f).

(G1a); on the other end of the spectrum, we experimented with “organic” looking branches (Fig. 2d), similar to [30], but our learning psychologists wanted to avoid a too literal interpretation by the visitors, while still conveying the idea that the tree of life is in fact an abstract scientific model (G1b, G5c). To strike a balance between visual appeal and meaningful representation, we tried different types of Bezier-curves. “Elbow”-like curves (Fig. 2b) were visually appealing, but feedback from both science educators as well indicators from visitor observations showed that these curves convey a “sudden” split of an ancestral species, while in reality, speciation is a gradual process. In our final exhibit, we use curves as shown in Fig. 8c. These curves seemed to strike a good balance between attractiveness, conveying an abstract impression, and illustrating the gradual nature of speciation.

The placement of species images in the tree also had conceptual impact. Initially, we had no images at all, which lead to a clean, but “empty” look. Adding images clearly increased visual engagement and provided a crucial motivator for free exploration, but the placement of the images also led to problematic misconceptions. Fig. 2e) shows one of our initial placements: tolweb.org assigns a sample of representative species for each internal node, which we positioned at the branching points. On the positive side, the images gave internal nodes more meaning and guided visitors' exploration: as images reoccur through zooming in, people can find their preferred species in the tree (for example one kid played a game of “chasing the monkey”). On the downside, placing the pictures on the internal node seemed to convey the idea that these species were “already alive” at that point in evolutionary history, which is wrong (the internal node represents common ancestors that lived in past). Our final layout is shown in (Fig. 2f). We anchor our pictures to the fixed canopy line, where they are constantly visible, while providing illustrating “directions” or “pointers” to the species positions in the tree. We display two types of image pointers: as soon as a terminal node comes into view, the species' image “sprouts” out of its location. Additionally, we permanently display 200 “signpost” species in the tree, which are scaled to convey a sense of distance: as visitors zoom deeper into the tree, these signposts grow in size. This way of positioning the pictures brought the illustration of all current “life” to the conceptually correct location in the tree, avoiding the mentioned misconception, while emphasizing the value of the picture in terms of aiding navigation and motivating free exploration. The pictures are a major attractor in our exhibit, which lead us to design a navigation technique around the images as well.

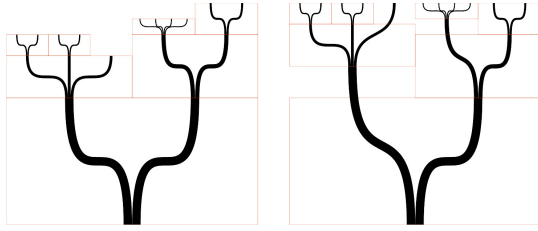


Fig. 3. Visualization of the DeepTree layout algorithm. Children are contained within the width of the parent node. (right) top aligned.

In order to reinforce the role of time in the tree (G9), we labeled 200 important internal nodes with their estimated time. We also only show labels for those nodes that exceed a certain screen size to minimize the amount of text that is simultaneously visible, reducing screen clutter (G1b).

6.2 Tree layout algorithm

The tree layout used by the DeepTree is shown in Fig. 3 (left). It is based on SpaceTree’s [45] “continuously scaled tree” – using fixed progressive scaling of the nodes. The principle governing this layout is that all children are fully contained within the width of the parent. This “fractal” rule leads to an exponential decrease of bounding box width based on the node’s level within the tree. For our purpose, this layout had several advantages. First, because of the rapid decrease of node size, only a few nodes are visible, as the lower levels rapidly shrink into sub-pixel “singletons”. This allowed us to maintain a clean, bare and intuitive look (G1) at all times. Secondly, the branches are laid out in a consistent coordinate system through which we can seamlessly zoom and pan (G2) – this was preferred by our learning experts over a layout with distortions (such as hyperbolic trees [41]) or frequent changes (such as expandable trees [45]) in order to avoid alternative interpretations by the learners. Due to the fractal nature of the layout, the same visual qualities apply to any given view, as the pattern of nested children continuously repeats itself. This enabled us to allow free exploration (G2), without compromising visual clarity and consistency (G1).

However, due to the size of our tree structure, which had 123 levels at its deepest point currently and will undoubtedly increase continuously, we ran into accuracy problems with the structure on which the bounding boxes of our nodes were based. As we are continuously sub-dividing the available width of a node to accommodate its children, we are also continuously decreasing the accuracy of the floating point of our bounding box. If we assume a perfectly bifurcated tree, in which every node has exactly two children, we would exhaust our floating point accuracy after 52 levels (a double floating point allocates 52 levels to the fraction), preventing us to further subdivide space for contained nodes. Accuracy problems on the implementation levels should be a concern for all fractal algorithms (such as [36][42][52]), however, we could not find any reference to this problem in prior work. Rendering “all life” – and being able to render both large and deep trees respectively was central to G5b & G6. Furthermore, we wanted to have a scalable layout and rendering engine that could accommodate future changes of the Tree of Life.

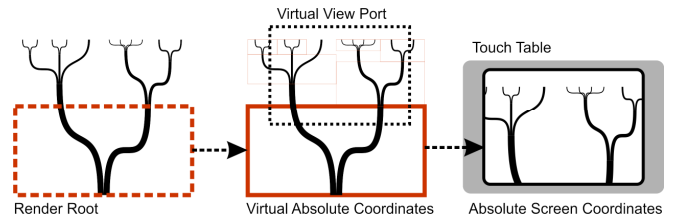


Fig. 4. Projecting relative coordinate system to absolute screen coordinate system.

Our solution was to implement a layout and rendering engine that is based on *relative* bounding boxes (a full technical description is available for download [3]): the bounding box of each node are expressed relative to the *top left corner* of its parent’s bounding box, and as multipliers of the parent’s bounding box’ *width*. In a first iteration, we calculated a relative distribution of nodes as shown in Fig. 2, left. However, our learning scientists criticized this layout as it positions species at different heights – which reinforces the misconception that some species are less evolved, while others are “higher” organisms. Top-aligning the tree removed this issue, as it moves every terminal node to the same vertical level (cf. Fig. 3, right). It also correctly conveyed time (G9) where the “canopy” embodies species that are alive today.

6.3 DeepTree Rendering Engine

Rendering any portion of our tree requires three basic steps: First we choose the lowest node that has to be visible – initially the root of the tree – and assign it absolute bounds in a virtual coordinate system (Fig. 4, left); second, based on the absolute bound of this *render root* and the relative definitions of their bounding boxes, we recursively calculate the absolute bounds of its children (Fig. 4, center); third, based on a viewport defined in the virtual coordinate system, we transform the virtual bounding boxes into screen space (Fig. 4, right). We can terminate the recursive calculation of bounding boxes when the size of a node’s bounding box is sub-pixel, or when it is horizontally outside of the viewport.

We can seamlessly navigate through the tree by translating and/or scaling the virtual viewport at each frame (basis for G2, G6), while applying two constraints. First, more detail can only be found in the very top of the tree – the canopy. Thus we always scale the viewport around the canopy, which causes the canopy to remain on the same vertical screen coordinate. Second, panning of the viewport is limited to the x-axis. These constraint had several benefits for us: 1) a portion of the canopy of the tree – the space in the tree where all the “life” is – would be always visible and at a consistent screen location, making it easy for visitors to keep it in focus, and use it as navigational aid (G5a); 2) it enabled a simple input gesture for manual navigation (G1&G2).

As we are zooming into the tree, portions of the tree will be outside the viewport (cf. Fig. 5, left, red highlight). When the viewport changes we define the deepest parent of all visible nodes as the new *render-root* (Fig. 5, left, “candidate”). The absolute virtual bounds of the new render-root, as determined in the previous render pass, is set as the new initial bounding box for the described calculations (Fig. 5, right). Additionally, both the viewport, as well as the initial

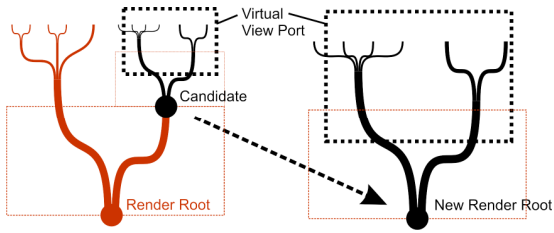


Fig. 5. Root transfer.

bounding box are multiplied by a factor, so that the accuracy of the floating point structures holding the bounding box is reset. This ensures that the structures holding the bounding boxes can always be sub-divided, at least until bounding boxes surpass pixel size, and the cut-off criteria is met, respectively. An equivalent process can be done when zooming out.

It is important to note that a root transfer is not visible to the viewer, as it simply recalibrates the viewport around a new visible root, which stays in a fixed screen location before and after the transfer. This was essential to support G2. The described rendering engine allows us to render and seamlessly navigate trees with unlimited depth and size (G5b&G6).

7 INTERACTING WITH THE DEEPTREE

The user interface of the DeepTree consists of three major components (cf. Fig. 1, left): the first is the main tree visualization, in which we provide basic interaction techniques to explore the tree; the second component on the very right is a scrolling image reel containing 200 species, which serves as the first entry point for learning; the third component is an “Action” button, centrally overlaying the image reel. Tapping the button reveals a sub menu with three items: “Relate”, “Find” and “Return”. Each of these components is described in the following subsections.

7.1 Basic Interaction Techniques

Interaction techniques should work for a single visitor and for a group of visitors equally well in museum settings. To satisfy G1 and G2, we wanted to provide simple and easy to understand means of navigating the tree. Initially, we drew on established gestures from multi-touch devices such as the iPad, where moving a single touch pans the view, and two touches moved away from each other/towards each other zoom in and out, respectively. These gestures, however, do not scale well to a multi-user scenario. As we cannot distinguish between touches of different users, two users trying to pan with a single finger look, to our touch mechanism, identical to a single user using two touches. Also, two users trying to zoom into different areas of the tree creates a conflict, as both compete for adjusting the viewport in different ways. To solve this problem, we utilize the fact that the canopy of our tree is fixed at a constant vertical screen coordinate. We created the following input metaphor: moving a finger left or right pans the tree left or right; moving a finger down “pulls” the tree downwards, revealing more branches at its canopy; moving a finger up “pushes” the tree upwards, shrinking detail and revealing nodes that are below the current view. Fig 6 illustrates this metaphor.

As both zooming and panning are expressed as a single directional gesture, we can also enable “flicking”, causing the motion of the tree to speed up until its momentum is depleted. This simple control for zooming and panning “scales” relatively well to multiple users: as soon as we sense multiple fingers, we can simply base our pan and zoom on the geometrical center of all touches (the average of all coordinate vectors). This enforces social cooperation and negotiation (G4): if two fingers move away from each other, they cancel each other out. If all users cooperate and “pull” into the same direction, the view is being updated accordingly.

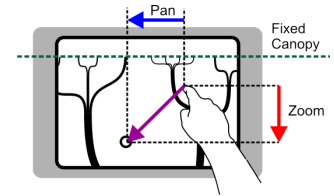


Fig. 6. Zooming and panning with a single finger gesture.

Our observation showed that visitors would spontaneously tap the images along the canopy, prompting us to facilitate this attraction to provide a complementary navigational aid. Initially, we experimented with automatically flying to a species once tapped, however, this method was discarded, as frequent accidental touches would trigger undesired effects. In our final exhibit, tapping only invokes a tooltip, prompting the user to hold the species. Once an image is held, it causes the tree to automatically zoom in towards the respective species. If the finger is released, the zoom stops.

7.2 Learning Entry Points

7.2.1 200 Signposts

While providing free exploration, we also wanted to introduce a series of entry points that would “lure” visitors to important points in the tree (PD), which were enriched with learning activities (G3). First, we added a scrolling image reel that contains 200 species. The species were selected by our evolutionary biologists and museum curators to represent major evolutionary groups, and to lead the visitors to areas in the tree that had additional learning content. The list can be scrolled manually by vertically sliding a finger along its elements. If a user taps a tile, it shows an animated arrow, prompting the user to drag the tile onto the tree (Fig. 7b). Once dragged, the tile detaches from the reel, and starts showing a “chord”, connecting the dragged tile with the actual position of the respective species in the tree (Fig. 7c). The current view automatically starts zooming towards the respective species, but only as long as the tile is held. If tiles are left untouched for several seconds, the tiles snap back into their space in the reel to prevent screen clutter (in response to kids frequently pulling out as many tiles as they could).

7.2.2 Relating Species

While visitors could effectively engage with our exhibit through free exploration, two of our core concepts – *Common Ancestry* and *Shared Traits* – and the corresponding design goals G7 and G8 were not commonly discerned by our museum audience. In response, we introduced a “Relate” function through an “Action” menu (Fig. 7a), which allowed users to drag any two species from the reel into a target UI slot (Fig. 7d), causing the tree to automatically fly to the most recent common ancestor of both species. Upon arrival, the

lineages of both species are visually highlighted and a bouncing button appears at the location of the most recent common ancestor. This is the entry point for a separate activity – the trait display – as shown in Fig 1, right. Upon tapping the button, the current view is shrunk into the top-left corner of the display, revealing a simplified tree that shows selected important groups, and the two selected species. Bouncing buttons appear at a series of shared ancestors that, when tapped, “flood” the respective groups with color. Information bubbles appear that point out that all highlighted organisms have inherited a special trait from a shared ancestor. A “learn more” button can be tapped to get a description of the trait’s evolutionary meaning (e.g. “Jaws are used for hunting and eating”), as well as illustrating the trait in members of this group.

7.2.3 Fly Me There

Based on visitor feedback, we also provided a “Find” function, which allows users to automatically fly to a species selected from the image reel.

7.2.4 Animation as attractor and “encoding”

Animation can attract attention, support object consistency, and be emotionally engaging which were all desirable attributes for our exhibit [23]. Both our “Relate” and “Find” function are based on an animated flight through our tree space. This fly-through takes varying amounts of time, from a fraction of a second when one flies to a close-by species up to several seconds when navigating between species that are separated by high numbers of branching points. We found that apart from attracting and engaging visitors, this animation had several learning effects. First, when making multiple successive “Relate”-queries (e.g. Human-Chimp, Human-Banana), visitors make inferences regarding the relative “closeness” of both species based on the direction of the fly-through: if the tree zooms out, the two species that are compared are further related than the previous pair, and vice versa (G7). We saw this type of inference frequently, for example, comparing humans and X. The length of the fly-through was also effective in conveying the size of the tree, and the vastness of biodiversity (G6).

Additionally, the path of the fly-through was chosen to fly from species to species via their common ancestor – enforcing G7. As the speed of the animated viewport comes to a temporary halt before it starts accelerating, visitors are also able to read the time label of the common ancestor, which adds the concept of deep time to automatic fly-through (G9).

7.2.5 Multi-user interface

Similar to our basic interaction technique, which scaled to larger groups by enforcing cooperation, we wanted to provide a touch interface to access our functions that would adhere to similar principles. In our initial designs we used buttons – hence tapping – as the primary mode of navigating to points of interest. However, buttons were prone to accidental activation [47] (e.g. through sleeves) and even when intended other collaborators often lacked the awareness for cause-and-effect in our interface, as tapping is easy to overlook. To remedy this issue we introduced the “slot-tile-drag” interface metaphor that are used for our Find and Relate actions. First, dragging is less prone to being accidentally invoked than tapping. Dragging elements towards a target slot in the center

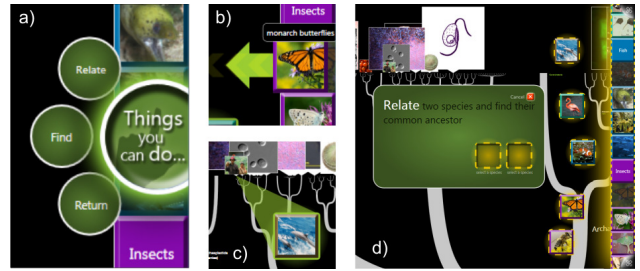


Fig. 7. DeepTree UI: a) action menu, b) image reel, c) chord to species location, and d) Relate dialog

of the screen is also easier to detect by all by-standers. It is also possible to anticipate and intervene, for instance, by physically blocking hands, or by covering the target slot with a hand. Generally, we found this system to work very well in practice as it encouraged consensual navigation of the tree.

Regardless of its suitability, tapping was the most common spontaneous way of interacting with graphical elements, and was observed to also be the first type of interaction with our species tiles on the side. Consequently, we used the tap modality to invoke visual instructions: if a tile is tapped, an animated arrow shows up for few seconds, and if a slot is tapped, and “shadow hand” performs a drag motion from the reel to the slot. This was usually sufficient instructions for users to drag the species tiles out onto the tree. We can generalize our UI interface principles as follows:

- Tapping is the most common spontaneous way of interacting with graphical controls, so buttons should be used for all *local* actions that do not affect the experience of all participants.
- Tapping should *not* be used for actions that trigger *global* changes, as it is a) prone to accidental touches and unintended action and b) easily goes unnoticed.
- Dragging visual elements to the center of the screen is the most suitable form of triggering a *global* change, as it enables anticipation and possibility for intervention.
- Dwelling can be used for elements that clutter the screen, as it requires active attendance to maintain an effect.

Based on these criteria, the final interface presented in this paper enabled the majority of visitors and visitor-constellation to effectively collaboratively interact with the DeepTree after an acceptable learning curve – it took some visitors a few seconds to learn about the action button, and dragging the species tiles, but even little children could perform required interactions with relative ease.

8 EVALUATION

In this section, we present an analysis of our observational data, which was conducted as part of our extended RITE method. We recorded conversations of 18 visitor groups to extract insights in regards to engagement and group discourse (6 multi-generational groups, 7 child dyads, 2 young adult dyads, 2 single older adults, and 1 single child). Most of the groups approached the table on their own. We then observed free exploration, and presented visitors with posttest questions. All interactions were recorded and utterances were transcribed and coded for 4 selected groups. We do not include discussions on demographics or group constellation in museums, as it is described in depth in [16,25].

8.1 User-Selected Level of Learning

A general observation we made was that the large dataset serves different purposes for different levels of learning. To visitors with basic biological knowledge, the size of the large tree encourages free exploration and conveys the vast size of biodiversity. Many college students have been exposed to phylogenies before, and are well versed in evolutionary biology. For this group of visitors, the tree allows them to see a seemingly complete tree of life for the first time. It is important to note that the size of the tree seemed to *enable* more advanced learners to make deeper connections with their preexisting knowledge, while *not hindering* the beginner in their discovery of more general and basic information. For example, when asked to describe the exhibit following exploration, beginners made comments such as “How anything, like anything, can relate to anything...like, for example, humans can relate to anything like a banana or coral fish” and “How far they go back...how long ago they have a common ancestor.” Advanced learners made comments such as “The relation between humans and bananas is something I never would have thought about” and “You learn in class that everything is connected...we all came from this little cell that started somewhere, but to think of it this way, we are all connected...from that direct line.” Both beginners and advanced learners commented on the deep time displayed: “Whoa! Fourteen million years ago...that’s a long time ago!” and “We’re going back to the distinction between animals and plants so we are going back a very, very, very long way.”

8.2 Engagement

Groups spent an average of 8:30 minutes at the exhibit (range 3:50 – 15:40). Groups accessed our “Relate” and “Find” function between 1 and 6 times.

Engagement through free exploration of a large dataset. The measured dwell times exceeded those of regular exhibits, and indicate that our exhibit could facilitate active prolonged engagement (APE) [29]. Children, in particular, engaged in manual exploration of the tree. Over the course of our iterative design, we have established that the size of the tree, and enriching the data with images and common names are both essential to facilitate exploration. In previous iterations, our dataset had significantly less imagery and common names. We also tested smaller trees (same layout and rendering engine, but only containing our 200 “signpost” species). While we did not continuously measure dwell times, our observation throughout several iterations showed a clear qualitative improvement regarding the level of engagement through providing an enriched large dataset.

Striking a balance between APE and PD. All groups used at least once our “Relate” and “Find” function, which led to planned discovery (PD) of our trait display. As these actions were triggered through visitor’s own initiative, and the parameters were chosen freely, we prefer to use the term Guided Discovery (GD), as it may appear to the user as if they bumped into the content by free choice.

8.3 Discourse Analysis

Based on four selected groups (1 multigenerational, 1 child dyad, 2 young adult dyads) we coded 264 utterances in total.

The utterances were categorized into biological content (23%), questions (16%), affective responses (9%) and other: e.g., UI statements (52%). We further analyzed all biological content, as shown in Table 1. The discourse analysis provided two more indicators:

Conveying our learning goals. The discourse analysis indicated that we had brought all core evolutionary concepts to the visitor’s attention (LG1, LG3, LG4 and LG5), albeit at different intensities: relatedness (LG1) was the most prominent topic, which we attribute to the introduction of the “Relate” function. Our results emphasize that interactions can be used to “encode” learning concepts quite effectively.

Affective effect of the size of the tree. Our discourse analyses revealed that for our four selected groups 9% of all utterances were affective statements. During fly-through, we frequently observed emotional utterances, such as “wow, this is big” or “woah”. This also indicated that we had met LG2, in conveying the vastness of the tree, while emotionally engaging our audience through our seamless animated flight.

9 DISCUSSION

To inform the design of information visualization for informal learning environments, we reflect upon lessons learned, insights gained, and design principles derived from our research.

From entry point to deep engagement

Existing work has highlighted the importance of providing *entry points* to entice people into engagement, and *access points* to enable users to join an activity [28,29]. In particular, [29] presented the APE (Active Prolonged Engagement) framework for museum exhibits and described the intricate relationship between designs for fluid entry points for initial engagement and trajectories for prolonged engagement to learn. Throughout our iterative design, we have experimented with classical entry points or “lures”, such as attract screens or entry-activities, which lose their role once initial engagement is established. Previous studies have demonstrated that this type of entry points may provide little in terms of visitor understanding of the underlying exhibit content [27]. We have found that particularly for a learning-based visualization, it is beneficial to embed learning concepts directly and clearly in the visual and interactive components so that these components can serve as *both* initial engagement lures *and* seamless transitional pathways into deeper cognitive activities. This design principle is reflected in our learning access points of “Relate” and “Experiment”. Our findings also show that the DeepTree visual representation itself provides not only initial attraction, but also induces engaged exploration, and remains as the primary visual anchor for visitors’ interaction activities.

Collaboration and Sequential Interaction

In the design of interactive museum exhibits, it is crucial to facilitate social play, meaningful interaction, and collaboration [22,29]. Collaboration on multi-touch tables is often associated with users *simultaneously* touching. Parts of our UI design may at the first glance appear to not facilitate this mode of operation as our visitors interact with the DeepTree functions in goal-directed short sequences. Our underlying design rationale is to create a set of shared,

consistent learning trajectories that visitors can walk through *together* to facilitate their collaborative learning, as opposed to providing an environment, in which visitors simply interact “alongside of each other”. We found that our DeepTree UI design leads to naturalistic and cooperative turn-taking, while encourages active discussions amongst visitors. Our drag-based selection of species tokens for the Find and Relate functions allowed episodic collaborative decision making, in which multiple participants would concurrently try to pick different species for the next learning and discovery step. Similarly, the DeepTree navigation mechanism employs a participatory approach, allowing all participants to at least influence (in the form of zooming or panning together) while not disrupt the navigation of the tree. Meanwhile, the tree visualization itself also provides opportunities for cognitive participation by everyone in a group. We found that the DeepTree UI design, with entry and access points that lead visitors into meaningful engagement was successful in fostering lively social interaction and collaboration [21,31] around the table.

User Interface as “Coding” for Learning Entry Points

The introduction of the Relate-function significantly changed the way in which visitors perceived and experienced our visualization. In early iterations, we did not provide a “Relate” function, but relied on visitors themselves to discern “Relatedness” from the tree branching patterns itself. This led to an *encyclopaedia*-style experience in which visitors simply looked up single species “at the tips” of the tree. After the introduction of the Relate function, this was still an issue as the Relate function was second in the menu of actions, which again favoured the Find action. Simply moving the Relate menu item to the top of the list, however, shifted the focus to relatedness, and the tree structure itself. This indicates that the user interface and the manner in which interface content is presented may be of high importance when designing visualizations for learning and education environments.

“The Bigger Picture” and Multiple Representations

We have considered providing a miniature “overview map” of the tree (a World in Miniature, WIM). There are no existing solutions for the design of a WIM for phylogenetic trees. There are two inherent difficulties to construct such a WIM. First, phylogenetic trees are congruent about the internal nodes; the subtrees can be rotated around their common parent node without changing the evolutionary relationship amongst the child subtrees or the terminal species. Therefore the left-right relationship amongst terminal species does not represent a constant distance relationship as in a geospatial map in general. Secondly, we could not utilize the fractal layout of the DeepTree, as deeper nodes and locations of terminal species quickly merge into a singleton pixel due to the exponential decrement of node sizes. In an experiment, we used a more conventional layout (similar to [34]) that allowed us to spread the tree more evenly. This allowed us to highlight distinct groups (e.g. Birds, Fish, Mammals, Insects), and the visitors’ current relative visual location within this “tree map”. While this approach created some sense of the big picture, visitors struggled to map the WIM to the DeepTree as the two representations used different layouts and had different visual rendering. Consequently, we concluded that for our case, the benefits of an overview could not justify the

cognitive load introduced by multiple representations. More generally, we think that when visualizing large data sets for learning, the need for visual simplicity might often outweigh the benefits of overview.

10 CONCLUSION

Through our research on the DeepTree exhibit, we have derived a set of generalizable insights and design guidelines for InfoVis in the domain of informal science education. We demonstrated RITE as a useful design and evaluation process for an inter-disciplinary, multiple-stakeholder InfoVis project. For learning and education, the particular style and rendering of the visual design and aesthetics have a strong impact on the viewer’s perception of the underlying scientific concepts. Efficiency in terms of data density and time-of-flight should be examined in light of their affordances for learning as well. Careful animation of a large structure can be emotionally engaging and play a role in a learner’s understanding of scale and time. The interplay of interaction and visualization should be at the center of a design for learning applications in order to engage and guide the learners through meaningful free-choice visual activities.

Natural history museums and science museums have a long history of designing exhibits that offer their visitors unique opportunities in informal science education. Visitors in these museums are a self-selected population that would like to or are brought to experience learning in an informal setting. Information visualization can play an important role and is becoming more commonplace in these museums. We hope that our experience and approaches reported in this paper can help designers of similar visualization systems in the future.

11 ACKNOWLEDGMENTS

We thank the Harvard Museum of Natural History, for allowing us to conduct this research in their galleries. We also thank our science advisers: Gonzalo Giribets, James Hanken, Hopi E. Hoekstra, Jonathan Losos, David Mindell, and Mark Westneat. Thanks to Sebastian Velez for selecting our signpost species and for his constructive feedback. We thank the National Science Foundation for their support of this project (DRL-1010889). Any opinions, findings and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation.

<i>Topic (%)</i>	<i>Example statement</i>
Relate (32%)	Let’s find out how tigers and people are related. You were related to a banana.
Tree (17%)	Are we on the same branch on the same tree?
Time (14%)	What do you want to trace back? That was a long time ago!
Branch (5%)	See, the two different branches here are so close to each other?
Species(2%)	Are these species?
Common Ancestor (3%)	Is this your common ancestor?
Common Thread (2%)	So, this is the common thread?
Other (20%)	It goes all the way back to fish. Hedgehogs, shrews, moles, and others are in between us.

Table 1. Analysis of biological utterances.

References

- [1] Life on Earth Homepage. <http://sdr.seas.harvard.edu/life-on-earth>
- [2] Encyclopedia of Life. <http://eol.org/>
- [3] The DeepTree Layout and Rendering Engine (technical appendix): <https://lifeonearth.seas.harvard.edu/downloads/DeepTree.pdf>
- [4] National Science Board. (2008). Science and Engineering Indicators 2008 (NSB 08-01; NSB 08-01A). Arlington, VA: US Government Printing Office.
- [5] NCBI Taxonomy. <http://www.ncbi.nlm.nih.gov/Taxonomy/>
- [6] Technische Universiteit Eindhoven, SequoiaView
http://w3.win.tue.nl/onderzoek/onderzoek_informatica/visualization/sequoiaview//
- [7] Tree of Life. <http://www.tolweb.org>.
- [8] TimeTree. <http://timetree.org/>.
- [9] Washington Post. The Kenedy Family Tree.
<http://www.washingtonpost.com/wp-dyn/content/graphic/2009/08/12/GR20090812000333.html>
- [10] Hu, Y., ATT Research Labs:
<http://www2.research.att.com/~yifanhu/TOL/>.
- [11] Understanding ToL. <http://evolution.berkeley.edu/UToL/index.html>
- [12] Andrews, K. and Heidegger, H. Information slices: Visualising and exploring large hierarchies using cascading, semi-circular discs. In *Proc. InfoVis'98*, pp. 9-12. IEEE Computer Society, 1998.
- [13] Aydin, B., Pataki, G., Wang, H., Ladha, A., Bullitt, E., and Marron, J.S. Visualizing the structure of large trees. arXiv.org e-print service, 1001.0951v2, 2010.
- [14] Balzer, M. and Deussen, O. Hierarchy based 3D visualization of large software structures. *Visualization'04: Poster*, pp. 81-82. 2004.
- [15] Boehm, B. (1986). A spiral model of software development and enhancement. *ACM SIGSOFT Software Eng. Notes*, 11(4), pp. 14-24.
- [16] Diamond, J., Luke, J. J., Uttal, D.H. Practical evaluation guide: tool for museums and other informal educational settings. *American Association for State and Local History book series*, Rowman & Littlefield, 2009.
- [17] Eichorn, E. Family tree visualization.
http://www.elisabetheichorn.de/_en/projekte/weiter/stammbaum/stammbaum.html
- [18] Evans, E. M., Weiss, M., Koke, J., Storksdieck, S., & Kennedy, J. (July, 2008). Conversations Across Disciplines: From Theory to Practice-The Spiral Model. Panel Presentation at the Annual Meeting of the Visitor Studies Association, Houston, TX.
- [19] van Ham, F. and van Wijk, J. J. Beamtrees: Compact visualization of large hierarchies. In *Proc. InfoVis'02*, pages 93-100, 2002.
- [20] Gregory, T. R. Understanding evolutionary trees. *Evolution: Education and Outreach* 1, 2 (2008), pp. 121-137.
- [21] Heard, J., Kaufmann, W., and Guan, X. A novel method for large tree visualization. *Bioinformatics*, 25(4), pp. 557-558, 2009.
- [22] Heath, C., vom Lehn, D. and J. Osborne (2005). "Interaction and Interactives: collaboration and participation with computer-based exhibits." *Public Understanding of Science* 14(1), 91-101.
- [23] Heer, J. and Robertson, G. Animated Transitions in Statistical Data Graphics. *IEEE Transactions on Visualization and Computer Graphics* 13, 6 (November 2007), pp. 1240-1247.
- [24] Heer, J. and Shneiderman, B. Interactive Dynamics for Visual Analysis. In *Queue* 10(2), 2012, ACM.
- [25] Hinrichs, U.; Schmidt, H.; Carpendale, S.; , "EMDialog: Bringing Information Visualization into the Museum," *TVCG*, vol.14, no.6, pp.1181-1188, 2008.
- [26] Horn, M.S., Leong, Z.A., Block, F., Diamond, J., Evans, E.M., Phillips, B., and Shen, C. (2012). Of BATs and APes: An interactive tabletop game for natural history museums. In *Proc. CHI'12*, ACM Press.
- [27] Hornecker, E. "I don't understand it either, but it is cool" Visitor Interactions with a Multi-Touch Table in a Museum. *Proc. of IEEE Tabletop 2008*. 121-128.
- [28] Hornecker, E., Marshall, P., Rogers, Y. Entry and Access – How Shareability Comes About. *Proc. of DPPP'07*, 328-342.
- [29] Humphrey, T. and Gutwill, J. Fostering active prolonged engagement: The art of creating APE exhibits. *Exploratorium* (2005).
- [30] Kleiberg, E., van deWetering, H., and van Wijk, J. J. Botanical visualization of huge hierarchies. In *Proc. InfoVis'01*, pp. 87-94. IEEE Computer Society, 2001.
- [31] Lee, B., Nachmanson, L., Robertson, G., Carlson, J. M. and Heckerman, D.. PhyloDet: A scalable visualization tool for mapping multiple traits to large evolutionary trees. In *Bioinformatics*, 25(19), pp. 2611-2612.
- [32] vom Lehn, D., Heath, C. and J. Hindmarsh (2001). "Exhibiting Interaction: Conduct and Collaboration in Museums and Galleries." *Symbolic Interaction* 24(2): 189-216.
- [33] Horn, M. S., Tobiasz, M., and Shen, C. Visualizing biodiversity with Voronoi treemaps. In *ISVD'09: Proceedings of the International Symposium on Voronoi Diagrams*, pp. 265-270.
- [34] Huson, D. and Richter, D. and Rausch, C. and Dezulian, T. and Franz, M. and Rupp, R. Dendroscope: An interactive viewer for large phylogenetic trees. *BMC bioinformatics* 8(1), pp. 460, 2007.
- [35] Jürgensmann, S., Schulz, H.-J. A Visual Bibliography of Tree Visualization 2.0. <http://www.informatik.uni-rostock.de/~hs162/treeposter/poster.html>.
- [36] Lamping, J. and Rao, R. The hyperbolic browser: A focus+ context technique for visualizing large hierarchies. *Journal of Visual Languages and Computing*, 7(1), pp. 33-55, 1996.
- [37] MacDonald, T. and Wiley, EO. Communicating Phylogeny: Evolutionary tree diagrams in museums. In *Evolution: Education and Outreach*, pp. 1-15, Springer, 2010.
- [38] Medlock, M. et al. The Rapid Iterative Test and Evaluation Method: Better Products in Less Time. Cost Justifying Usability, An Update for the Internet Age. Boston, Morgan Kaufmann, 2005.
- [39] Munzner, T. A Nested Model for Visualization Design and Validation. In *Visualization and Computer Graphics, IEEE Transactions on* , vol.15, no.6, pp. 921-928, Nov.-Dec. 2009
- [40] Munzner, T., Guimbretiere, F., Tasiran, S., Zhang, L., and Zhou, Y. TreeJuxtaposer: Scalable Tree Comparison using Focus+Context with Guaranteed Visibility. In *Proc. SIGGRAPH 2003*, published as ACM Transactions on Graphics 22(3), pp. 453-462, 2003.
- [41] Munzner, T. H3: laying out large directed graphs in 3D hyperbolic space. In *Proc. InfoVis'97*, pp. 2-10, 1997.
- [42] Neumann, P., Carpendale, S., and Agarawala, A. Phyllotrees: Phyllotactic patterns for tree layout. *Proc. EuroVis'06*, pp. 59-66, 2006.
- [43] Nguyen, Q. V. and Huang, M. L. EncCon: an approach to constructing interactive visualization of large hierarchical data. *Information Visualization*, 4(1), pp. 1-21, 2005
- [44] Page, R. Phylogenetics & Phylogeography, Presentation, VizBe 2011.
- [45] Plaisant, C.; Grosjean, J.; Bederson, B.B. SpaceTree: supporting exploration in large node link tree, design evolution and empirical evaluation. In *Proc. InfoVis 2002*, pp. 57- 64, 2002.
- [46] Pousman, Z., Stasko, J. T., and Mateas, M. Casual information visualization: Depictions of data in everyday life. *IEEE Transactions on Visualization and Computer Graphics*, 13(6): pp. 1145-1152, 2007.
- [47] Ryall, K., Forlines, C., Shen, C., Morris, M. R., and Everitt, K. Experiences with and Observations of Direct-Touch Tabletops. In *Proc. TABLETOP '06*, pp. 89-96, 2006.
- [48] Sandberg, A. Hilbert tree of life.
<http://www.flickr.com/photos/arenamontanus/1916189332/in/set-72157594326128194/>, 2007.
- [49] Shneiderman, B. Tree visualization with tree-maps: 2-d space-filling approach. *ACM Transactions on Graphics*, 11(1), pages 92-99, 1992.
- [50] Schulz, H.-J.; Hadlak, S.; Schumann, H. Point-based tree representation: A new approach for large hierarchies. *Visualization Symposium*, 2009. PacificVis '09. IEEE Pacific , vol., no., pp.81-88, 20-23 April 2009
- [51] Song, H., Curran, E. P., and Sterritt, R. FlexTree: visualising large quantities of hierarchical information. In *SMC'02: Proceedings of the IEEE International Conference on Systems, Man and Cybernetics*, IEEE Computer Society, 2002.
- [52] Teoh, S.T. and Ma, K.-L.. RINGS: A technique for visualizing large hierarchies. In *Proc. GD'02*, pp. 51-73. *Lecture Notes in Computer Science*, Springer, 2002.
- [53] Nguyen, Q. V., and Huang, M. L. EncCon: an approach to constructing interactive visualization of large hierarchical data. *Information Visualization*, 4(1), pp. 1-21, 2005
- [54] Wang, W., Wang, H., Dai, G., and Wang, G. Visualization of large hierarchical data by circle packing. In *Proc. CHI'06*, pp. 517-520.
- [55] Wigdor, D., Wixon, D. Brave NUI World | Designing Natural User Interfaces for Touch and Gesture. Morgan Kaufmann, 2010.