Combining Interactive Hierarchy Visualizations in a Web-based Application

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Abstract: In this paper we describe a web-based tool combining several hierarchy visualization techniques. Those run in a browser and support the communication of hierarchy data that is omnipresent in many application fields like biology, software engineering, sports, or in algorithmic approaches like hierarchical clustering. To this end we provide node-link diagrams, Pythagoras trees, circular, as well as 3D treemaps also called 3D step-trees to give several visual perspectives on the same data and to improve data exploration tasks. The visualizations are interactive and linked, while the tool is available online, making it easily accessible for people all around the world without installing extra software or relying on additional libraries and frameworks. Hierarchy datasets can be uploaded to a server and shared with others. The visualizations were primarily implemented using JavaScript, and more specifically, rendered using the D3.js library. We illustrate the usefulness of the interactive visualization by applying them to the NCBI taxonomy and the Influenza dataset.

1 INTRODUCTION

In this paper we describe a visualization tool capable of producing several data visualizations for hierarchical data, implemented such that users can interact with them online. For reasons of better visual communication we implemented four different visualizations to show a dataset in several perspectives, as only one may provide a limited view. All visualizations are linked, which is especially practical for comparing datasets. Moreover, the tool can easily be extended by extra hierarchy visualizations.

To this end we support node-link diagrams (Reingold and Tilford, 1981; Burch et al., 2011), Pythagoras trees (Beck et al., 2014a), circular treemaps (Zhao and Lu, 2015; Hlawatsch et al., 2014) as well as 3D step-trees (Bladh et al., 2004) (see Figure 1) based on the general concept of treemaps (Shneiderman, 1992). All of the provided visualizations have their strengths when it comes to visual communication and hierarchy data exploration tasks. For example, node-link diagrams give a detailed overview of the whole dataset and can be particularly useful if the dataset is relatively small because then all connections and relationships can be seen easily and clearly. The circular treemap on the other hand can give a more global picture of the structure of a dataset, and can be useful if individual connections are not of major importance. The Pythagoras tree gives an aesthetical overview of a dataset, especially when using an appropriate coloring. Lastly, the 3D step-tree shows the data in a 3D visualization, giving the possibility to rotate around 360 degrees and interact with the data dynamically. Moreover, due to their similarities to trees in nature and color codings, Pythagoras trees and 3D step-trees might be considered aesthetically appealing which is an important criterion for effective visual communication (Brath et al., 2005).

All of these visualizations are interactive in order to support dynamic visual communication and hence, to make them even more useful in trying to learn about the data. The user is given the possibility to zoom, pan, hover, and rotate the visualizations and clicking the nodes of the visualizations helps to import or export data. Another aspect of dynamic communication is user friendliness, hence we provide our techniques online in a web browser avoiding the challenges of installing extra software. Users can upload their own hierarchy data to a web server that can then be shared with all the other users to explore some other unfamiliar datasets for example. Snapshots of the visualizations can be produced easily allowing the data to be visually presented and disseminated, for example in a scientific publication or when giving an

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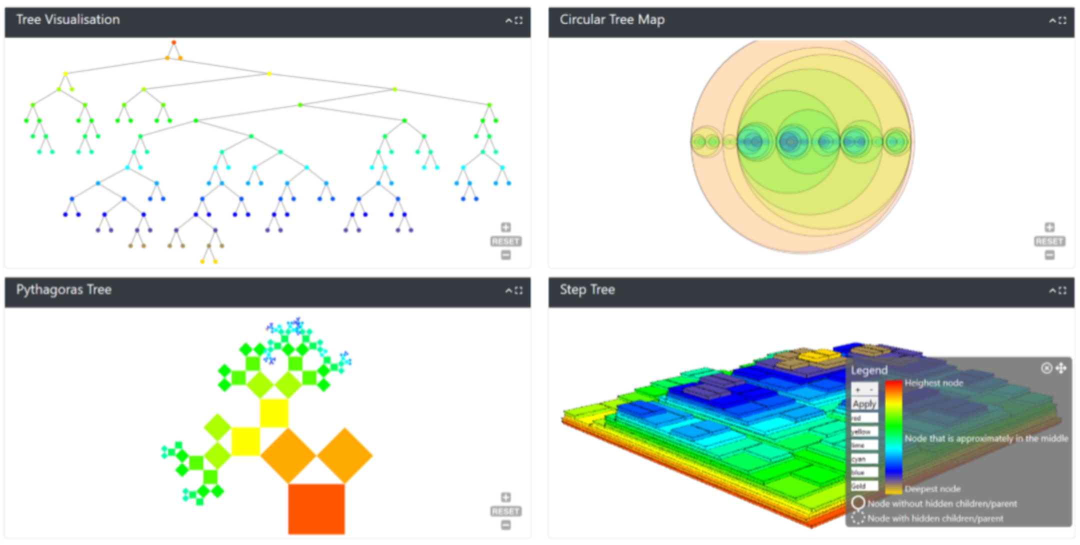
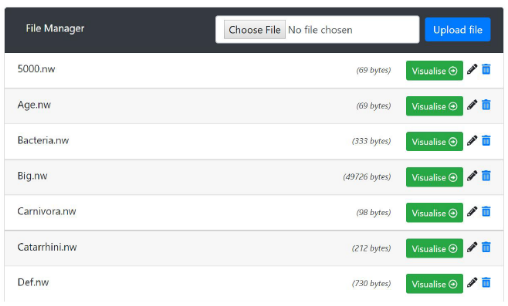


Figure 1: A screenshot of the default view of our visualization tool with a dataset about carnivores, nodes colored according to depth. Each card can be repositioned, collapsed/expanded, and set to full-screen mode. In the legend the meaning of the colors is described which can also be changed interactively and adapted to the dataset scenario at hand.

oral presentation to a larger audience.

The visualizations were implemented in JavaScript, more specifically by using the D3.js library. To test our tool, we let it run on a couple of example datasets, from relatively small to relatively large sizes. The largest of these datasets, the NCBI taxonomy dataset, consists of over 300,000 hierarchical elements that describe species living on earth having a total depth of 42. Although this tool is not primarily built for data analysis, but more for communicating hierarchical structures in different visual perspectives, we are aware of the fact that it might be extended to a data analytics tool if, for example, more algorithmic concepts like tree comparison (Beck et al., 2014b), tree restructuring, or automatic filtering were integrated.



File Manager | Choose File No file chosen | Upload file

5000.nw	(69 bytes)	Visualise
Age.nw	(69 bytes)	Visualise
Bacteria.nw	(333 bytes)	Visualise
Big.nw	(49726 bytes)	Visualise
Carnivora.nw	(98 bytes)	Visualise
Catarrhini.nw	(212 bytes)	Visualise
Def.nw	(730 bytes)	Visualise

Figure 2: An overview of the file manager. In the top bar users can upload new files, underneath an alphabetically ordered list of uploaded files is shown. To the right, options are provided to delete, rename, or visualize each file, and furthermore, the size of each file is also shown.

2 RELATED WORK

The field of data visualization is one that has a long history and where a lot of research is still being conducted. Because of this, a large variety of visualization techniques were developed, and are still being developed. A lot of examples of hierarchical data visualizations can be found in (Jürgensmann and Schulz, 2010; Schulz, 2011). The most well-known types of hierarchical visualizations are node-link (Reingold and Tilford, 1981; Burch et al., 2011; Eades, 1992), stacking (Kruskal and Landwehr, 1983; Stasko and Zhang, 2000), nesting (Shneiderman, 1992; Nocaj and Brandes, 2012), and indentation techniques (Burch et al., 2010; Burch et al., 2012). There are also combinations of these forms, usually called hybrid forms, that try to exploit the benefits from several, but at least two, approaches (Nguyen and Huang, 2005).

An example of a node-link diagram is the well-known tree visualization (Wetherell and Shannon, 1979). The advantage is that, at a quick glance, individual relations between nodes of the data can be seen, so they offer a lot of detail. However, this comes with a drawback as the drawing of these trees, more specifically 'tidy' drawing of trees, is not something trivial. Especially, when the trees become larger, then this results in a big challenge (Supowit and Reingold, 1982). Several different solutions exist for drawing tidy trees, as in (Wetherell and Shannon, 1979) and the Reingold-Tilford algorithm (Reingold and Tilford, 1981). The latter serves as the base for our implementations, as the D3.js library uses a modified version of this algorithm.

Another problem with visualizing trees is that when the dataset is large, the visualization tends to use a lot of space to be drawn, or becomes cluttered (Rosenholtz et al., 2005). Many overlapping nodes make it nearly impossible to understand the data on a communicative basis. Other approaches, like nesting, are more space-efficient when working with large data sets. The circular treemap, which we used in our implementation, is an example of a nested visualization (Zhao and Lu, 2015). In these types of visualizations details are less apparent, but they give a better overall view of the structure of the data. If larger datasets are used with circular treemaps, they look more structured and tidier than, for example, a node-link diagram, however, details can get lost, because each subsequent level is drawn in a smaller way. Another advantage is that they use a fixed amount of space, as the circles representing the data are recursively drawn smaller for each new level. This means that drawing them is more space-efficient than drawing trees, which tend to take up more space when the dataset becomes bigger (McGuffin and Robert, 2009). Therefore these visualizations are sometimes preferred over node-link diagrams.

An example of a more hybrid form of visualizations is the 'Elastic hierarchy' (Zhao et al., 2005), combining both node-link and nesting properties into a hybrid visualization. In this example it is clearly visible that these hybrid visualizations have advantages over, for instance, the node-link visualizations. In this case, the visualization is more space-efficient than a tree visualization, and the screen does not get cluttered that easily when compared to the tree visualization. This leads to the effect that these types of visualizations are sometimes preferred over other types, because of the greater efficiency in terms of space and clarity. If only limited space is available, for example, on a website with a small window for the visualization, it might even be necessary to use a visualization like this.

3 VISUALIZATION TOOL

The visualization tool runs online in a web browser making it easily accessible to anyone all over the world. Users can also switch easily between different datasets and visualizations, to make the tool as user-friendly as possible.

3.1 Graphical User Interface

The file manager provides a view on all files shared on the server while new files can be added (see Figure 2). At the top there is a file selection button, next to which is another button to submit the selected file for uploading. Below is a list of all files which have been uploaded so far to the server. For each file, there is a link to visualize the dataset and two extra options to either rename or delete the file. For each dataset the file size is also displayed, which can give the users some indication of how long they have to expect to wait until the dataset is loaded or how complex a hierarchy visualization might look like in case they plan to quickly show some figures for illustration purposes.

The visualizer page is where the visualizations are displayed. The layout (see Figure 1) consists of three main sections, the visualizations themselves, the settings bar, and the legend. The settings bar is collapsible, which allows for the full width of the page to be used for the visualization. Within the settings bar, there are many options to apply to the visualization. With these settings the user can select the file being displayed, select the coloring that is applied to the visualization, change the effect of left and right clicking on a node, and the depth limitation for the drawing of the tree. There are also two buttons to collapse and expand the subtrees, to make it easier to apply these actions. There is also a button to make the 3D step-tree and Pythagoras tree dependent on the branch weight of the tree, and a setting to adjust the minimum weight for all nodes. Some datasets may have a branch length attached to the parent-child relationships, which gets incorporated in these visualizations if this option is selected. This might be important for biologists or bioinformatics researchers.

When starting the visualization tool, the legend will be shown in the bottom right of the screen (see Figure 1). To ensure easy usage of the legend, the user can position it anywhere on screen as to not obstruct and occlude the visualizations.

The visualization panel consists of four cards, each with a different visualization (see Figure 1). These cards each have a tab at the top, with a name at the top left, and on the right, options to make the visualization cover the full page, and an option to collapse or expand the card. The cards can also be dragged by grabbing these tabs, in case a certain order or layout is preferred.

3.2 Interaction Techniques

Under the tab we can see the major view of the visualizations. Each one has zoom buttons in the bottom-

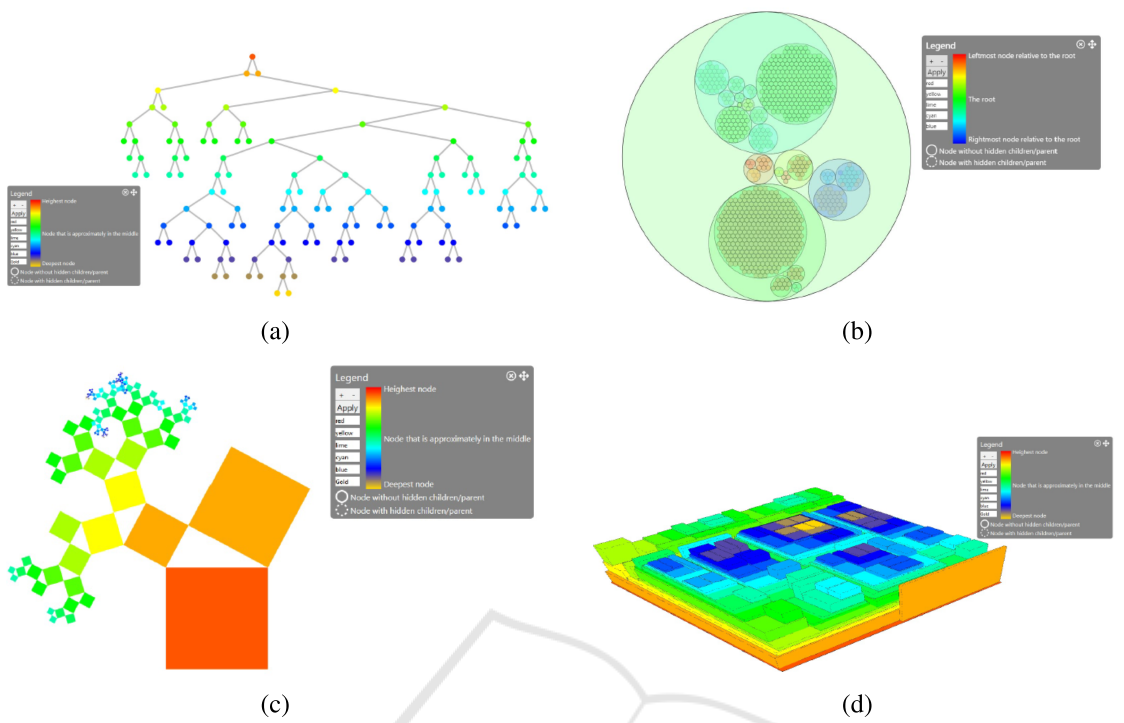

Legend
Heighest node
Node that is approximately in the middle
Deepest node
Node without hidden children/parent
Node with hidden children/parent
Apply
red
yellow
lime
cyan
blue
Gold
(a)
Leftmost node relative to the root
The root
Rightmost node relative to the root
(b)
(c)
(d)

Figure 3: The visualization supports node-link diagrams (a), circular treemaps (b), Pythagoras trees (c), and 3D treemaps (d).

right corner, and a button to reset the zoom and pan to the default settings. Each visualization can be panned around using the left click and also zooming is supported. The 3D step-tree visualization can be rotated around using the left click, and panned around using the right click. Also in each visualization, if a node is hovered over, details about that node are shown. This data includes the name, number of children, depth, height, color, and weight of the node. This is displayed in a grey balloon to make it easier to read, as otherwise the colors of the visualization might interfere with the readability of the text.

In all of the visualizations if a node is hovered over, the path to that node from the root becomes highlighted. In the tree visualization this is accomplished by increasing the size of the nodes and thickness of the connecting lines in the path, while in the circular treemap and Pythagoras tree visualization this is shown by increasing the thickness of the border of the circles/rectangles in the path. In the step-tree every node in the path is colored red. Every node's subtree can be expanded and collapsed by left-clicking the node, or the tree will be rerooted to that node depending on the left-clicking mode that is set in the settings menu. A right-click on a node will either collapse or expand the whole subtree that the node is connected to, depending on the mode set in the settings. When it is the case that the user collapsed parts of a subtree with multiple left-clicks, expanding the root of this subtree with a left-click will result in the subtree expanding nodes without expanding previously collapsed subtrees of these nodes. If the user had performed right-click expanding instead, it would have expanded the entire subtree, including those previously collapsed subtrees of child nodes.

3.3 Visualization Techniques

The major visualization technique is a traditional node-link diagram since it is easy to understand and serves as a navigation aid but negatively, it suffers from visual scalability problems (see Figure 3 (a)). Drawing a tree is done by using the D3.js function .tree(). It is an implementation of the Reingold-Tilford algorithm (Reingold and Tilford, 1981). This assigns x- and y-coordinates to each node, such that each node is centered over its children, has a non-overlapping subtree, and is as evenly spaced as possible with respect to its siblings.

Another visualization (see Figure 3 (b)) is the circular treemap. This is a variation of the traditional treemap. D3.js also provides an implementation for this type of map, by using the .packed() function. Its algorithm can be described as the continuous optimization of disk packing (Zhao and Lu, 2015). A good disk packing algorithm is much harder to implement by ourselves than, say, the Reingold-Tilford algorithm, which is why we are lucky D3.js also provides a function for this. If we were to use an even better and more complex disk packing algorithm, we should fear losing the relatively good performance we are achieving now.

The third visualization is a Pythagoras tree (see Figure 3 (c)), a method in which each node is represented by a rectangle. Our implementation of this visualization is based on the work by (Beck et al., 2014a). In this paper a generalized recursive algorithm was given for the calculation of the positions of each node. We implemented an iterative version of this algorithm in JavaScript, using the D3.js library. First, the tree is passed through the D3.js function .hierarchy(), so that children of the nodes are easier to be called in JavaScript. Then, the angles for the spreading of the squares are calculated and the length of the side of each node is computed.

The fourth visualization is a 3D treemap, also called 3D step-tree (Bladh et al., 2004) (see Figure 3 (d)). A step-tree is an extension of a treemap to the third dimension. This visualization may provide a lot of insights into (large) datasets which may have no emergent characteristics in two dimensions. To draw 3D objects, we used the well-known three.js library. Starting from our hierarchical data, we use D3.js to obtain a treemap of it using .treemap(). Then, we do some arithmetic in finding suitable height attributes for each object depending on whether the option is set to use the branch length properties or not, assuming it is provided in the input file, of course. If the option is set to incorporate branch lengths, then the height of a node is scaled relative to the branch lengths of that node and its parent. We also add black lines to stress what the bounding box of a node is, which could have been hard to see with some colorings and large datasets. We have added the options for several colorings of the dataset. The absolute depth coloring is based on the depth of the nodes. For each node, we look at its depth and add a relative amount to the hue of the node. This amount is scaled by the maximum depth of the dataset, hence the name absolute. How the colors change from the root to the leaves can be chosen by the user by interacting with the legend. When using this coloring, nodes with the same depth will have the same color. It may be noted that the legend has two purposes, i.e., informing about the graphical primitives and the visual variables while also serving as means for adapting parameters and visual encodings.

When displaying multiple visualizations on the same page, the exact same data is displayed, but in a different visualization like in multiple coordinated views. This is achieved by using only one data object, and when necessary updating only that data object and then every visualization is required to fit that data object. Another technique we use to increase performance, is to limit the depth of the original data we plot such that we plot at most 3,000 nodes in the initial plot. Of course the user will be able to plot all data, although the tool will not do this from the start. We do load all the data into the data object, however, expanding beyond the initial depth is no problem.

Finally, to enhance performance, we also only update the visible visualizations, so if a card is collapsed, then its visualization is not updated. If the user, at a later point, decides to reopen the card, then the pending changes are applied immediately. This feature is useful to reduce the runtime for layouting and rendering the dataset.

3.4 Implementation Details

Our website's user interface was written in PHP, HTML, CSS, and JavaScript. We chose PHP for our file manager back-ends because it allows for file manipulations at the server side and we used HTML, CSS, and JavaScript because they are the de facto languages in the development of web applications.

We used the Bootstrap framework to create the user interface of our visualization tool, to ensure that the page would look roughly the same on all devices and that the page would be appropriately scaled. To create our four-visualization card layout, we used the Bootstrap cards design to which we added the dragging, expanding/collapsing, and full-screening functionalities using the Lobicard library. As the Lobicard library was developed for the 4.0 beta version of Bootstrap and we have used the Bootstrap v4.1.1 release version, the Lobicard library did not work correctly at first. We have had to adapt the library to work correctly with the Bootstrap v4.1.1 cards and furthermore, we have had to extend the functionality of the Lobicard library, using jQuery to make sure it also scaled the visualization cards correctly to fill the whole screen. We chose to use jQuery because it allows for easy manipulation of DOM elements.

Tether was also used, as it is a dependency for the Lobicard library, which allows for easier absolute positioning of DOM elements without messing up the rest of the layout. Our settings bar and legend were custom-built using Bootstrap components as a base, which we then extended using our own CSS and jQuery code to make them function correctly. Finally, we used the Font Awesome library to create good looking and easy-to-interpret icons in the user interface of our visualization tool.

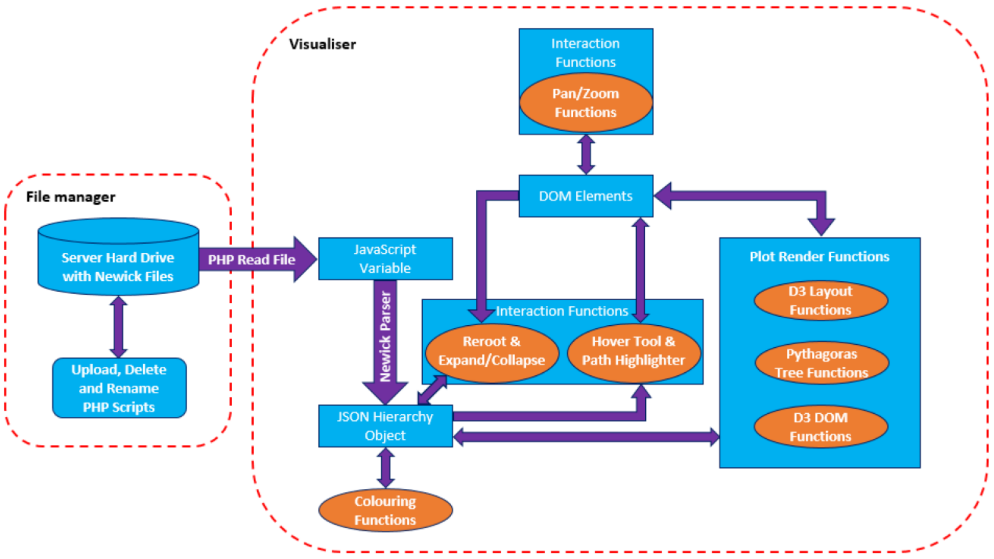
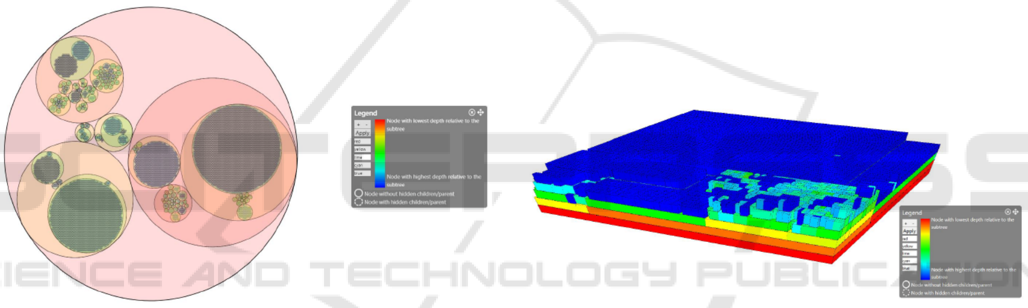


Figure 4: A UML diagram showing the connections of data and visualization components.



(a) (b)

Figure 5: The NCBI taxonomy shown as a circular (a) and a 3D (b) treemap.

Our visualizations were implemented using the D3.js JavaScript library, therefore, all of the visualizing aspects are processed at the client side. The work flow is visualized in Figure 4.

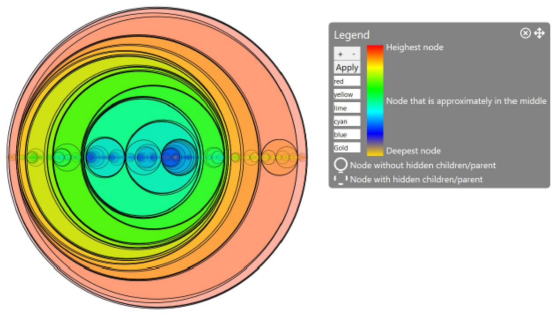
4 APPLICATION EXAMPLE

We illustrate our visualization tool by applying it to the NCBI taxonomy and a smaller hierarchical dataset referred to as Influenza.

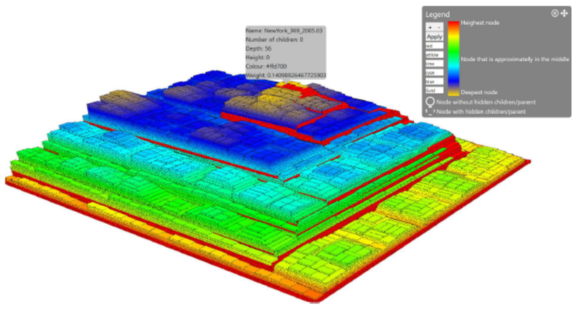
4.1 NCBI Taxonomy

Suppose a user or company has a hierarchical dataset and wants to visualize the data when, e.g., giving a presentation to a customer. This visualization has to be unambiguous and informative. Visualizations of larger datasets often get cluttered easily and may lead to misinterpretations, hence in our first case, we decide to use the circular treemap and the step-tree. In this first application example, we will use the NCBI taxonomy dataset, since this is quite a large dataset and therefore, a real stress test. To get an image which gives a rather clear structure, we set the depth limit to 4 and afterwards expanded some nodes. This visualization can be seen in Figure 5 (a).

In this circular treemap, we see the general structure of the dataset. The size of a circle gives the relative size of the subtree rooted at this node. We can hover over the different circles to see which taxa have most children or sub-taxa. Also, when a certain circle is crowded with smaller circles, we know that there is a large number of children for this specific node. When we zoom in we will see that some of these children still have subtrees that are collapsed. If the user desires to look at the more specific structure of the data, it is possible to expand these subtrees. This ex-


Legend
Apply
red
yellow
lime
cyan
blue
Gold
Heighest node
Node that is approximately in the middle
Deepest node
Node without hidden children/parent
Node with hidden children/parent

(a)


Legend
Apply
Heighest node
Node that is approximately in the middle
Deepest node
Node without hidden children/parent
Node with hidden children/parent

Name: NewYork_369_2005.03
Number of children: 0
Depth: 56
Height: 0
Colour: #ffd700
Weight: 0.1409892646772590З

(b)

Figure 6: The influenza dataset shown as a circular (a) and a 3D (b) treemap.

pansion was applied to a couple of children for the step-tree (see Figure 5 (b)).

Due to the fact that not all nodes are expanded and the maximal depth of the tree is higher than 40, we cannot see the structure of the whole dataset, which might be misleading. Nevertheless, to see the structure of specific nodes (think of the amount of children), you get a good overview, which makes the choice of this visualization applicable on large datasets. In the step-tree, we expanded some nodes that had a collapsed subtree. This can, for example, be done when these nodes are of particular interest, like when researching a specific branch of species.

We now clearly see that a lot of nodes are already leaves because they are colored in blue. We also see there are still some nodes that have a collapsed subtree, for example in the left corner, because they are not colored in blue. These nodes were, however, purposefully left collapsed. If the user wanted to get a more detailed view of a subtree, then the user could also reroot to the corresponding subtree in order to get a more detailed view on this part of the dataset, excluding the rest of the dataset. This can be particularly useful when the user is for instance particularly interested in a specific taxon, for example the kingdom of Animalia.

4.2 Influenza

In the second case we want to graphically depict an arbitrary dataset we found online which is named Influenza. Its size is not very small, but definitely not as big as the NCBI taxonomy dataset. It has 1,373 nodes, spread over 56 levels, against the 324,276 nodes over 42 levels of the NCBI dataset. We have uploaded it to our website, so you can interact with it. Clicking the visualize button from the file manager brings us to the visualization page.

From the circular treemap, we can immediately infer it is a binary tree (see Figure 6 (a)). We know this because all circles have its center on the horizontal axis, which means every parent has precisely two children. Notice that the coloring we use here, which is explained in the legend, does not produce an aesthetically looking visualization. Perhaps choosing a color scale with only two colors would look better.

Looking at the step-tree, we find that there is a sort-of-pyramid structure, with attached to it some small stacks of nodes on the steps of the pyramid. The pyramid has one peak which is colored gold. From this, we can infer that the tree was created around a central path on which small subtrees were attached. Hovering over one of the peak nodes, we can find the maximum depth of the tree (see Figure 6 (b)). In this case, we find that the maximum depth of the tree is 56. Looking at the regular treemap we see that the tree seems to be relatively deep for the amount of nodes it has. Its depth is greater than the one of the NCBI dataset, while the amount of nodes is less than a hundredth of it. This enables for a nice interaction with the Pythagoras tree as we can keep on zooming in on this longest path to fully enjoy the recursive structure.

Notice the nodes colored red in Figure 6 (b) are the path from the root to the selected node. Also, notice a text box with information about the selected node is displayed above the selected node. Because of the medium size of this dataset, we are perfectly able to interact with it in all visualizations. If we explore further by hovering over more nodes, we can see a general structure in the names given to the nodes. Also, enabling branch lengths shows that the branch length value seems to be determined by the size of the subtree, although if this is actually the case remains unknown as it does not seem to hold for all nodes.

5 CONCLUSION AND FUTURE WORK

To achieve the goal of this project we set up a web page using Bootstrap, HTML, PHP, and CSS. We created visualizations using D3.js. By using four different visualizations and by making these visualizations interactive in a variety of ways, we have achieved a tool that can be used to visually communicate hierarchy data. By making the layout adjustable to the user's needs and by using industry-standard icons we have tried to give the user a great and hassle-free experience. There are still some things that we would have wanted to implement. Some aesthetic aspects have room for improvement, for instance the circular treemap could be made to have opaque nodes, such that the coloring corresponds better to the color scale depicted in the legend. Furthermore, we would have liked to implement some sort of search function, so that users can easily find nodes. Moreover, we think that adapting our tool such that it can edit, extend, and export datasets would add a whole new dimension of practical uses for our website. Also a user evaluation by applying eye tracking techniques (Blascheck et al., 2015) might be an option for future work.

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