VisFCAC: An Interactive Family Clinical Attribute Comparison

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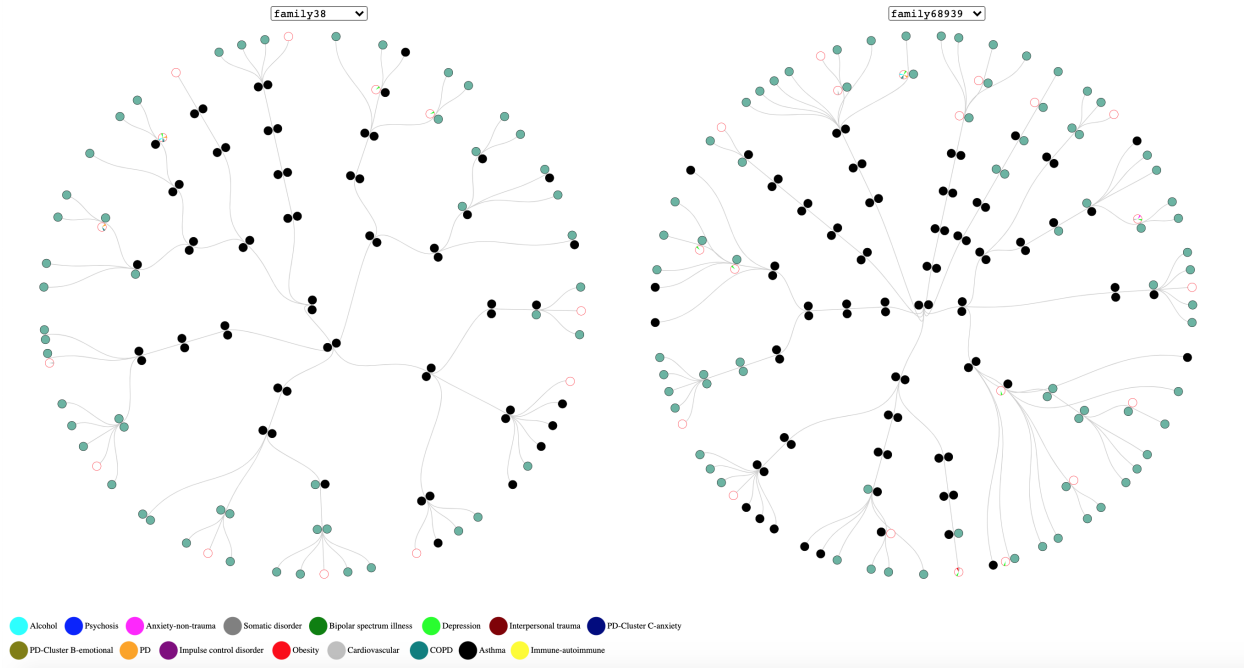

Fig. 1. The VisFCAC interface. The system presents the structure of the family tree that is selected. Family members that are deceased are represented by a black circle, family members that are alive are represented by green circle, and family members that have committed suicide are represented by a radial chart displaying their diagnosed clinical attributes, or if the person does not have clinical attribute data they are represented by a red circle.

Abstract—This paper presents VisFCAC, an interactive visual analytics system that displays family structures along with clinical attribute of family members to effectively uncover patterns related to suicide deaths for submission to the BioVis 2020 Data Challenge. VisFCAC facilitates pattern tracing to offer insight on potential clinical attributes that could be connected to previous deaths by suicide in attempt to prevent future suicides by at risk people with similar detected patterns. This paper lays out an approach to compare family members within a family tree structure to uncover patterns that may appear in clinical diagnosis within the family. This approach also compares two different families and their family structures to see whether there are patters in suicide cases amongst clinical attributes outside family structures. Our solution implements a radial tree with clinical attributes displayed on radial charts to provide in depth visual analysis, and offer a comprehensive insight for underlying pattern discovery.

Index Terms—BioVis challenge, Visual analytics, Family structure, Clinical attribute, Radial tree, Radial chart, Suicide.

1 Introduction

The BioVis 2020 Data Challenge focuses on public health to uncover the underlying patters of disease that may play a role in the rate of suicide. The challenge tasks participants to create a novel visualization to compare family tree structures with diagnosed clinical attributes of the family members to determine patters that involve suicide cases. Because it is important to clearly show hierarchical relationships influence other elements [1], a radial tree visualization was used to show the hierarchical structure of the family tree data obtained from the Utah Population Database. To tackle this challenge, a radial tree visualization was created to display two family tree structures side by side for comparison. For a family member who fell victim to suicide, a radial chart showing the person's diagnosed clinical attributes was used to represent them on the family tree structure.

We built a comprehensive web-based visual analytics system that allows users to compare two family trees and the family members that have fallen victim to suicide in order to uncover underlying patterns in diagnosed clinical attributes. The systematic views of VisFCAC is shown in Figure 1. The general workflow includes 1) selecting a family to be displayed on the right and one to be displayed on the left, then 2) analyze family members that have fallen victim to suicide and analyze their diagnosed clinical attributes, and 3) compare the clinical attributes contained amongst family members who have committed suicide to uncover patterns of clinical attributes both within the family structure, and within other families. A similar analytical approach with visualizations on social media data can be found in [2]. The complete source code for the visualization can be found at `https://gist.github.com/JakeTTU/b66df4ad837043273db34733cfe67e08`.

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2 System Architecture

2.1 Radial Tree

The view is presented in Figure 1. This allows the user to select two of the nine families whose data was given in the challenge in order to compare the family hierarchical structure of the two families. Each family unit is represented as two circles, a mother and a father. Or if the person is a child that is not found to be with a spouse, they are represented my an individual circle. The color of the circle is representative of whether the individual is alive, deceased, or has fallen victim to suicide. A green circle represents the individual is alive, a black circle represents the individual is deceased, and a red circle or a radial chart represents a suicide. The root of the tree is representative of the first generation that was given in the data from the Utah Population Database, and each subsequent generation is located at the end of a link from the previous generation. If a family line stops and there is no more generations, the nodes appear on the outer rim of the radial tree visualization.

2.2 Radial Chart

Figure 2 describes visualization used to display the clinical attributes of a suicide victim to the user. A user can simply hover the mouse over an individual who has committed suicide and has clinical diagnosis data. The chart represents sixteen different clinical attributes that include: alcoholism, psychosis, anxiety-non-trauma, somatic disorder, bipolar spectrum illness, depression, interpersonal trauma, PD-Cluster C-anxiety, PD-Cluster B-emotional, PD, Impulse control disorder, obesity, cardiovascular, COPD, asthma, and immune-autoimmune. Each of these clinical diagnosis are represented by a unique portion of the radial chart, and are represented by a unique color. For the user's reference, a legend of what diagnosis each color represents is displayed at the bottom of the visualization.

Using this platform, the user can analyze if there was a point in the family tree where a clinical disease appeared in the family, and which family members might have inherited genes that also make them susceptible to the same clinical disease. Also, if a clinical disease appears in different branches of the family tree, the user is able to easily determine who the last common ancestor was to offer a deeper insight.

2.3 Side-by-side Comparison

To more effectively compare two family structures to determine how clinical attributes effect families differently, the visualization incorporates a side-by-side comparison view of two selected families. This becomes useful when tracking clinical diagnosis within a family to determine if that clinical attribute follows a similar pattern amongst the other families in the given data set. Each family tree structure varies greatly, thus patterns in disease heredity can easily be uncovered. By comparing different family structures, some environmental factors can also be investigated to determine if they play a role suicide rates and clinical diagnosis. For example if a family member commits suicide, the likelihood of a family member later on in that family structure committing suicide could potentially be evaluated.

3 Challenge Findings

With the aid of the created visualization, we can determine that depression is one clinical attribute amongst family members who have fallen victim to suicide that can easily be passed from one generation to the next. Even if a person in the previous generation does not contain the data to definitively determine if they suffered from depression, we can see that there may very well be a gene that predisposes offspring to suffer from the disease. We can see in families 27251 and 68939 that there are different family members of the same generation that have fallen victim to suicide where each of them were diagnosed with depression. This may be caused by biological factors, or may be caused by environmental factors. In the case of family 27251, we can see that both offspring of a suicide victim were diagnosed with depression, and then also fell victim to suicide.

While it is difficult for us to determine how the diagnosed individuals came to have these diseases whether being biological or environmental

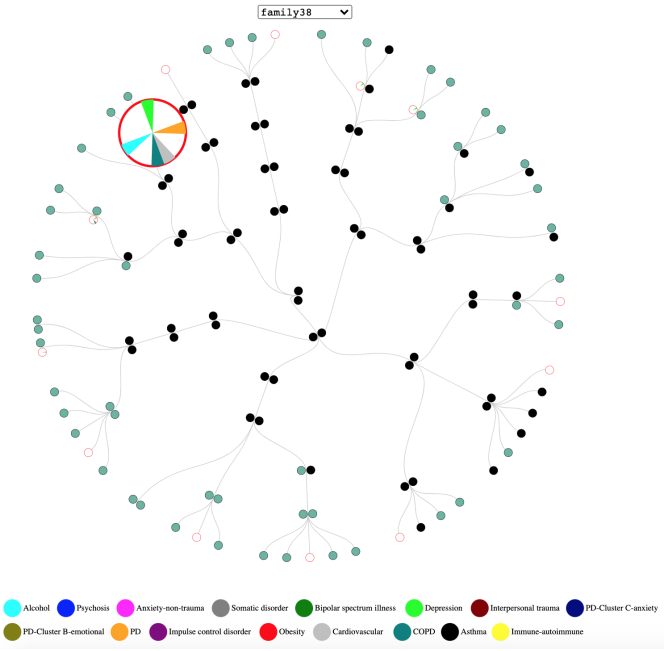

Fig. 2. When analyzing the diagnosed clinical attributes of a family member who has committed suicide, mousing over the radial chart enlarges the graphic to more clearly see the colored portions what can be referenced with a color key toward the bottom of the visualization to determine the diagnosis

factors, the user of the created visualization can easily uncover patterns of clinical diagnoses and suicide to know where to focus deeper investigation. It can also potentially offer some insight on why some members of a family within a generation seem healthy with few deaths, but have one family member who committed suicide and suffered from numerous clinical diseases. For example in family 149 in the ninth generation a family member was diagnosed with 5 different clinical diseases before committing suicide, while all members of that generation, the previous generation, and the second previous generation were still alive.

4 Conclusion and Future Work

This paper presents VisFCAC, an interactive system for uncovering underlying patterns in suicide rates amongst different family structures was implemented in HTML5 with D3.js. The system enables a quick overview of the structures of the different families in the Utah Population Database and shows which of the family members are alive, deceased, and have fallen victim to suicide. With investigation by the user, the radial chart offers insight into why patterns of suicide cases may exist within a family structure. While it difficult to determine the underlying cause of these clinical disease diagnoses, whether being biological or environmental, patterns of illness and suicide can be traced to determine if family members of the current or future generations may be at risk of suicide or illness. With the side-by-side comparison view of different family structures, the user can easily determine what clinical diseases are more prone to inheritability by comparing how a given clinical attribute forms patterns in different family structures.

References

[1] T. Dang, P. Murray, R. Etemadpour, and A. G. Forbes. A user study of techniques for visualizing structure and connectivity in hierarchical datasets. pp. 45–59. VOILA@ ISWC, 2017.

[2] H. N. Nguyen, J. Gonzalez, J. Guo, N. V. Nguyen, and T. Dang. Vismca: An interactive visual analytics system formisclassification correction and analysis. In *2020 IEEE Conference on Visual Analytics Science and Technology (VAST)*, 2020.