



Proceedings of the 2013 Workshop on Visual Analytics in Healthcare:

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Preface

As medical organizations move to electronic medical records and embrace new health information technology (HIT), the amount of data available to clinicians continues to grow at a rate not seen before. The vast amount of observational data we now collect promises many benefits. However, there are also many challenges. The large amount of clinical data captured just for a single patient poses a challenging task for clinicians trying to make sense of the patient's condition and understand the patient's medical history. Similar challenges of scale and complexity are faced by those performing population studies over large collections of historical electronic health data.

Visualization and visual analytics show great potential as methods to analyze, filter, and illustrate this vast sea of electronic medical data. By tapping into the human ability to visually perceive and interact with data, these technologies promise to help unlock the hidden insights buried within the large and heterogeneous data sources we are collecting. These insights can help with diagnosis and decision support for physicians. They can help patients and caregivers manage their health. They can help generate and confirm hypotheses for researchers, and they can help institutions improve efficiency, performance, and outcomes.

Visualization and visual analytics can potentially provide great benefits to each of these constituencies. However, to be successful, visualizations must be carefully designed to meet the challenges of the healthcare domain. This event, the fourth annual VAHC Workshop, provides clinicians, medical informaticists, and visualization researchers with a venue to gather, share ideas and results, and discuss directions for future work.

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Invited Speakers	
	<p>Dr. Ben Shneiderman, PhD University of Maryland</p> <p>Ben Shneiderman is a Professor in the Department of Computer Science and Founding Director (1983-2000) of the Human-Computer Interaction Laboratory at the University of Maryland. He is a Fellow of the AAAS, ACM, and IEEE, and a Member of the National Academy of Engineering, in recognition of his pioneering contributions to human-computer interaction and information visualization.</p> <p>Ben is the co-author with Catherine Plaisant of Designing the User Interface: Strategies for Effective Human-Computer Interaction (5th ed., 2010). With Stu Card and Jock Mackinlay, he co-authored Readings in Information Visualization: Using Vision to Think (1999). His book Leonardo's Laptop appeared in October 2002 (MIT Press) and won the IEEE book award for Distinguished Literary Contribution. His latest book, with Derek Hansen and Marc Smith, is Analyzing Social Media Networks with NodeXL. (2010)</p>
	<p>Dr. Howard Wainer, PhD Distinguished Research Scientist of the National Board of Medical Examiners</p> <p>Howard Wainer is a statistician and author. 'Medical Illumination: Using Evidence, Visualization and Statistical Thinking to Improve Healthcare' is his 20th book. His first two medical books (technical works in pediatrics) were published almost 40 years ago. He has been working primarily on medical topics since 2001 as the Distinguished Research Scientist of the National Board of Medical Examiners. At various times in his career he has taught at Princeton, The University of Chicago and the Wharton School of the University of Pennsylvania. He has a PhD from Princeton and is a fellow in the American Statistical Association and the American Educational Research Association. He has been the recipient of many awards for his broad ranging research and has served internationally on many editorial boards of leading statistical journals as well as a consultant to both government and industry. He has also written a column in the magazine 'Chance' for the past 22 years.</p>

Agenda:

Session I: Behavioral Health and Visual Analytics Chair: Jesus J. Caban, NICoE / Naval Medical Center	
8:30 - 8:45	Welcome – VAHC 2013 Paper presentations
	<i>"Visualizing the Overview of Temporal Patterns of Patients' Activities"</i> Kazuo Misue, Yuta Kanai and Hideaki Takagi
	<i>"Visual Exploration of Common Behaviors for Developmental Health"</i> Yi Han, Agata Rozga, John Stasko and Gregory Abowd
8:45 - 10:00	<i>"Visual-based Interactive Clinical Decision Support Tools: Developing User-centric Approaches"</i> Ketan Mane, Vincent Carrasco and Javed Mostafa
	<i>"BEDA: Visual analytics for behavioral and physiological data"</i> Jennifer Kim, Melinda Snodgrass, Mary Pietrowicz, Karrie Karahalios and Jim Halle
	<i>"Visualizing Patterns of Social and Communicative Behavior in Children Using Plexlines"</i> John Lee, Sanny Lin and Karrie Karahalios
10:00 - 10:30	Coffee Break
Session II: Visualization Systems and Dashboards Chair: David Gotz, IBM Research	
10:30 - 11:15	Keynote: Dr. Ben Shneiderman University of Maryland
	Paper presentations
	<i>"Visualization of EHR and Health Related Data for Information Discovery"</i> Vivian West, David Borland and W. Ed Hammond
11:15 - 12:00	<i>"Interactive Dashboards: Using Visual Analytics for knowledge Discovery and Transfer"</i> Samar Al-Hajj, Ian Pike and Brian Fisher
	<i>"VisXplore: Flexible Visualization System for Analyzing Complex Clinical Datasets"</i> Filip Dabek and Jesus Caban
12:00 – 1:00	Lunch break

Session III: Poster and Demonstrations Chair: Paul Nagy, John Hopkins University	
1:00 – 1:45	Fast forward Presentations – Posters and Live Demonstrations
1:45 – 3:00	Poster and Demo Session (see next four pages for list of posters & live demonstrations)
Session IV: Temporal and Drug Visualization Chair: Janusz Wojtusiak, George Mason University	
3:00 – 3:45	Keynote: Dr. Howard Wainer Distinguished Research Scientist National Board of Medical Examiners
3:45 – 4:30	Paper presentations
	<i>"Temporal Search and Replace: A Graphic-Based Solution to Temporal Event Data Wrangling and Incremental Querying"</i> Megan Monroe, Rongjian Lan, Hanseung Lee and Allan Fong
	<i>"Dydruma: A Dynamic Drug Map for Exploring the Associations Among Drug Therapeutic Indications and Side-Effects"</i> Fei Wang, Ping Zhang, Nan Cao, Jianying Hu and Robert Sorrentino
	<i>"Visualizing Patterns of Drug Prescriptions with EventFlow: A Pilot Study of Asthma Medications in the Military Health System"</i> Tamra Meyer, Megan Monroe, Catherine Plaisant, Rongjian Lan, Krist Wongsuphasawat, Trinka Coster, Sigfried Gold, Jeff Millstein and Ben Shneiderman
4:30	Closing Remarks

Poster Presentations (1:00 – 3:00pm)	
<i>Poster #1</i>	<i>"Interactive visualization for understanding and analyzing biomedical research collaboration networks - a pilot study"</i> Jiang Bian, Mengjun Xie, Umit Topaloglu, Teresa Hudson and William Hogan
<i>Poster #2</i>	<i>"Topic Modeling and Network Visualization to Explore Patient Experiences"</i> Annie Chen, Laura Sheble and Gabriel Eichler
<i>Poster #3</i>	<i>"Data Exploration of a Notifiable Condition Detector System",</i> Yuni Xia, ShiaoFen Fang, Mathew Palakal, Roland Gamache, Thanh Nguyen, Sam Bloomquist, Anand Krishnan, Jeremy Keiper, and Shaun Grannis.
<i>Poster #4</i>	<i>"StickWRLD : Interactive Visualization of massive parallel contingency data for Personalized Analysis to facilitate Precision Medicine",</i> William Ray and Christopher Bartlett
<i>Poster #5</i>	<i>"A research pipeline of information extraction for visualization of narrative clinical reports on a timeline "</i> Jianlin Shi, Ruth Reeves, Edna Shenvi, Melissa Sharp, Robert El-Kareh, Zia Agha and Wendy Chapman
<i>Poster #6</i>	<i>"Detecting Comorbidity of Chlamydia from Clinical Reports for Health Terrain Visualization"</i> Mathew Palakal, ShiaoFen Fang, Yuni Xia, Anand Krishnan, Sam Bloomquist, Thanh Nguyen, Roland Gamache and Shaun Grannis
<i>Poster #7</i>	<i>"Use Cases for Public Health Data Visualization"</i> Jeremy Keiper, Yuni Xia, ShiaoFen Fang, Mathew Palakal, Shaun Grannis, Roland Gamache, Thanh Minh Nguyen, Sam Bloomquist and Anand Krishnan

Poster Presentations (cont.)	
<i>Poster #8</i>	<i>"Perceived Usefulness and Usability of a Visual Analytical System for Toxic Chemical Identification: Results from a National Survey of First Responders"</i> Suresh Bhavnani, Bryant Dang, Kai Zheng and Chris Weber
<i>Poster #9</i>	<i>"How Graphical Visualization Can Aid in Understanding and Developing Clinical Ontologies: Exploring the Overlap Between ICD and SNOMED"</i> Evan Minty, Marco Cusumano-Towner, Dean Yergens and Bill Ghali
<i>Poster #10</i>	<i>"COPTADS: Clinical Online PTSD and TBI Analysis and Decision System"</i> Banaszak Steven, Vadim Kagan, Andrew Stevens and V.S. Subrahmanian

Live Demonstrations (1:00 – 3:00pm)	
<i>Demo #1</i>	<i>"Harnessing patient-reported outcome data to project and visualize disease course"</i> Timothy Vaughan (PatientsLikeMe)
<i>Demo #2</i>	<i>"Live Demonstration: A Day in the Life: Understanding and Improving Clinical Workflows Through Visualizations of Integrated EHR Activity"</i> Nick Stepro and Michael Simon
<i>Demo #3</i>	<i>"Demonstration of Visualization of EHR and Health Related Data for Information Discovery"</i> David Borland, Vivian West and W. Ed Hammond
<i>Demo #4</i>	<i>"Visualizing the Overview of Temporal Patterns of Patients' Activities"</i> Kazuo Misue, Yuta Kanai and Hideaki Takagi
<i>Demo #5</i>	<i>"Visual Exploration of Common Behaviors for Developmental Health"</i> Yi Han, Agata Rozga, John Stasko and Gregory Abowd
<i>Demo #6</i>	<i>"Visualizing Patterns of Social and Communicative Behavior in Children Using Plexlines"</i> John Lee, Sanny Lin and Karrie Karahalios
<i>Demo #7</i>	<i>"VisXplore: Flexible Visualization System for Analyzing Complex Clinical Datasets"</i> Filip Dabek and Jesus J. Caban
<i>Demo #8</i>	<i>"Temporal Search and Replace: A Graphic-Based Solution to Temporal Event Data Wrangling and Incremental Querying"</i> Megan Monroe, Rongjian Lan, Hanseung Lee and Allan Fong

Live Demonstrations (cont.)	
<i>Demo #9</i>	<i>"EventFlow"</i> Tamra Meyer, Megan Monroe, Catherine Plaisant, Rongjian Lan, Krist Wongsuphasawat, Trinka Coster, Sigfried Gold, Jeff Millstein and Ben Shneiderman
<i>*Demo #10</i>	<i>"Topic Modeling and Network Visualization to Explore Patient Experiences"</i> Annie Chen, Laura Sheble and Gabriel Eichler
<i>*Demo #11</i>	<i>"A research pipeline of information extraction for visualization of narrative clinical reports on a timeline"</i> Jianlin Shi, Ruth Reeves, Edna Shenvi, Melissa Sharp, Robert El-Kareh, Zia Agha and Wendy Chapman
<i>*Demo #12</i>	<i>"COPTADS: Clinical Online PTSD and TBI Analysis and Decision System"</i> Banaszak Steven, Vadim Kagan, Andrew Stevens and V.S. Subrahmanian

*Demonstration together with poster presentation.

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PAPER PRESENTATIONS

Visualizing the Overview of Temporal Patterns of Patients' Activities

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Abstract

It is necessary to determine patients' activities for effective management in hospitals and affiliated regional medical institutions. The purpose of this study is to support the identification of features from temporal patterns of patients' activities using information visualization. This paper introduces a technique called "ChronoView" for visualizing temporal patterns. ChronoView provides an overview of many temporal patterns and enables us to easily determine the similarity and anomaly of temporal patterns. In order to illustrate a use case, temporal patterns of patients' activities were extracted from an actual data set of patients of the University of Tsukuba Hospital. This paper reports some features of the temporal patterns identified using ChronoView.

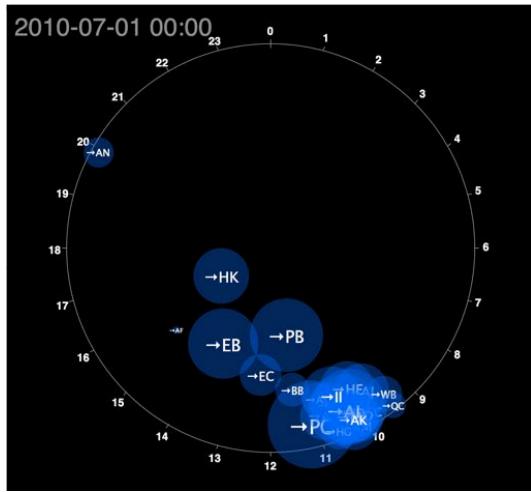


Figure 1. Daily temporal patterns of admission visualized using ChronoView. Each blue circle represents a clinical group. Admission time of most clinical groups is concentrated between 10:00 and 11:00. Admission time for Group HK (Emergency group) and a few other groups is independent of the time of day.

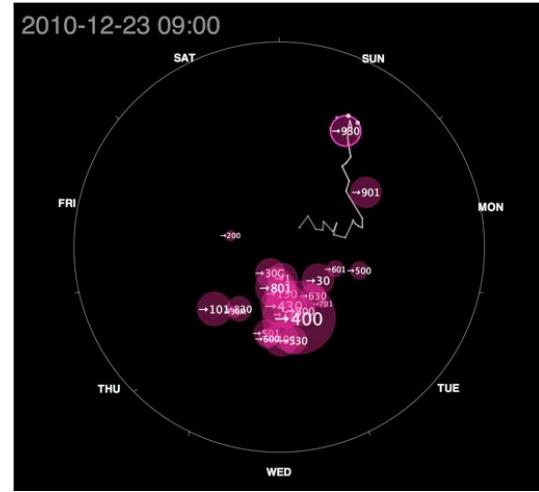


Figure 2. Weekly temporal patterns of transition into wards. Each red circle represents a ward. Transition into most wards is independent of the day of the week. Transition into Ward 930 changed and was concentrated on the weekend. The gray polyline represents the moving history of Ward 930.

1 Introduction

It is necessary to determine activity patterns of patients for effective management in hospitals and affiliated regional medical institutions. Activity patterns need to be determined from various viewpoints. It is important to determine the temporal patterns of patients' activities. What type of features does each clinical group have in temporal patterns of admission? What kinds of differences exist among wards in temporal patterns of moving in? Are temporal patterns of admission changing? Determining patients' activities and their changes with respect to the previously mentioned viewpoints is necessary to manage clinical groups that are accepted and to allocate beds in wards.

Date and time can be expressed as simple numerical data. However, understanding the significance of date and time converts the analysis of temporal patterns into a complex process. Time is a linear as well as periodic entity. Thus, we cannot disregard the periodicities of date and time in the temporal patterns of human activities. Therefore, even for a single pattern, we have to observe the pattern from several viewpoints such as a day-period, week-period, and month-period. Moreover, it is difficult to observe many temporal patterns simultaneously. Consequently, the analysis of temporal patterns can be very complicated and problematic. To solve these problems, we need certain techniques to visualize the overview of many temporal patterns.

The purpose of this study is to support the analysis of patients' activities. In particular, we aim to improve the efficiency of identifying features from many temporal patterns by focusing on the temporal aspects of activities.

We have already proposed a technique called “ChronoView” for visualizing many temporal patterns¹. This technique represents a temporal pattern, i.e., a set of time-stamps, using a position on a two-dimensional plane. Therefore, it provides high space efficiency and contributes toward determining the similarity between temporal patterns. We have developed an analysis tool that provides ChronoView. Using this analysis tool, we have been able to visualize a data set of patients.

2 Related Work

Powsner and Tufte proposed a graphical summary of patient status². They used small repeated graphs with identical formats to show the time-oriented status of a patient. Plaisant et al. proposed LifeLines, which provides a general visualization environment for personal patient histories³. These seminal works focus on offering information about an individual patient. There are certain studies that focus on patients’ activities. For example, Brodbeck et al. presented a case study using Masterplan, which provides several different views of patients’ flows⁴. In this study, we aim to determine the features of temporal patterns of patients’ activities such as admission, transition, discharge, and other clinical events.

For visualizing temporal patterns, various visualization techniques have been developed. One of the most common techniques is plotting each event on a time axis⁵. LifeLines adopted this technique. A time axis can be drawn as a circle or a spiral to reveal the periodicity of temporal patterns⁶. Another technique adopted a representation similar to a river to express the time-oriented quantitative data⁷. There are various techniques similar to those mentioned above; however, it is difficult to represent many temporal patterns together using these techniques. The scalability of visual representations for a large number of temporal patterns is an important issue.

3 Temporal Patterns and Their Overview

This section presents a formal definition of a temporal pattern, and describes an issue of visualizing the patterns.

3.1 Formalization of Temporal Pattern

Events or activities related to inpatients are accompanied by date and time, i.e., time-stamps. Every event is recorded using a time-stamp. Assume that a patient p of Group PB (obstetric group) is admitted to Ward 300 at time t . This is considered as an event and is accompanied by a time-stamp t and other attributes such as *patient p*, *admission*, *PB*, and *Ward 300*. Events that satisfy certain conditions are considered as an *event group*. For example, events of all admissions into Ward 300 comprise an event group. A *temporal pattern* is a set of time-stamps that accompany an event group. We define a temporal pattern as follows: Let E be a set of events. Each event $e \in E$ has a time-stamp $t(e)$. Each event may also have certain other attributes: a patient, one or two ward(s), action (admission, transition between wards, discharge, and so on), and a clinical group. Let, $a(e)$ and $g(e)$ denote an action and a clinical group related to an event e , respectively. For example $E_{PB,Adm} = \{e \in E | g(e) = PB \text{ and } a(e) = Adm.\}$ denotes a set of events that represent admissions to Group PB. Moreover, $T_{PB,Adm} = \{t(e) | e \in E_{PB,Adm}\}$ denotes a temporal pattern that accompanies events in $E_{PB,Adm}$. By analyzing the set, we determine a pattern of admission related to the obstetric group.

3.2 Overview of Many Temporal Patterns

If we focus on a single temporal pattern, plotting every time-stamp in the pattern on a time axis allows us to easily determine the pattern. A histogram is also useful to understand the frequency distribution of events. For example, when we want to identify the monthly distribution of admission to the obstetric group, such methods work well. However, we want to identify not only the distribution of an event group but also the remarkable features in many event groups. There are many sets of events to be observed and the temporal patterns of these sets should be observed with respect to various periodicities. One naive method for our requirement is to draw all possible histograms and to compare them. This impractical method fills the computer display with many histograms for large groups. We require a more practical method to observe an overview of all event groups efficiently.

4 ChronoView

ChronoView is a technique for visualizing many event groups with time-stamps. This technique represents each event group as a position on a two-dimensional plane. Event groups are placed on a plane similar to the clock face of an analog clock. First, we give the twelve o'clock position on the clock face to the time-stamp t_0 . Then, moving

clockwise, we then place all time-stamps on the circumference according to the time elapsed from t_0 . If we suppose that U is the set of all time-stamps, the position of the time-stamps is expressed by the function $f_0: U \rightarrow \mathbb{R}^2$ given by

$$f_0(t) = (r \cdot \cos \theta, r \cdot \sin \theta)$$

where r denotes the radius of the clock face circle, and

$$\theta = \frac{\pi}{2} - 2\pi \frac{t-t_0}{c}.$$

Suppose that T is a finite set of time-stamps, i.e., $T = \{t_1, t_2, \dots, t_n\}$. We assign the barycenter of the positions of t_i ($i = 1, \dots, n$) to the set T . The positions of a set of time-stamps can be represented by the function $f: 2^U \setminus \{\emptyset\} \rightarrow \mathbb{R}^2$.

$$f(T) = \frac{1}{T} \sum_{t \in T} f_0(t).$$

For example, let us consider the case where $c = 24h$. Figure 3 illustrates the basic idea of ChronoView and shows two event groups: A and B. If events in Group A occurred at 00:00, 08:00, and 14:00, the group is placed near the center of the clock face. If events in Group B occurred at 18:00 and 22:00, then the group is placed close to 20:00 on the chord between 18:00 and 22:00. It is easy to observe whether events in the group have occurred in a wide range of time-periods, or only during certain times, by representing an event group using such positions. In Figure 3, a period c is set to 24h and t_0 is 00:00 (midnight). When c is seven days, it represents a diagram of a one-week period. In a similar way, ChronoView can represent a one-month or one-year period.

5 Visual Tool for Temporal Patterns

We have implemented ChronoView in a visual tool. The tool provides some functions as follows.

- A time-period can be selected from one-hour, one-day, one-week, and one-month.
- Individual time-stamps are plotted. ChronoView has some ambiguity in representation, because it represents a set of time-stamps by a position on a two-dimensional plane. To eliminate this ambiguity, bullets that represent individual time-stamps are drawn on the circumference of a circle expressing an event group (see Figure 4).
- Moving averages of event groups are shown. ChronoView shows the barycenter, i.e., the average of time-stamps. The length of the range to compute the average can be selected using a slider. The range can also be changed. Movement of the barycenter according to the movement of the range can be presented as an animation.
- The moving history of an event group can be drawn. Moving averages are presented as an animation. However, the animation is not helpful in determining an exact route of a moving average. The tool draws the trajectory of the moving average of a selected group explicitly (see Figure 5).

6 Use Case

UTH is affiliated to the University of Tsukuba, and is located about 40 miles northeast of Tokyo, Japan. It has approximately 30 clinical groups and 23 wards consisting of 800 beds⁸. A complete data set of all inpatients' activities (with encrypted id's), ranging over a two-year period from April 2010 to March 2012, was provided by UTH. The Ethics Committee of UTH has approved the statistical treatment of this data and the resulting publication of research findings in our project. We extracted various event groups from the data set and visualized temporal patterns of the groups using the analysis tool.

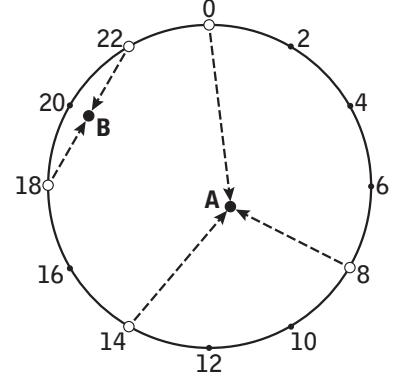


Figure 3. Basic idea of ChronoView.

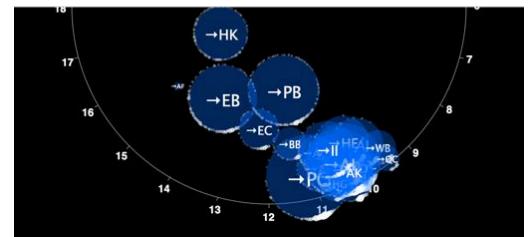
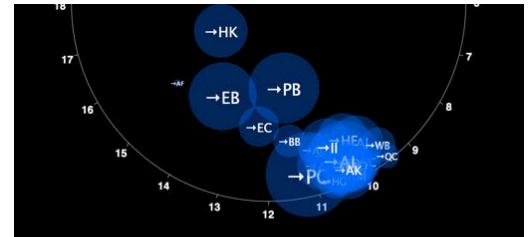


Figure 4. (Above) Normal view, without individual time-stamps. (Below) Individual time-stamps are plotted on the circumference of each blue circle.

6.1 Remarkable Features of Event Groups

We consider admission to each clinical group as an event group. Figure 1 shows temporal patterns of all event groups represented as a ChronoView. The time range is three months from April 1, 2010 to June 30, 2010. Each blue circle represents a clinical group. As is shown, most circles are concentrated from 10:00 to 11:00 on the circumference of the clock face. We can infer that the admission time of most clinical groups is concentrated between 10:00 and 11:00. This shows that admissions of planned hospitalization are performed in the morning.

In contrast, Group AN (Sleep Disordered Breathing group) was placed close to 20:00. This suggests that all the patients of Group AN were hospitalized for tests. Group HK (Emergency group) was placed close to the center of the clock face. This suggests that the admission of Group HK occurred independent of the time of day. This feature is in the nature of the role of Group HK. Group PB (Obstetric group) and Group EB (Child Health group) were also placed near the center of the clock face. We can say that the admission of these groups also occurred independently of the time of day.

6.2 Change of Features of Event Groups

Here, we consider transitions to each ward as an event group. Figure 2 presents the temporal patterns of all event groups represented in a one-week period. Each red circle denotes the moving average of a ward for three months. In addition, the moving history of Ward 930 is drawn with gray lines. We see that Ward 930 moved to Sunday and then returned to the center of the clock face (see Figure 5). This suggests that in late December 2010, the transition to Ward 930 was concentrated on the weekend.

7 Conclusion

We have shown that we can understand the overview of features of patients' activities by visualizing temporal pattern data extracted from the data set of movement of patients. The results of the study shown so far are based only on the temporal patterns extracted from the data set. We did not use the expertise of the hospital for our conjecture. We have two objectives for future work. The first is the improvement of visual representation to efficiently express the information required by medical professionals. The second is to design a smooth connection between ChronoView and other visual representation methods for detailed information because ChronoView can only show the overview of temporal patterns.

We thank the following staff of the University of Tsukuba Hospital: Dr. Tetsuya Igarashi, Dr. Hiroyuki Hoshimoto, and Mr. Masaki Suzuki. This work was partially supported by JSPS KAKENHI Grant Number 23241047.

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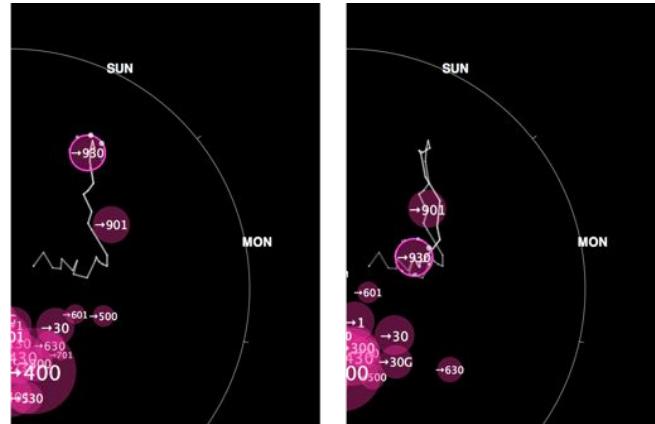


Figure 5. Moving history of Ward 930. (Left) Ward 930 moved to Sunday in late December 2010 and (Right) Ward 930 returned to the center of the clock face.

Visual Exploration of Common Behaviors for Developmental Health

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Abstract—**Detecting early signs of developmental issues in a child is critical for successful interventions.** Using behavior capture technologies such as video cameras, microphones and wearable sensors, it is increasingly possible to record and analyze human behavior in unprecedented detail. However, the analysis of such rich and complex dataset poses new challenges for developmental psychologists. We present the initial design of a visualization tool aimed at supporting the exploration of digitally captured behavioral data for studying developmental health.

I. INTRODUCTION

Developmental psychologists seek to understand how people's behaviors change over the human lifespan. Developmental problems in childhood are particularly important as they could influence the rest of a child's life. One way to assess problems by psychologists is to observe how a child interacts with others. For remote and retrospective assessments, today these interactions are often captured on video. However, reviewing video is time-consuming and one video camera can only capture behaviors from one angle. As a result, as part of a multi-site, interdisciplinary project, we are exploring how to use additional sensing technologies such as multiple high-resolution video cameras and wearable sensors to capture more subtle, non-obvious behaviors [3]. The richer, more complex captured behaviors make it more challenging for data annotation and analysis. As a result, we are also creating new computational methods to help automatically detect and label behaviors of interest to support behavior analysis for psychologists. Nevertheless, along with the vast amount of automatically labeled behaviors comes new challenges in how to effectively explore them to study typical and atypical behavioral patterns.

Through discussions with developmental psychologists, we learned that they are particularly interested in finding typical or atypical behaviors among and between groups of children. There are two reasons: 1) they need to know what is considered a typical behavior among a large group of children in order to tell when they see an atypical behavior, 2) when they find an atypical behavior in a group of children, they are interested in seeing how this behavior correlates with the diagnosis of developmental disorders. The task of finding typical and atypical behavior patterns is normally achieved through human observations. However, with today's new behavior capturing technologies, psychologists want to investigate if they can find subtle, non-obvious behavior patterns that are difficult to identify through human observation, especially across a large group of children. The current tools being used for exploring behavior patterns, such as video annotation tools [6], are only effective in looking at behaviors of a small number of children. Therefore, we see an opportunity for a new visualization tool

that can effectively support the exploration of typical and atypical behavior patterns exhibited by groups of children. Information visualization (infovis) represents a natural fit to the problem because it leverages humans' superb visual cognitive ability in finding insights from a large information space [2]. By interactively exploring the data, new interesting questions may arise from discovering unexpected visual patterns.

The application of infovis has been widely studied in understanding physiological health but largely overlooked in psychological health. Shneiderman highlighted three overlapping application domains in improving healthcare: personal, clinical and public health [5]. Specifically, extensive work has been done in analyzing the temporal events in electronic health records [4]. However, little work in infovis has focused on psychological health, not to mention developmental health that emphasizes behavior pattern exploration. As part of a project that aims to understand human behaviors through novel computational methods, we believe infovis can play a key role in supporting the exploration of the digitally captured behaviors for developmental health¹.

II. BEHAVIOR DATA

We used a short social play protocol to collect social and communicative behaviors for analysis. To date we have collected data from over 140 children aged 15-30 months (>190 sessions, each child could have up to two sessions recorded at different ages.) The protocol is a five-minute interaction between an examiner and a child at a table [3]. There are five stages in the protocol: 1) greeting the child, 2) rolling a ball back and forth with the child, 3) reading a book with the child, 4) placing the book on one's head and pretending it's a hat, and 5) tickling the child. The child's reaction to the examiner's speech or intentional pause are scored by the examiner based on the expected responses such as whether the child gazed back at the examiner when his or her name is called.

We instrumented a lab to capture the behaviors exhibited by the child, the parent (who is often in the same room) and the examiner. The lab contains 13 video cameras, an overhead Microsoft Kinect sensor and two microphones. During the sessions, we additionally equipped the child and examiner with a lapel microphone and Affectiva Q sensors on both wrists that capture temperature, electrodermal activity and accelerometry.

¹Another paper (Lee et al.) submitted to this workshop also describes a visualization tool for the same dataset. This paper considers the problem of being able to create understanding across multiple sessions while the other focuses on individual sessions

The onsets and offsets of the child's behaviors during the play sessions are annotated frame-by-frame by multiple research assistants in ELAN [6], an open-source data annotation tool, on four key behavior variables: (1) Gaze (examiner's face, examiner's hands, parent's face, ball, book); (2) Speech (vocalizations, verbalizations), (3) Gestures (e.g., pointing, reaching); (4) Vocal affect (crying/whining, laughing). The specific subcategories such as "Gaze at Examiner Face" and "Gaze at Ball" in the Gaze behavior variable are the basic unit for annotation. These annotations are being used as ground truth by the rest of the research team that are designing computational techniques to automatically identify the behaviors. Note that at this point the number of fully annotated sessions (~ 40) is smaller than the total number of recorded sessions (> 190).

In this visualization prototype, we used the human annotation data for the exhibited behaviors. In the future, these annotations will be replaced with behaviors automatically detected by computational methods which better capture subtle, non-obvious behaviors [3].

III. UNDERSTANDING NEEDS IN PSYCHOLOGY RESEARCH

We spoke with developmental psychologists informally to learn about their interest in studying social and communication behaviors. We discovered two interests that guided our design: 1) Responsive behaviors in social interactions and 2) Modes of communication used in the response.

Psychologists look for responsive behaviors in social interactions when studying developmental health in children. As a result, we used a unit of analysis called an "Examiner Bid (EB)" which is a time window that bins the responsive behaviors. This time window is similar to what is commonly used in developmental psychology research for coding responsive behaviors. In the social play protocol, the examiner uses specific phrases to introduce activities to the child (e.g., "Look at my ball!"), to guide the child through each stage (e.g., "Ready, set, go!"), and even to prompt the child to engage in specific behaviors (e.g., "Can you turn the page?"). A complete list of these speech bids can be found on the x-axis of the Multiples View in Figure 1 and Figure 2. The examiner also engages in specific behaviors to elicit a response from the child, such as pausing the ball and book activity to see whether and how the child will react. Therefore, we defined an EB as a window of time that includes the examiner's speech/pause and a configurable amount of seconds afterwards. For example, the EB "look at my ball" includes the time when the examiner utters the words, holds up the ball, and a few seconds afterwards when the expected response should occur.

Psychologists look at four modes of communication in a child's response to assess social behaviors: 1) Attention 2) Speech 3) Gesture and 4) Affect. The four key variables in the human annotation (gaze, speech, gesture, vocal affect) are designed to code these modes of communication. It is important to understand how the different modes are used together in social interactions.

We created our design based on these research interests. Additionally, we also found that psychologists typically only



Fig. 1. Subgroup Selection in the Distribution View. (a) Using the slider to focus on the aggregation of behaviors in the Ball stage EBs (b) A group of sessions that showed laughing behavior is selected (c) None showed verbalization but it is not uncommon (d) Few showed reaching behavior while many others do (e) The six sessions in the selected group are highlighted.

use statistical visualizations in their research for communication purposes. Therefore, we thought leveraging their familiarity with bar charts would be a good place to start as it may lower the barrier of entry in using the visualizations.

IV. VISUALIZATION DESIGN

The visualization tool contains three views as shown in Figure 1: 1) Multiples View that shows how common a behavior is among a group of children over the social play protocol, 2) Distribution View that shows how common the frequency of a behavior is over a consecutive set of EBs and 3) Sessions View that shows how individual sessions are selected and visualized. In addition, there is a control panel for filtering the data and configuring the views. Using a user-centered design, we present the visualization design progressively based on the needs of developmental psychologists. The visualizations are implemented with the D3 visualization library [1].

Multiples View

Psychologists want to see which behaviors are commonly exhibited in each EB over the course of the social play protocol. The Multiples View (Figure 2) shows this information. The four modes of communication are displayed in four vertically-stacked bar charts. The x-axis of the view is the list of EBs. They are in the order of when they should appear in the play protocol. The y-axis of each bar chart shows the number of children that exhibited the behavior. In Figure 2 (a), for example, at a glance a psychologist can immediately notice that there are more sessions showing laughing behaviors at the tickling EBs. This behavior is expected because the examiner is engaging the child in a tickling game. Such expected typical behavior patterns were very useful in helping us demonstrate

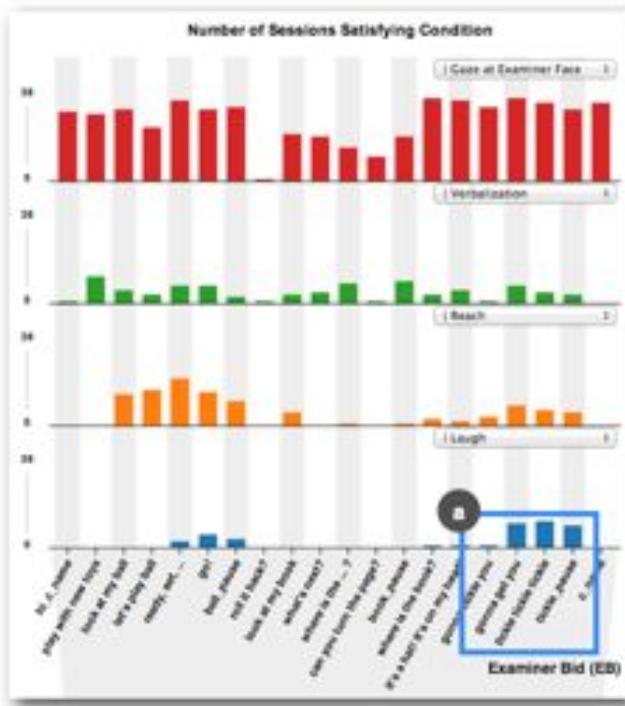


Fig. 2. MultiplesView. (a) More sessions showing laughing behavior at the tickling EBs.

the utility of the visualization prototype and establish trust in the visual representations. To inspect other subcategories of behaviors such as “vocalization,” a psychologist can use any of the dropdown boxes above the bar charts to select them. If a psychologist would like to know how many sessions exhibited a behavior more frequently, they can tune a threshold with a slider in the control panel to find children that exhibited more behaviors in each EB.

Distribution View

Psychologists also want to find subgroups of children that show different amounts of behaviors over a group of EBs in the social play protocol. This information is shown in the Distribution View that is located beneath the Multiples View as shown in Figure 1 and Figure 3 (a). This view shows the distribution of sessions over the total amount of behaviors across a number of consecutively selected EBs. The EBs can be selected from the range slider above the Distribution View. The four selected behaviors in the Multiples View are shown on the x-axis. The y-axis shows the aggregated behavior amount. The sessions are distributed among 10 equal-sized bins over the y-axis accordingly. An additional bin at the bottom holds all the sessions that did not exhibit the specified behavior.

Sessions View

After finding a group of sessions of interest from the Multiples or Distribution View, psychologists will need to identify those specific sessions for further investigation. The Sessions View shows the list of sessions that are loaded into the system as shown in Figure 1 and Figure 3 (b)(c). Each session includes two visual components next to a session label: (1) A bar showing the amount of behaviors of the session and (2) A circle indicating whether the session is selected.



Fig. 3. Distribution and Sessions View. (a) Session distribution illustration (b) Bar: behavior amount of a session in a selection (c) Circle: selection status of a session.

V. USAGE SCENARIOS

We present two usage scenarios of the visualization tool that explores how different groups of children exhibit common typical or atypical behaviors.

A. Is a group of children behaving atypically?

When psychologists see an atypical behavior exhibited by a group of children, they are interested in learning about who these children are and what other behaviors they have in common. In Figure 1 (b), a group of six sessions has been selected in the Distribution View after observing this group of children is behaving differently than the others. This group of sessions have children showing laughing behavior in the Ball stage EBs as selected by the range slider in Figure 1 (a). As there is only a small subset of sessions showing this behavior, we assume it is an atypical behavior that should be further investigated. When the six sessions in the bar are selected, these sessions are highlighted everywhere in the visualization tool while keeping the prior visualization faded behind in place. This design allows the psychologist to see if the selected subgroup of children in these sessions is behaving differently than the rest of the children. If more sessions are highlighted in a longer bar (typical behavior), it means the selected children behave similarly to the larger group. From Figure 1 (c) in the Distribution View, it seems that all these children that laughed did not verbalize at all over the entire social play session! However, when they are highlighted in a longer bar, the visualization implies that it seems typical for children to not verbalize in the social play session. On the other hand, few of them showed reaching behaviors that are common in the Ball stage as shown in Figure 1 (d). Are these children behaving atypically? From the highlighted six sessions in Figure 1 (e), the psychologist can see exactly which sessions they are in and either further the exploration by looking at different behavior variables, tuning other parameters or examining the video data of those sessions to better understand what might have caused these children to behave differently from others.

B. How do children at different ages behave in the social play session?

To assess developmental progress, it is important for developmental psychologists to understand how children should behave at different ages. By adjusting the age range slider on the control panel in two side-by-side windows as shown in Figure 4 (a), we can easily see the differences in common behaviors exhibited by younger and older children. Notably, (1)



Fig. 4. Comparing Younger to Older Children. (a) Different age ranges selected (b) More older children verbalized in their sessions (c) More younger children vocalized at the Ball stage (d) More younger children whined and cried.

more older children verbalized over the course of the session (Figure 4 (b)), (2) more younger children vocalized at the Ball stage (Figure 4 (c)) and (3) more younger children whined and cried (Figure 4 (d)). (1) and (3) can be expected but (2) might be interesting in exploring further. Why do children tend to vocalize more when they are younger and playing ball?

VI. DISCUSSION

One key challenge in our work is that psychologists are not accustomed to using visualization to explore data. They typically only use statistical visualizations for communicating their research findings. Even though occasionally they use video annotation tools with a timeline visualization, it is not part of their standard workflow. As a result, we have encountered some initial reluctance toward using visualization for exploration. Nevertheless, after seeing an interactive demonstration of the visualization and how it provides additional opportunities for finding new research questions through visual exploration, psychologists started to become intrigued by the idea of using visualization in this new way in their work.

VII. CONCLUSION

Infovis is a promising new approach in supporting psychologists explore social and communicative behavior patterns for studying developmental health. Currently we are only using the human annotation data to create the visualizations. In the future, we would like to add computationally generated labels to the visualization because they could capture subtle behaviors that are not currently coded by the human annotators [3]. With more uncertainty and complexity in the these behavior labels,

we foresee a great deal of opportunities for infovis to make an impact in developmental health down the road.

ACKNOWLEDGMENT

This work was supported by the NSF Expedition Award number 1029679. We would like to thank Opal Ousley, Lauren Adamson, Daniel Messinger, Karrie Karahalios, John Lee, Sanny Lin and the Ubicomp research group at Georgia Tech for their valuable feedback to this work.

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Visual-based Interactive Clinical Decision Support Tools: Developing User-centric Approaches

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Abstract

A new visual-based clinical decision support (CDS) tool was designed and is undergoing phased usability testing. It extracts clinical data, constructs medical historical timelines, maps treatment guidelines and presents outcomes data. Phase I presented here, evaluates our test methodology to better understand user-interface (UI) alignment with clinical workflow. Lessons learned about gaps in methodology, along with refinement needed prior to a comprehensive Phase II evaluation is covered here.

Introduction

Visual analytics approaches offer potential to quickly aggregate data, and help health practitioners interpret clinical data through an interactive UI. Using anonymized real-world Major Depressive Disorder (MDD) patient data, visual analytics approach was designed to extract retrospective clinical data, analyze it and aggregate therapeutic recommendations, and ultimately display it in a meaningful format to help deliver personalized care¹.

In medical domain, the adoption of a UI in practice is dependent on how well it fits in the clinical workflow². Therefore, it is critical to understand the clinician's workflow tasks, and the support UI offers to support it. Figure 1 shows stages of a typical clinical workflow (upper half), and different UI features or data views (bottom half) embedded to support tasks at each workflow stage to gain data insight.

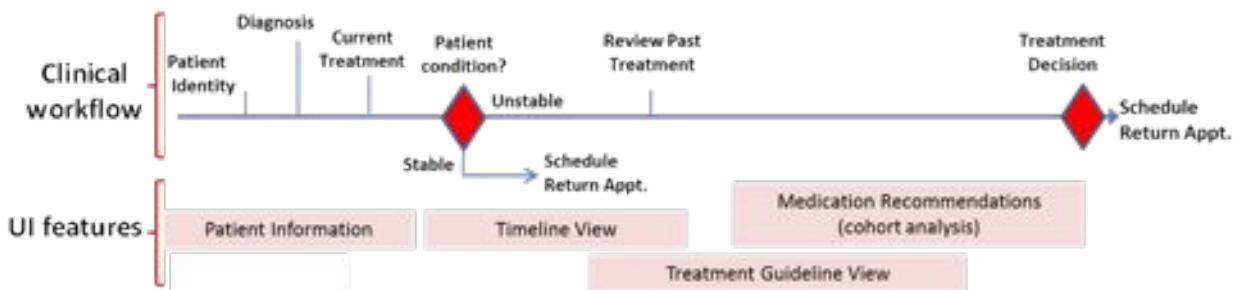


Figure 1. Clinical Workflow for Mental health follow-up visit ("Med-check")

To better understand value contribution of a new visual-based UI, we took a two phase strategy to UI evaluation, see Figure 2. Phase 1 was designed to test our evaluation methodology through a set of feedback to user tasks. The intent was to gain insight about methodology, refine it as needed prior to conducting a Phase 2 comprehensive study.

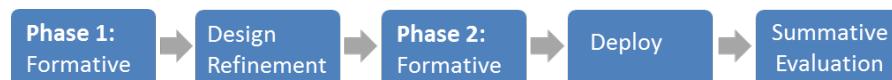


Figure 2. Design phases of UI evaluation

Figure 3 shows our UI design that is populated with anonymized real-world patient data on Major Depressive Disorder¹. Following the patient's demographic section in the UI, the first data view displays a comprehensive summation of the individual patient's treatment history, derived from their electronic medical record (EMR) and presented as 'Medical Historical Timeline'. The second section, 'Medication Recommendations' data view displays evidence about cohort population aggregated at the medication level, along with other details. In this view, an individual recommendation can be selected to gain insight about projected treatment outcome. The projected outcome to selected treatment is shown in the form of an extension to the patient's historical timeline. The third

section “Guideline View” maps the patient’s treatment to established guidelines. In our case, we used TMAP³ treatment guideline for MDD patients, and mapped the patient’s treatments to it. The patient’s historical therapeutic outcome was based on the Clinical Global Index (CGI)⁴.

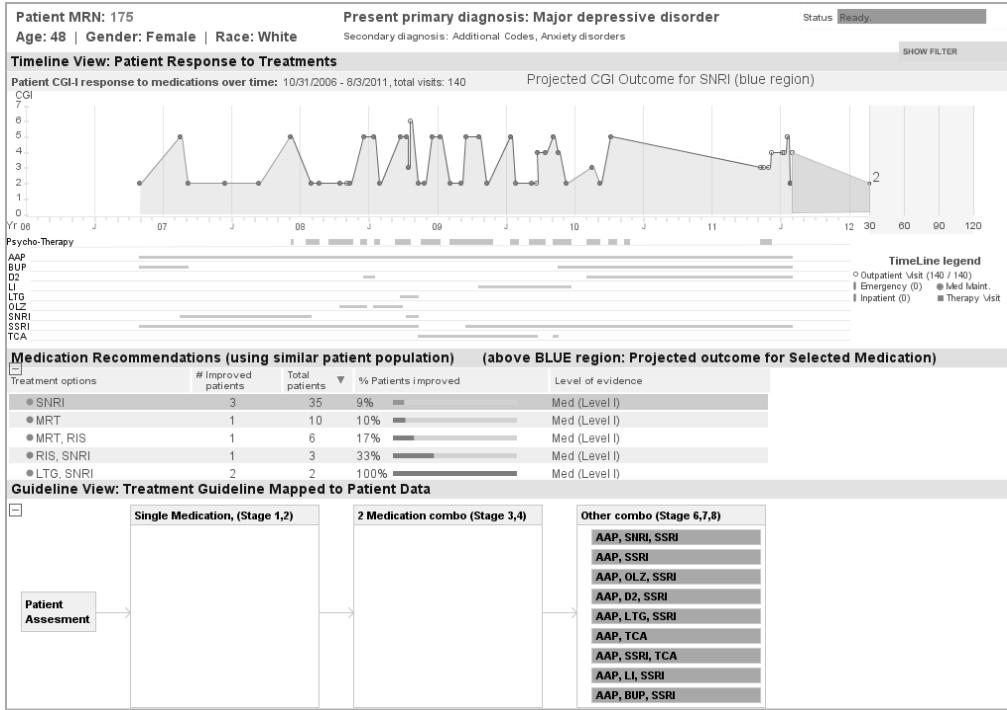


Figure 3. User-Interface designed to aggregate treatment evidence and to facilitate decision making process by displaying the patient’s demographics, a longitudinal display of patient treatments and responses to therapy. Aggregated evidence of response to various therapeutic options within the patient’s cohort can be selected as medication recommendations. The cohort can be refined and predicted CGI response to selected treatments (in yellow displayed using the filter option)

Evaluation Study: Methodology

An expert review usability study employing “med-check” scenario was designed with two observers recording the subject’s behavioral responses during their interaction with the UI. Six subjects, having significant clinical experience (MD’s, and Nursing) were selected.

Each of the six subjects completed 4 simple steps: 1) *Pre-test questionnaire*: designed to collect demographic data and clinical experience; 2) *Short demonstration of the UI*: was designed to familiarize the subjects with various features of the UI; 3) *Task questions* - each subjects was asked to complete an identical set of seven tasks (see Appendix 1) using a “talk-a-loud strategy”, while interacting with the UI. No time limit was imposed for completion for each task. The act of the subject ending interaction with the UI and writing down the answer was considered as a successful completion of each task. A screen capture tool recorded audio and screen activity for post analysis, and 4) *Post-test questionnaire*: to capture user feedback about their UI experience. In addition two behavioral observers noted the subjects’ individual interactions with the UI. Each subject was compensated \$25 at completion of the study.

Results

The pre-test questionnaire verified that all subjects were clinically active and experienced with clinical guideline use. Figure 4.A tally’s the subjects’ task responses: correct responses are shown in texture pattern and incorrect responses are shown in plain pattern. In Figure 4.B, column 3 highlights that timeline data view with its lows user success rate for task 1 needs more optimization as compared to others to help with data interpretation. The table

quantifies the user-experience, and post-video analysis highlights improvement is needed to some data view to enhance user-experience. For example, zoom-in feature needed in the timeline data view.

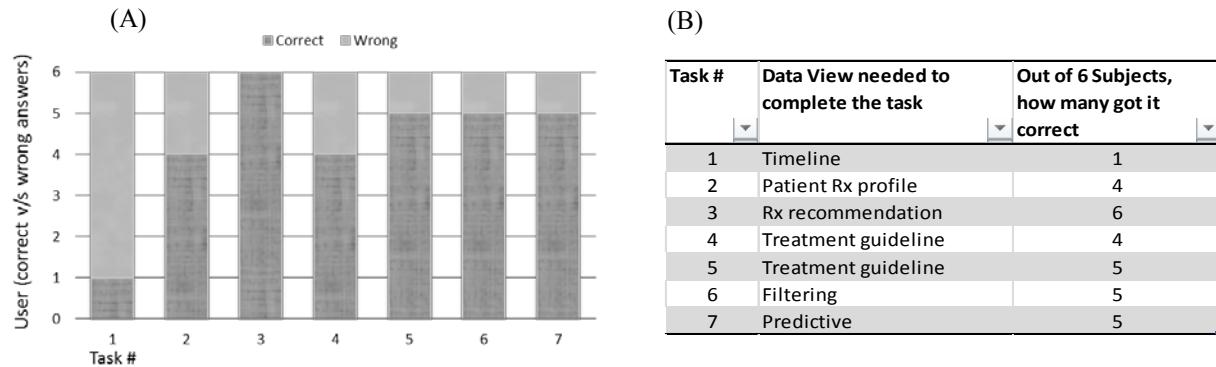


Figure 4: (A) Highlights the subjects' performance to different tasks, and (B) Data views needed to answer each task question, along with subject count who got it correct.

All subjects progressed sequentially through the clinical scenario without impediment using the UI, commenting throughout the process. Comments and behavioral observations are summarized as follows:

Comments:

- Many subjects were overwhelmed when all data views were displayed at once.
- Subjects uniformly commented that the metric used to measure patient outcomes (CGI) was counter intuitive and unfamiliar. CGI range is 1 through 7, value of 1 corresponds to better, and 7 correspond to worse outcome.
- Subjects wanted the option to review the original treatment guideline along with the displayed guideline view.

Behavioral Observations:

- Most subjects had difficulty resolving portions of the data view, in particular – the end of the timeline where the last group of points appeared crowded.
- Hitting refresh button was needed to refresh the cohort data in the filtering panel, but some subjects were hoping that the filtering will take place by mere selection of attributes.
- As we began to fine tune the message given in the demo portion of the study, we experienced that subjects had a good understanding of the UI features and experienced less cognitive overload.
- As subjects progressed through their task, each subject showed some degree of adaptation.
- Overall subjects were universally excited by: the ability to view patient's entire treatment course, the ability to map patient treatment to established guidelines, receive recommendations for treatment, and have the ability to view forecast potential treatment outcomes based on various treatment options.
- Most of the subjects did feel that for some data view (in particular, timeline and guideline), some optimization was needed.

Overall feedback from all subjects on the UI was - ease of use, understandable display format, less learning curve in understanding its features. All agreed that the UI offers potential to help with patient diagnosis. However, the subjects were split in which UI they thought was most and least informative. Inspite of difficulty in answering task 1 (based on timeline), most subjects found timeline view that showed trend in patient history to be most informative; followed by the predictive data view in second position. The guideline view was recorded as the least informative data view by a majority of the subjects owing to lack of insight about treatment guideline.

Conclusion

Phase I demonstrated that the UI mapped well with the established clinical workflow. However, subjects' responses to task questions reflected a high degree of cognitive overload and significant problems with interpreting portions of the visualization. It is interesting to note that a subject's ability to manage cognitive overload, correlated with their clinical experience. They were also influenced by their enthusiasm for features that provided new therapeutic options, guideline mapping, the treatment timeline and outcome forecasting. This enthusiasm facilitated adaption to the UI. Despite the complaint of cognitive overload, the subjects requested access to additional information (specific

guidelines). Future iterations of the UI will include “on-demand” options allowing the user to customize the content of the initial view by choosing the density and nature of the presented data.

The authors conclude that the UI maps well to clinical workflow, no conceptual fatal flaws were identified in the UI, and that task questions need refinements to certain extend to better align them with the workflow. The UI can be significantly improved with additional presentation options. Having resolved the methodology through these insights; and optimizing some data views would help us conduct a more comprehensive phase 2, with targeted focus on UI and its ability to communicate the intended information effectively.

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Appendix 1: Tasks for Phase 1 Evaluation

1. Is the patient’s condition better or worse than it was at the previous visit? Use the patient time line.
2. Looking at the patient’s treatment history, was there a time that this patient received psychotherapy alone?
3. This task requires looking at aggregative information on treatment options. Find the relevant data view. Find the treatment option with the best outcome (highest percentage %- value for patients improved)?
4. Refer to Guidelines Mapped to Patient View answer the following question: How has the patient responded (better or worse) to any medication regimen with medication class ‘TCA’?
5. Interact with the Guidelines Mapped to Patient view and determine the number of days the combination ‘AAP, TCA’ was prescribed.
6. Now, use the “Show Filter tab” to limit the gender to this patient’s gender. Do you see any change in the highest percentage %- value for patients improved? (hint: compare with task 3 answer, which represent default view)
7. You decide to go with the treatment option with the highest total patient count. Having selected this option, what predictive insight do you have about the patient’s potential treatment outcome, meaning their CGI value, at the end of 30 days on the selected medication? Don’t forget to use clickable features.

BEDA: Visual analytics for behavioral and physiological data

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Abstract— We present BEDA, a tool to help researchers synchronize, visualize, and analyze data sources for single or multiple sessions of behavioral and physiological data. We developed this tool to assist in a study exploring the efficacy of sensory integration (SI) therapy in a school setting. The tool integrates human-coded behavioral data and sensor-generated physiological data from therapy sessions in a 12-week longitudinal study. SI, as a specialty area of occupational therapy, has been widely used to help individuals with developmental disabilities that have difficulties regulating sensory input and modulating arousal levels. There is a lack of research supporting the use of SI; we chose to explore SI further using physiological measures in addition to traditional measures. Conducting studies that rely on many modes of data (video, audio, human-coded behavioral data, physiological measures, etc.) becomes an organizational challenge, especially over a period of several months. Some of these challenges arise in the synchronization, visualization, and analysis of the multiple data sources. BEDA aims to facilitate easier data analysis. Early feedback suggests this tool has potential in clinical and research settings. To date, we have not found evidence that pressure vests increase engagement or decrease undesired behaviors in our school setting. We have also not found correlations between pressure vest use and our physiological measures.

Keywords—Visual analytics; behavioral coding; physiological data analysis; sensory integration therapy; single-subject research design; longitudinal data analysis

I. INTRODUCTION

Children with autism and other developmental disabilities often have difficulties in regulating sensory input and modulating behavior [1]. An individual who has difficulty regulating sensory input may also have difficulty fully participating in all aspects of their communities. Occupational therapists have tried to address issues with sensory regulation through the use of sensory integration (SI) therapy [2]. Few studies, however, explore the cause and effect relationship between the use of SI therapy and behavioral and physiological data concurrently with rigorous analysis [3]. One example of a physiological measure, electrodermal activity (EDA), measures change in electrical skin conductance produced by changes in sweat production. The sweat glands are controlled by the sympathetic nervous system, and researchers have suggested that changes in EDA may, therefore, reflect changes in arousal [4]. Analyzing an individual's EDA data along with behavioral data may help researchers identify how SI therapy affects both internal states and external behaviors. However, there are

numerous challenges when analyzing longitudinal data with multiple data sources (video, sensor data, human-coded behaviors, and sensor data analysis results). Researchers may have to use manual techniques to synchronize several data streams (e.g., a software package to annotate videos, a statistical package to analyze results, etc.). With data streams residing in different software environments, it can be cumbersome to move between analysis results and actual data streams. BEDA is designed to mitigate these difficulties. It supports (1) synchronization, visualization, and navigation of different sources of data, (2) visual analysis of both outwardly observable behaviors and internal physiological data, and (3) record-keeping activity.

II. RELATED WORK

Several existing tools support the visualization and analysis of different sources of data (video and time-coded sensor data) [5], [6], [7]. A video annotation tool, Vcode/Vdata, optimizes the video annotation workflow and supports convenient annotations by allowing users to define behaviors and insert them into the video timeline [5]. In addition to supporting annotation, another software application, Elan, provides synchronization between video and time series data and visualization of both video streams and time series data [6]. BEDA is most similar to Chronoviz, which aids in annotation, visualization, navigation, and analysis of multimodal time-coded data [7]. None of these tools, however, support record keeping and analysis of multiple data sessions in a longitudinal study. Below we describe the use of BEDA in a case study exploring SI therapy in a school setting over a 12-week period. BEDA was designed in collaboration with special education researchers to support an ongoing longitudinal study.

III. CASE STUDY

Sensory integration (SI) techniques, such as the application of pressure vests, are common practice in educational and therapeutic settings for individuals who have difficulty regulating sensory input. However, we lack rigorous research showing cause and effect relationships between these techniques and changes in either arousal level or behavior of the individual receiving the intervention [1], [3]. A pressure vest is a commonly used SI intervention that gives the wearer the sensation of receiving a hug but can be worn with little inconvenience in any setting [1]. An interdisciplinary team of professionals from Special Education and Computer Science conducted a case study with a 9-year-old child, Eddy,

diagnosed with a developmental disability in a school setting. The child's occupational therapist (OT) specifically recommended pressure vests for his therapy. One purpose of this study is to explore whether wearing a pressure vest would produce predictable and measurable changes in EDA levels and, if it did, how these changes related to observable changes in behavior. In this paper, we will present how BEDA can support researchers to investigate more rigorous data analysis in longitudinal studies.

We conducted a controlled study in a public school in collaboration with the child's teacher and OT. We identified undesired behaviors and observed their occurrence when the pressure vest was worn. These behaviors included yelling, hitting the table, and other disruptive and potentially sensory-based observable behaviors. We also identified behaviors that indicated Eddy was engaged in the educational activity at hand, such as manipulating materials and looking at the teacher. We then recorded the occurrence of both undesired and engaged behaviors during intervention sessions across different conditions to determine if the pressure vest produced the hypothesized effect on undesired and engaged behaviors. EDA data was also collected through a sensor attached to Eddy's ankle.

We used a single-subject reversal experiment design to evaluate the effect of the pressure vest on Eddy's behavior and EDA levels [8]. We analyzed 20 sessions of data for this study across the following four different conditions: (1) structured teaching while wearing the vest without pressure, (2) unstructured teaching while wearing the vest without pressure, (3) unstructured teaching while wearing the vest with pressure, and (4) structured teaching while wearing the vest with pressure. We discovered that the structure we imposed on the context produced improvement in Eddy's behavior, so in the second condition, we simulated a context similar to that existing in the classroom. When Eddy's behavior worsened, a rationale for the use of the pressure vest existed. When his behavior remained stable (i.e., no improvement) with the pressure vest, we re-introduced the structured teaching to assess whether we could produce a reversal to improved levels of behavior. In the following section, we illustrate the functionality of BEDA and demonstrate how we used the tool to support the data analysis for our case study.

IV. SYSTEM DESIGN AND DATA ANALYSIS WORKFLOW

Through discussions with researchers, clinicians, and Eddy's teachers, we iteratively designed BEDA to support this study. We highlight the features of BEDA in this section.

A. Visualization, synchronization, and navigation

The users first load video and sensor data into BEDA. Figure 1 shows the BEDA interface after loading a video and EDA sensor data. In Figure 1(e), BEDA visualizes the entire sensor data stream in a line graph in a single view, which gives users an overview of the data. Users can zoom in and out as needed using the buttons in Figure 1(b). Users can change the color and the range of the graph. Synchronization is the next problem people encounter when using multiple streams of data. Because researchers often collect behavioral data of

participants through video recording and physiological data through external sensors, these data need to be synchronized or aligned on the same timeline for analysis. BEDA allows for one-click synchronization by providing both a navigation and a synchronization mode; users can easily change modes by clicking the button in Figure 1(a). In synchronization mode, users can navigate the video timeline using a playhead located below the video (see Figure 1(c)) and the sensor timeline using the orange playhead (see Figure 1(d)). After users put each playhead at the time point that aligns the two data streams, they synchronize the individual streams by switching to navigation mode (Figure 1(a)). In navigation mode, users can navigate the synchronized video and sensor data together.

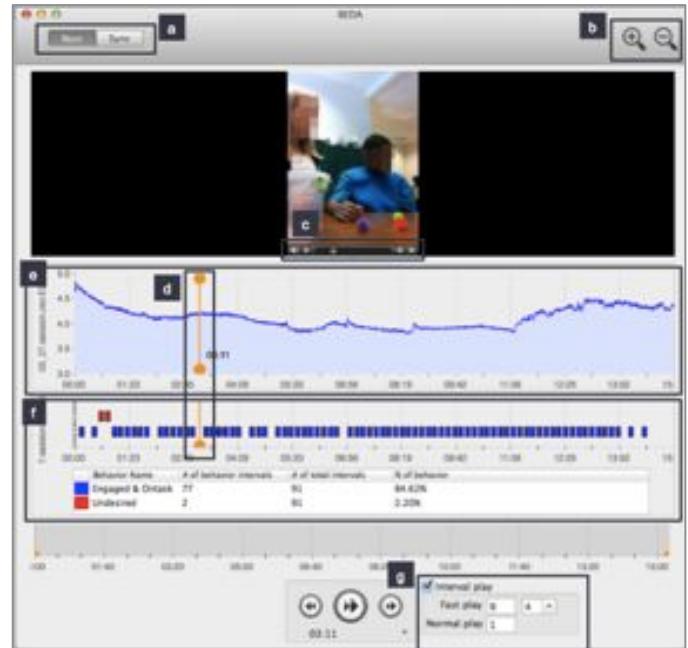


Fig. 1. BEDA interface with a video, EDA sensor data, and human-coded behaviors.

B. Behavioral coding (analysis of outward behaviors)

Behavior coding from video can be time consuming and organizationally challenging. Researchers typically code behavioral data by hand on paper. In our case study, we coded two behaviors, undesired and engaged (on-task) behaviors, using momentary-time sampling (see Figure 2). That is, we recorded whether the identified behaviors occurred during the last 1 second of every 10-second interval in the video. If, for example, the engaged behavior occurred in the 1-second interval, users entered '+' in the corresponding square on the sheet shown in Figure 2. In some cases, researchers were independently moving through video files every 10 seconds by hand, using a media player such as QuickTime¹. Using this approach, two independent coders attempting to code the same interval would often code different time intervals. Tools for consistent indexing of video were needed.

BEDA supports behavioral coding via keystroke. Users define intervals of video play (see Figure 1(g)). In this case

¹ <http://www.apple.com/quicktime/>

study, the interval was set to a fast play speed for 9 seconds and a normal speed for 1 second. These rates are reconfigurable by the users. This automated approach ensures consistent indexing of video because researchers no longer have to move a playhead by hand. BEDA also allows users to define the name, color, and hot key for targeted behaviors. In our case study, we coded undesired and engaged (on-task) behaviors using the hot keys “u” and “e” in red and blue respectively on the annotation timeline. Figure 1(f) shows many annotations of engaged behavior (blue rectangles), and few cases of undesired behaviors (red rectangles) in this session. During the behavior coding, the tool automatically calculates the percentage of the annotated behaviors by calculating the number of coded behaviors out of total number of intervals in the video. This was previously done by hand and labeled on the score sheets (see bottom of Figure 2).

Date: 3/6/2013		Key: + is target behavior present - is target behavior absent	
		Total Clip Time: 10:58	
Engaged & On Task		+ - + + + + - + - + - + + + + -	
		1 2 3	
Undesired Behaviors		- - - - - - - - - - - - - - - - - -	
Engaged & On Task		- + - + + + + + + + + + + + + + +	
		4 5 6	
Undesired Behaviors		- - - - - - - - - - - - - - - - - -	
Engaged & On Task		+ + + + - + + + + + + + + + + + + +	
		7 8 9	
Undesired Behaviors		- - - - - - - - - - - - - - - - - -	
Engaged & On Task		+ + + + + + + - - +	
		10 11 12	
Undesired Behaviors		- - - - - - - + + + + -	
Engaged and On Task:		52 / *100 = 80.0 % of time engaged and on task (# of + intervals) / (total # of intervals)	
Undesired Behavior:		2 / *100 = 3.08 % of time in undesired behavior (# of - intervals) / (total # of intervals)	

Fig. 2. Behavioral data coding sheet.

C. Analysis of physiological data (analysis of internal state)

EDA signals can be separated into phasic skin conductance response (SCR) and tonic skin conductance level (SCL) components [4]. The changes in SCR, often appearing as peaks in the signal, are associated with short-term stimuli or non-specific stimuli. In contrast to SCR, SCL responses denote gradual changes in EDA. SCR and SCL features are often used as proxies to infer arousal and engagement. Common extracted features from SCR and SCL are peaks per minute (PPM) and area under the curve (AUC), and others [9].

Figure 3 shows the Data Analysis interface. Users can select a pre-programmed analysis script (see Figure 3(b)) and click the ‘Analyze Now’ button; analysis results appear in the data analysis window (see Figure 3(a)).

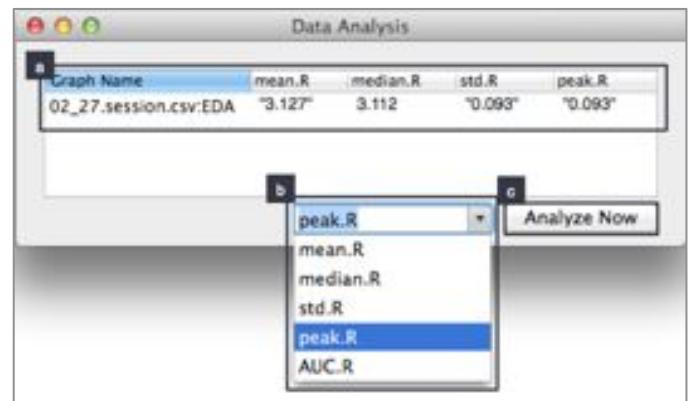


Fig. 3. Physiological (e.g., EDA) data analysis interface.

For users who are familiar with signal processing and want to conduct more specialized analysis, BEDA allows users to write their own scripts using MATLAB² and R³. After they import the scripts into BEDA, the name of the script appears in the combo box shown in Figure 3(b). Users can then select the script name and run it. This allows users to extend functionality by importing scripts. This also supports rapid iteration of algorithms in the same environment. The user can extract new features from EDA and compare them to existing measures.

D. Switching between the summary-graph view and the multi-sessions view

Researchers studying individuals’ behavior in applied settings (e.g., school, home) often use single-subject study designs; they collect data for multiple sessions across different conditions to test the effectiveness of interventions [8]. In our case study, we had four conditions. Continuous data collection and coding are crucial when using this methodology, because the decision to change conditions is made based on the incoming data [8]. For example, if we identified consistent behavioral or physiological patterns within a condition (e.g., wearing a pressure vest), we then can make a decision to change the condition to, for example, not wearing the pressure vest. Thus, simultaneously visualizing both behavioral and EDA analysis across different conditions helps researchers identify patterns within a condition and across different conditions. This also helps researchers identify whether a condition (e.g., wearing a pressure vest) produced changes in the individual’s behavioral and EDA data. After looking at the summary-graph view (see Figure 4), researchers often want to return to the actual video and sensor data streams to investigate sessions in more detail. Currently, this process is cumbersome because researchers must manually find the video and sensor data and load the data. BEDA allows users to switch between the summary-graph view and actual data streams with a click.

² <http://www.mathworks.com/products/matlab/>

³ <http://www.r-project.org/>

A) Summary-graph view

With BEDA, users can manage multiple sessions from diverse data sources in one environment. Users create conditions and label session data with the corresponding condition (e.g., wearing a pressure vest). When a user loads several conditions in the summary-graph view list box (see Figure 4(a)), BEDA includes the sessions in those conditions in the summary-graph view visualization (see Figure 4(b) and (c)). In the graph in Figure 4(b), different coded behaviors are represented as different colors. Data points in the same condition are connected to each other, and there is a gap between conditions. In Figure 4(c), we see the EDA analysis results, PPM and AUC, visualized as a bar graph. Users can compare relationships between coded behaviors and EDA analysis results across different conditions.

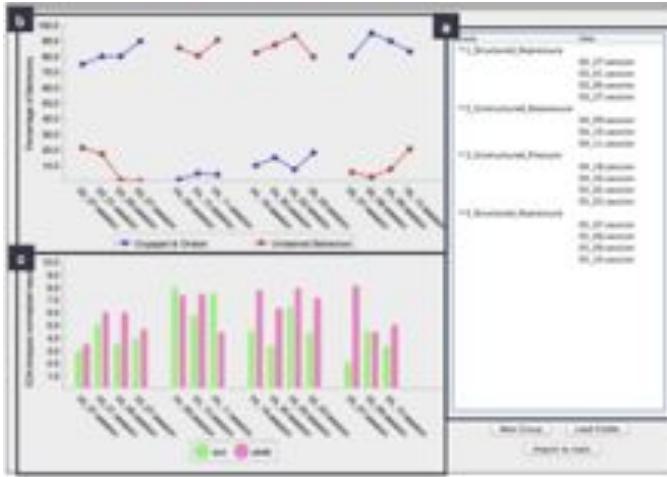


Fig. 4. Summary-graph view: visualizing behavioral and EDA data analysis results of multiple sessions across different conditions. (a) List box of conditions and corresponding sessions. (b) Line graphs showing coded behaviors. The x-axis lists the sessions in chronological order. The blue graph represents percentage of engaged behaviors and the red graph represents percentage of undesired behaviors. Data points in the same condition are connected to each other and a space appears between conditions. (c) Aggregate EDA results for PPM (pink graph) and AUC (green graph).

B) Multi-sessions view

In the summary-graph view, users can find patterns or outliers to investigate in more detail. For example, while both sessions on May 7 and May 9 show higher engagement behaviors and fewer undesired behaviors, the EDA analysis of these two sessions is very different. Clicking the names of these sessions via the list box in Figure 4(a) opens them in the multi-sessions view (see Figure 5). From this multi-sessions view, users can probe sessions and see specific video, sensor data, and human-coded behavioral data. If users drag one of the orange playheads (see Figure 5(a-2)), the video, sensor, and human-coded behavioral data related to this session (see Figure 5(a-1) and (a-2)) move together. Users can navigate each session separately and compare one session with others. Finally, the users can configure the size and order of the graphs.

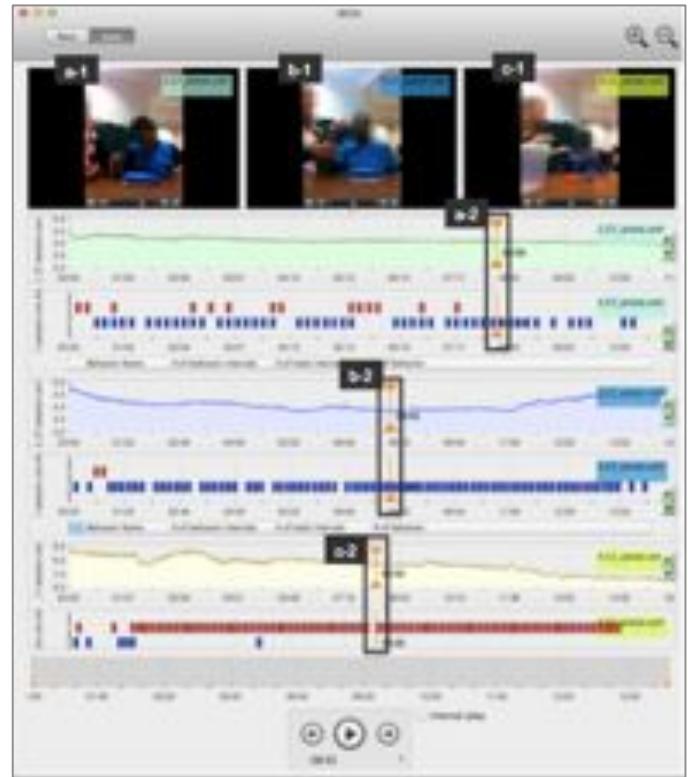


Fig. 5. Multi-sessions view: navigating multiple sessions of original data. If users drag the orange playhead in the Figure 5 (a-2), the video (Figure 5 (a-1)) and data for this session (Figure 5 (a-2)) move together.

V. CONCLUSION AND FUTURE WORK

We presented a tool, BEDA, that supports analysis of longitudinal data from different sources of data, such as video and sensors. We used this tool to support research that examined the efficacy of SI therapy with a rigorous concurrent analysis of behavioral and physiological data. While closely working with special education researchers, we identified the challenges encountered in this style of studies and developed a tool to mitigate them. This tool supports visualization, synchronization, and analysis of diverse data sources (video and physiological data (e.g., EDA)). The tool further supports annotation of behavior from video and sensor signal analysis in the same environment. Finally, the tool permits users to analyze multiple sessions by interactively switching views between the summary-graph view and the multi-sessions view of multiple study sessions.

We have not found evidence that pressure vests increase engagement or decrease undesired behaviors. To date, we have also not found correlations between pressure vest use and EDA with the default EDA measures shown in Figure 3(b). The next step is to explore variations on these measures.

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Visualizing Patterns of Social and Communicative Behavior in Children Using Plexlines

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Fig. 1. The main view of Notables with one Plexline selected. Each Plexline highlights the interactions between the child and the examiner during a Rapid ABC session. The red, green, and blue circles each represent the child’s gesture, gaze, and vocalization respectively, and the size of the spheres denotes the duration of each action.

Abstract—We present a system to visualize the annotations of videos of children engaged in a 3–5 minute interactive protocol that assesses communicative behavior, the Rapid ABC. Rapid ABC session videos are annotated to capture the child’s gestures, gaze, and vocalization — important developmental indicators for a young child. From these annotations, we create a graphical fingerprint for each session. In doing so, we introduce Plexlines, a technique for visualizing multiple types of information layered compactly as timelines. Our tool highlights points of interest to probe Rapid ABC sessions that require more attention. Early feedback suggests this system has potential as a tool for communicating developmental concerns to parents and as a training tool for clinicians.

Keywords—Visualization, Multimedia Systems, Time series analysis

I. INTRODUCTION

Diagnosing Autism Spectrum Disorder (ASD) is a

challenging task, requiring a significant investment of time and an experienced professional to make a diagnosis [10]. The Rapid ABC (RABC) is a semi-structured play protocol to assist a clinician in observing the social communicative behavior of a child aged 9–30 months [11]. Compared to traditional instruments—such as the Autism Diagnostic Observation Schedule and Autism Diagnostic Interview, Revised — that may take over an hour, a RABC session can be completed in under five minutes [9]. The child and examiner go through a series of semi-structured activities while the entire interaction is recorded and observed. The RABC is short and has a consistent structure. It lends itself well to exploring new methods of data visualization to highlight patterns of behavior.

To do this, we developed Notables, an online tool designed for researchers, clinicians, and parents that allows for comparison of many RABC sessions at a glance using data gathered from video annotations. Each session is presented as a Plexline, a layered, timeline-based representation where behaviors are represented as abstract graphical elements.

[†]Both authors contributed equally to this work.

Notables was designed with three main goals: To create (1) a child-centered, time-based visualization that (2) highlights communicative behaviors known to be warning signs for developmental delay, and (3) compared across a population of children on and off the autism spectrum.¹ We found that abstracted visualizations are highly functional and early probes suggest clinicians and researchers are excited to explore them in their analysis process. We will explain the methodologies and techniques used to meet these goals, the feedback we have received from our preliminary evaluation, and our plans for future work.

II. RELATED WORK

There has been extensive work visualizing time series data. In this section, we will discuss our main inspirations, though it is not an exhaustive list of work in the field. We are especially interested in social visualization, which is defined as “the visualization of social information for social purposes,” or in other words, visualizations for the everyman [3]. Time series data visualization has come a long way, from simple hand-drawn visualizations, such as Playfair’s line graphs and bar charts [14], to Chat Circles, which visualizes time series data in real-time [3]. We take an approach similar to Chronovis where data is imported into the visualization [5]. We found that the abstracted, linear graphical representations of temporal data in Loom, Chat Circles, and CloudLines were evocative and functional, so we embraced functional abstraction in presenting each child’s visualization as a personal time stream [3, 6].

In the field of medical visualizations, we were inspired by LifeLines, one of the first visualizations of medical records [12]. Its second iteration, LifeLines2, allows users to visually inspect multiple health records in a consolidated view, with additional functionality to align, rank, and zoom to examine the records [15]. Its depiction of multiple medical records of time series data as a list is perhaps the biggest inspiration for Notables.

III. PROJECT BACKGROUND

Notables visualizes data from the RABC, a protocol created for direct observation of social communicative behavior of young children. Videos of RABC sessions were coded using ELAN, an annotation software package. The export of this coding is the input to our system.

A. Rapid ABC

RABC was developed as an easy to administer 5-minute pre-screener for ASD that was designed to be accessible to all doctors and theoretically, can be conducted in a routine doctor’s visit [9]. It consists of five stages of play (greet, ball, book, hat, tickle) wherein the examiner evaluates the child’s responses to social bids (an attempt by the examiner to initiate a response) and the ease of engaging the child. This research is part of a larger research initiative, an NSF Expeditions project involving 9 universities and an autism center. The RABC data was collected as part of this effort. Over a hundred RABC sessions were recorded in a specially instrumented room

containing multiple cameras, microphones, and a Kinect. Affectiva Q-Sensors on both the examiner and child recorded electrodermal activity (EDA), temperature, and acceleration. For our visualizations, we utilize the camera facing the child and the human coded RABC video annotations.

B. Annotations & ELAN

The RABC videos were hand coded by three independent coders and checked for inter-rater reliability. We grouped the annotated behaviors into three categories: child’s gaze, vocalization, and gesture. Of these annotations, we highlight the ones that indicate communicative intent and interactions directed toward the examiner. We further explain this in the Annotation Taxonomy subsection.

The RABC videos were annotated using ELAN, a software tool to annotate video [16]. It allows for multimodal analysis through the creation of an annotation hierarchy. We export this ELAN data to create Plexlines.

IV. PLEXLINES

Plexlines were developed specifically to reveal temporal patterns available in the RABC annotations. In this section, we discuss the design decisions and the framework behind the visualization.

A. The Power of Abstraction

Visualizing one child’s data in ELAN requires the entire screen. This layout prohibits comparison of several RABC sessions at a glance. Our approach is to create a simple, legible fingerprint of each RABC session. To do this, we abstract the annotations, through the use of simple shapes and symbols, that allow us to provide a complete picture of the annotated behaviors at a glance [1].

We have evolved to perceive perceptual structure—patterns of quantities, color, relative size, and shapes [1]. In a way, shapes and symbols are more concrete than numbers. The latter uses single units while the former operates as a whole, through our cognitive ability to quickly perceive visual relationships. The abstracted visualization is a concrete representation of an internal mental model of social-communication behavior. A new representation of a familiar model can also help clinicians become more attuned to spotting abnormalities, revealing patterns faster than what would typically be hidden in text and numbers [8, 17].

Our goal with Plexlines is to visualize timeline data, functionally and legibly. Plexlines capture the essence of behavior while providing a detailed picture of many types of information. In the context of this work, one Plexline visualizes over 30 different annotation codes, while still providing information on actions, duration, behavioral patterns, and initiation-response sequences.

B. Annotation Taxonomy

We categorized the RABC annotations to create a graphical framework. To focus on interpersonal interaction, we separated child-related annotations into primary and secondary annotations. We define primary annotations to be cases where the child is engaged in social interaction directly with the examiner or with intent, including: gaze at examiner,

¹ Another paper (Han et al.) submitted to this workshop also describes a visualization tool for the same dataset. This paper focuses on visualization and understanding of the individual session, while Han et al considers the problem of being able to create understanding across multiple sessions.

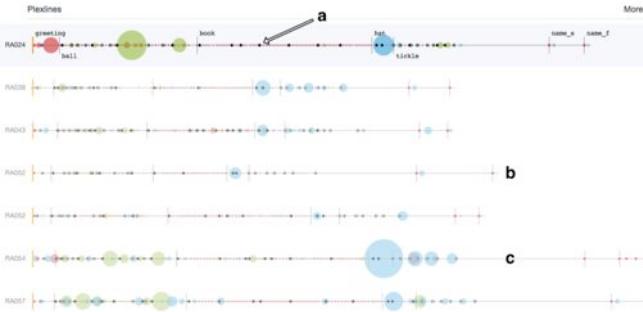


Fig. 2. A series of Plexlines. Each Plexline represents a single RABC session. (a) Instance of an examiner bid signal (b) A shorter Plexline with minimal gaze, gesture, and visualization of the child (c) A longer Plexline with instances of overlapping actions during a RABC session.

responding to a question, or calling for attention. Primary annotations are further separated into three categories: vocal, gesture, and gaze, which are color-coded red, green, and blue respectively. Secondary annotations are all other annotations not categorized as primary, representing moments in which the child is engaged in an activity, but not in direct communication with the examiner, such as turning the page of a book. This distinction between primary and secondary is the basis for the visual hierarchy of the Plexline. Primary information will be represented more prominently to distinguish the nuances between each child.

Annotations relative to the examiner are categorized similarly, separating annotations into two types of examiner bids or requests: those in which there is an expected reaction from the child, and all else in which there may be any number of reactions from the child. The former usually consists of a question or a demand—such as “Can you turn the page?” or “Look at my hat!”—and is marked by a filled black point. All other annotations fall into the latter category and are represented by a hollow point (see Fig. 1). Additionally, calling of the child’s name is highlighted separately from other examiner annotations. This bid was added to the end of the RABC by the research team.

C. Graphical Design

Visualizations of medical records have shown that graphical time scales are one of the most intuitive approaches for telling a narrative and comparing large datasets [12, 6]. However, rather than comparing many sets of data within one child’s timeline, we are comparing different categories of information in one child, and those patterns across several children. In order to maximize screen real estate while creating a legible visualization, we developed a technique for layering salient information onto one line. By layering and combining multiple types of information on a line using different stylizations of plotting symbols, we are able to display all the annotation data continuously while maintaining legibility [1, 7]. Each unit can be read individually, or as part of its group on a linear time scale.

1) Symbolic Markers: One of the biggest challenges of the Plexline is separating the different categories of information visually. However, legibility can be achieved through careful selection of different styles of circular plotters. Circles are

used as the main representation of data for aesthetics and scalability. It lends itself well for displaying multiple units of different sizes over a linear path of time. By using the diameter of the circle to indicate the duration of the annotation, we can create a visual pattern in which more visual density indicates more child activity.

Secondary child annotations show that the child is still participating in the activity and are aggregated and represented by small hatch marks on the Plexline so they are not emphasized as much as the primary annotations. Examiner bids signal initiation of a social interaction (See Figure 2 (a)); they are represented by circles to match the child, who may follow with a response. However, since the examiner is scripted and standardized (as much as is possible), the size of the examiner’s circle is fixed and does not include duration. The examiner’s bids serve as landmarks so the viewer focuses on the child’s data.

2) Color: Because this is a child-centered visualization, only the child’s primary actions are colored, drawing attention to the child’s pattern of interaction. Vocal, gesture, and gaze behaviors are coded red, green, and blue, respectively. These behaviors are critical in identifying autistic behavior. For example, lack of vocalization or non-verbal vocalization is one of the biggest indicators of autism [10]. With vocal being the least expected action, it is coded the brightest and boldest color, red, for ease of reference. A slight transparency to each circle allows for spotting overlapping of actions since it is not unusual for a child to express all three primary interactions at once, showing high engagement.

V. ONLINE WEBTOOL

We developed a beta of Notables, to explore the effectiveness of the visualization. It is a fully functional system implemented primarily using D3. We discuss the details of the tool in the following sections.

A. Video Supplement

The Notables online tool can be seen in Figure 1. The Plexlines appear as a list below the video screen. Selecting a specific Plexline, loads its corresponding video. The Plexline then becomes both an interactive scrollbar and visualization. The video proved useful in explaining specific visualization patterns. For example, in Figure 3 (b), the child gazes at the examiner primarily in the middle of the session. When viewing the video, the user can see the gaze in context. The visualization’s reliability is strengthened by the ability to cross-reference points of interest with key moments in the video.

B. Comparison

Plexlines are displayed as *small multiples*, a term Tufte coined describing a series of small visualizations with the same design structure. This “economy of perception” allows the viewer to focus on information changes within and across Plexlines [14]. For example, in Figure 2 (c), the last Plexline depicts a longer RABC session, with more gazes from the

child. However, in Figure 2 (b), the RABC session is much shorter, lacks gesture and vocalization behaviors, and displays minimal gaze behavior from the child.

The default order of the visualizations is sorted by the child's ID number. To compare a small selection of children, one can reorder Plexlines by drag-and-drop. It is possible to compare one child across the entire population by comparing the Plexlines of one child to an aggregate visualization of the rest (except that of the individual child). In this view, the Plexlines are layered on top of each other (see Figure 3 (b)). From the aggregate view, one sees that children are more likely to gesture during the initial stages of the session, a behavior missing in the first Plexline in Figure 3 (a).

VI. INITIAL EVALUATION AND FUTURE WORK

As of the writing of this paper, 190 children have participated in the RABC recording, of which 68 sessions have been annotated. We presented a demonstration of Notables with these annotation data to a clinician and a panel of researchers. The clinician's response was enthusiastic. From this discussion, we identified key ideas to drive future

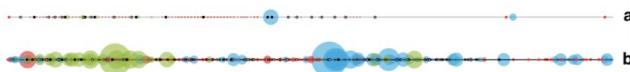


Fig. 3. Comparing one child (a) with a layered aggregate of the rest (b). A lack of green on the individual Plexline shows that this child lacks gestural engagement in the first quarter of the RABC session, which is unusual when compared to the aggregate.

development.

A. Annotating Plexlines

The clinician found the Plexlines interpretable and expressed a desire to further annotate points of interest along a Plexline. This would be useful for noting and describing specific events to parents after a session.

B. Notables as a Training Tool

Early feedback introduced a new use case for the visualization. The clinician suggested the potential of using Notables as a training tool for clinicians. Trainees can see a series of Plexline visualizations to understand a typical session, thereby understanding the structure of the protocol and the expected behaviors.

C. Segmenting Stages

The entire RABC session is represented continuously on one Plexline. The Plexlines are aligned at the beginning of the RABC greeting stage. The protocol, however, consists of 5 stages. Aligning the Plexlines about any of the specific stages across multiple children would provide more detailed information about that stage. That is especially helpful as children proceed through the RABC at different rates.

D. Limitations

We realize annotations are imperfect and not inclusive of every possible behavior. Coding schemes improve iteratively over time. The features we are coding may not be optimized for our screening goals. The taxonomy for our visualization is

highly influenced by the taxonomy of the existing RABC annotations. We currently distinguish between gaze, gesture, and vocalization behaviors. Smiling is an example of an annotation that may be useful, but not yet annotated.

Additionally, since users tend to perceive longer duration by observing larger surface area rather than by longer diameter, there are concerns that using circles may exaggerate the child's engagement level since area doesn't scale linearly with diameter. However, it allows clinicians to spot trends and unusual patterns faster and easier, from which they can go into a more detailed analysis, which is our goal.

The time it requires to code the RABC videos is another limitation. Ideally, a clinician may want to show a parent their child's session visualization immediately following the session. Other members of the research team are exploring vision and audio techniques to automatically extract annotations from the RABC. Until we can reliably annotate data automatically, we depend on a less convenient, but more consistent framework through hand-coded annotations.

VII. CONCLUSION

We presented a browser-based tool for visualizing RABC sessions using Plexlines, a new technique for visualizing multiple layers of social and behavioral interaction. We focused on understanding the child's intent and preferred patterns of communication through their gestures, gaze, and vocalization. The Plexline for each individual child can be viewed in the web browser for comparison across multiple children to identify points of interest for further examination. Early feedback suggests Plexlines are (1) interpretable, and useful in providing a quick overall summary of RABC sessions and (2) a useful tool for teaching and explaining the RABC protocol.

We continue to make the tool more robust and flexible, by integrating sorting, filtering, and semantic zoom features. A larger formal study is planned to consider how the tool is integrated into the clinicians' existing workflow in a way that is unobtrusive and useful.

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Visualization of EHR and Health Related Data for Information Discovery

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Abstract

In this paper we describe research we are conducting in response to a Program Announcement solicited by the Assistant Secretary of Defense for Health Affairs, Defense Health Program. The amount of information in Electronic Health Record (EHR) systems is growing rapidly with the inclusion of disparate forms of data from a number of new sources, i.e. genomics and imaging data. EHR systems will continue to grow as more healthcare data is digitized. As data in EHRs grows, there is increasing interest in understanding what information and knowledge these large data sets represent.

Data visualization techniques offer an opportunity to explore and understand large data through novel approaches. Our research seeks to visualize health care data from electronic health records (EHR) and other health related data. Our approach is informed by retrospective data queries using DEDUCE, a query tool developed at Duke University.

Keywords: Electronic health records, health related data, information visualization

Introduction

Visualization of genomic data is used to understand data structures. Geospatial applications have revealed patterns related to risk factors in environmental health,^{1,2} and visualization methods of limited data sets have been used for clinical decision support.^{3,4} Data from EHRs and other health related data, however, are displayed primarily through techniques that have been used for many years, e.g. fishbone diagrams for lab values, or by using charts and graphs. There have been few successful attempts to visualize massive amounts of disparate health care data.

Effective visualization techniques of large health data sets will allow users to see patterns they would not otherwise see. With many sources of health related data containing many parameters, the ability to visually explore the collective data has the potential to reveal valuable information.⁵ There are many data elements and attributes in healthcare data. We propose that grouping and aggregating related data elements via a priori categorization (e.g. laboratory results or vital sign data) or data-driven methods (e.g. correlation) will facilitate developing visualization techniques that will allow users to see patterns in large data and elicit further inquiry of the data. We also believe the user should be able to further explore the data by opening the visual representation of a set of data elements to see trends representing aggregated data and drilling down even further to the subsets of the data. By having an interactive visualization, the ability to explore and gain a deeper understanding⁶ of what the data represent will encourage adoption of the visualization technique, assuming the visual presentation minimizes cognitive burden.

Related Work

There are numerous reports in the literature related to data visualization in health care, most focusing on the technical aspects of visualization, medical imaging, and genomics. A number of prototypes have been also been reported. LifeLines, first described in 1996 by Plaisant and colleagues,^{7,8} was used to visualize health data across a personal health record using timelines. Lifelines evolved to become Lifelines2, a visualization tool using categorical point event data across multiple records. More recently, Eventflow, similar to Lifelines2, also addresses the need to have a system to support interval events.⁹

Novel visualization techniques using EHRs was somewhat limited until 2009 when the HITECH Act mandated EHR implementation. In addition to evolving changes to LifeLines, several prototypes are in various stages of development. Most reported techniques are interactive, allowing the user to explore data incorporated as one visual display. For example, Zhang, et. al.¹⁰ use a radial starburst visualization of multiple data points from one health record permitting users to drill down on data to single time points. Klimov and Shahar describe a prototype called VISITORS (Visualization of Time-Oriented Records) using time-oriented data sets with an interface to explore longitudinal values.¹¹ These approaches are similar to that we are taking, but we believe the historical queries and identification of the data elements and clusters will enhance visualization of relevant data.

Methods

Using historical data queries of Duke's EHR system (called DEDUCE) we will identify what data elements are in queries and classify them according to the types of information sought (e.g. outcomes, outliers of treatment

methods). Groups of related data elements will be incorporated into a visualization that allows a quick comparison of the data from a large population with the ability to view trends over time within a chosen measure.

The following example illustrates our approach using the Department of Defense mock EHR data. We will look at aggregated health related data from an Army unit pre- deployment using visualization to discover differences within the group. We will then compare the same data elements post-deployment to identify changes. These time periods can be compared with the group later diagnosed with post-traumatic stress disorder to identify outliers and what data elements might have caused the outlier. In this example, Army personnel between 25-30 years old who have been deployed can be compared to the population of all adults in the system, or all Army or Marine or Navy personnel. We will employ visualization methods that show aggregated groups of data elements with a distribution per population, with the ability to drill down in the data and display longitudinal data for selected data elements.

The key to selecting the most effective method of visualization is to understand how to address the informational value of the data. We expect classes of data elements with the greatest variation to stand out. We will statistically pre-process data as an enhancement to visualization, eliminating null associations and unimportant variables (statistically). In comparing groups, the visualization method should clearly show differences. Further examination of data should also permit the easy application of different filters and the ability to hone down on subsets of data.

Discussion

1. Radial Coordinates Visualization. We have developed an initial multivariate visualization tool in the statistical programming environment R, using the RGL package to enable real-time interactive visualizations. This radial-coordinates visualization prototype is inspired by parallel-coordinate^{12,13} and star plot¹⁴ multivariate visualization techniques.

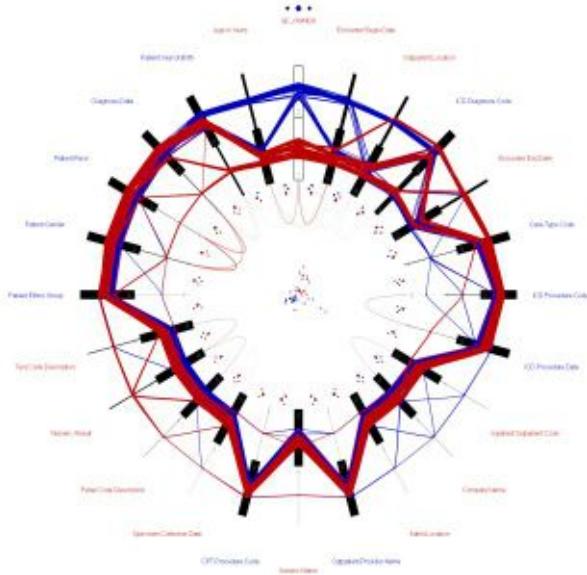


Figure 1: Radial coordinates visualization of DEDUCE queries.

Figure 1 shows an example radial coordinates visualization using queries from the top two users in Duke’s DEDUCE EHR query tool. Each line represents a query, and the value for each axis represents how often that data element was used in the given query (typically zero or one). The lines are colored by system user. A circular layout of the axes has the advantage of a square aspect ratio when compared to standard parallel coordinates axes, which can be beneficial for large numbers of axes. Within this framework we have looked at additional improvements to standard parallel coordinates techniques, such as showing data distributions directly for each axis based on data type. For continuous data we display a box-and-whiskers plot (not shown in Figure 1), for discrete integer-valued data we display a histogram with bin width proportional to number of entities with that value, and for categorical data we display a stacked bar chart, with bar length proportional to number of entities with that value. This enables rapid evaluation of the various data types for a heterogeneous dataset, and of the distribution for each variable. In addition, we introduce line spreading to mitigate the problems of multiple lines collapsing to a single data point for discrete and categorical data, extending the parallel sets method (<http://eagereyes.org/parallel-sets>) to enable visualization of individual data entities, and the incorporation of non-categorical data.

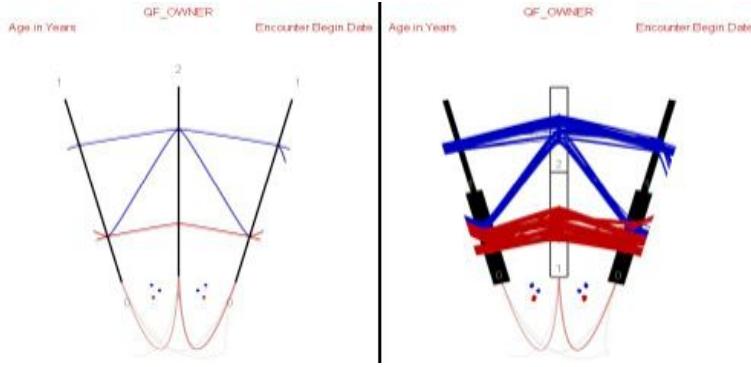


Figure 2: Line spreading (right) for discrete and categorical data enables improved visualization of multiple entities with the same value.

The close-up in Figure 2 illustrates the improvement possible using axis visualization with line spreading (right). The “QF_OWNER” categorical data (user 1 vs. user 2) is displayed using a stacked bar chart, with segment length proportional to number of entities with that value (there are slightly more queries from user 1), and individual lines are spread out within each bar segment based on their position on neighboring axes. The other two discrete integer-valued data elements are displayed using a histogram with bin width proportional to number of data entities with that value, and individual lines are spread out within each bin. With the visualization on the right it is much easier to follow individual lines between axes, and to see clustering of lines.

Axis-ordering is a well-known problem with parallel-coordinates techniques. We have experimented with a number of techniques for clustering axes based on correlation between axes. We also utilize correlation to flip axes to try to minimize line crossings, based on positive or negative correlation with a given axis. To enhance these techniques we also draw curved arcs connecting axis pairs, with opacity and line width proportional to correlation magnitude, and color based on correlation polarity (blue = negative, red = positive). Colored axis labels indicate whether the axis has been flipped (blue) or not (red).

The central space in the radial coordinates visualization enables the display of supplemental visualizations. Inspired by Holten and vanWijk,¹⁵ we draw pair-wise scatterplots just below neighboring axes, and in the center we draw a scatterplot of the first two principal components. In the future, we plan to enable a number of different visualizations to be placed here, chosen interactively by the user. Each scatterplot and the radial coordinates visualization are linked together, such that selection in any visualization is reflected in the other visualizations.

2. Force-Directed Network Visualization. We have also developed a force-directed node-and-link network visualization to investigate queries from DEDUCE queries, implemented in the Processing programming environment. Figure 3 shows the same data as Figure 1, with individual query data elements drawn as circles, and de-identified system users (in this case the top two users of the system) as squares

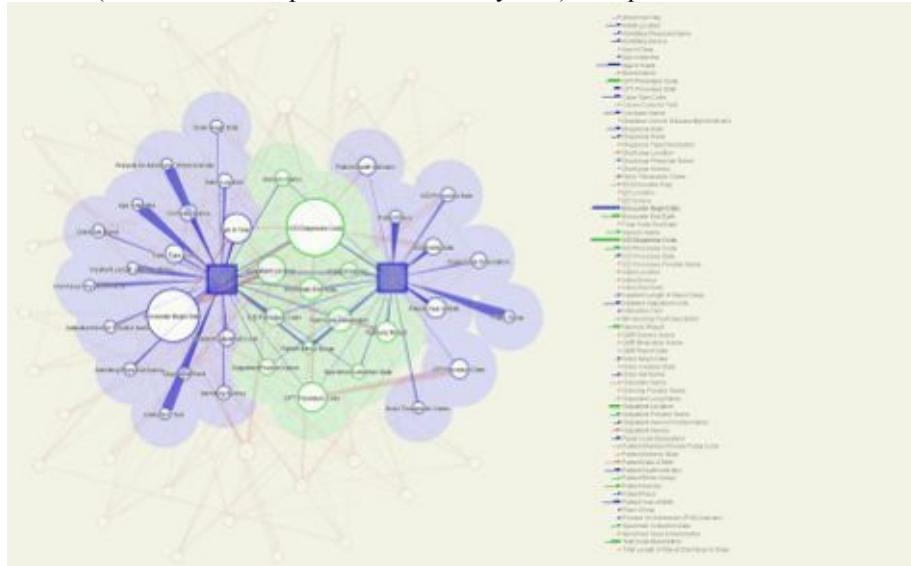


Figure 3: Force-directed layout visualization of DEDUCE queries.

The size of each circle represents how often it was used as a query element across all queries, and the size of each square represents the number of queries made by that user. Links between circles represent how often each element was used together in a series of queries, with each end scaled based on the relative importance at each end of the link. Links between circles and squares represent how often each user made a query on each element. Nodes are placed via a force-directed layout based on the overall strength of each link. In this example the user has highlighted the two users, which in turn highlights nodes connected to those users, while deemphasizing all other nodes. Nodes that are connected to both users are highlighted in green, whereas nodes that are connected to just one user are highlighted in blue. A full list of data elements is shown to the right, with horizontal lines representing the number of times each element was used across all queries (equivalent to circle size), and the number of other elements connected to. The user can interactively select nodes via the node-link diagram or the list of elements.

Some relationships are more easily discernible in one representation vs. the other. E.g. it is perhaps more readily apparent in Figure 3 that ICD Diagnosis Code is the most-used query element, and both users used that element, whereas in Figure 2 it is more apparent that Patient Gender, Patient Race, and Patient Diagnosis Date are all strongly correlated (i.e. they tended to be used together in queries), and that one of the users (red) included those elements more than the other. Our approach going forward will therefore combine such visualizations to enable multiple linked views of the data.

Conclusions

Compressing petabytes of health care data representing many data elements into various groups of related data presented visually with an interface that allows the user to interactively explore the data elements, to our knowledge never been done. There is the potential to detect causal relationships between various sets of data, which may lead to improved health care costs.

Acknowledgements

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Interactive Dashboards: Using Visual Analytics for knowledge Discovery and Transfer

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ABSTRACT

With the advancement in information technologies, complex and multidimensional data are generated at an unprecedented rate. The public health sector deals with complex and dynamic health data that impose a challenge on health professionals to understand and make informed decisions about complex health problems. This study synthesizes the Delphi method approach and the Visual Analytics methodology to solicit experts' inputs in a collaborative setting and focus their skills and expertise to inform the design of a visual analytical tool that can be employed to help health professionals to understand complex and heterogeneous health data, build knowledge and make informed decisions. Findings generated from this study will help to inform the design of innovative dashboards that can be used as a knowledge discovery and transfer tool within the public health sector.

Keywords: Visual Analytics, Public Health, Group Analytics, knowledge Discovery, Knowledge Transfer.

1 INTRODUCTION

With the advancement in information technologies, complex and multidimensional data are generated at an unprecedented rate. In this data rich world, from intelligence to finance to healthcare, multidimensional and dynamic datasets impose a challenge on data analysts and decision makers to understand and make informed decisions about complex events and situations.

To effectively approach multidimensional and complex problems, visual analytics methods have been adopted to expand the shortcoming of analytical and computational approaches [Keim et al., 2010]. Visual Analytics (VA) is defined as the "Science of analytical reasoning facilitated by interactive visual interfaces" [Cook and Thomas, 2005]. The emerging science of visual analytics leverages human's perceptual and cognitive capabilities to reason, analyze and make sense of complex datasets. Visual analytics integrates advanced visualization techniques and interactive graphical interfaces with mathematical and computational analytics to support humans' analytical reasoning processes [Thomas and Cook, 2006; Keim et al., 2008]. Visual analytics helps analysts to gain insights into dynamic datasets and ultimately support knowledge discovery and transfer. [MacEachren et al., 2004; Boulos et al., 2011]

An example of a multidimensional and dynamic problem in public health is injury. Injury is the leading cause of death among North Americans age 1-44 and results in the greatest number of potential years of life lost, compared to other causes of death

[Health Canada, 1999]. The causes of injury are many, including motor vehicle crashes, poisoning, drowning and falls, among others [Pike et al., 2010]. Furthermore, injury is associated with numerous individual, social, environmental and policy related factors, and present multi-dimensional ill-structured problems to public health professionals and researchers. These ill-structured problems are interconnected and interdependent; they combine various health elements and require a careful study of related factors in order to make appropriate decisions.

Effective analysis of injury data is critical to the development of successful prevention strategies. This includes the discovering and identifying trends and patterns in injuries – who is being injured, how they are being injured, and an understanding of the leading causes and associated factors of injury - in order to monitor and improve the health and well being of children and youth in Canada [Pike et al., 2010]. The BC Injury Research and Prevention Unit (BCIRPU) at the Child and Family Research Institute (CFRI), BC Children's Hospital has a goal to provide injury researchers, public health practitioners and policy makers with an interactive decision-support technology solution that can help injury stakeholders visually explore, discover and interpret dynamic injury datasets. As such, we designed the Analytical Injury Dashboard (AID) as a tool that will empower injury stakeholders and allow them to understand and synthesize critical information from complex injury data in order to inform fundamental policies and programs and to strengthen child and youth injury surveillance, prevention and future research.

This study synthesizes theories from the Delphi method and the visual analytics methodology to evaluate the use of the AID dashboard to help injury stakeholders build and exchange knowledge in order to make informed decisions about dynamic health situations for child and youth injury prevention initiatives.

The preliminary results of this study are outlined in this paper as follows. The first part of this paper describes the proposed AID dashboard and demonstrates its application using real multidimensional public health data retrieved from the Canadian Hospitals Injury Reporting and Prevention Program (CHIRPP). The remainder of this paper shows the results of the AID pilot testing using the Group Analytics sessions that synthesize multiple injury stakeholders' inputs and enable them to collaboratively work on various scenarios to evaluate the proposed AID dashboard.

2 CHIRPP DATA

Canadian Hospitals Injury Reporting and Prevention Program (CHIRPP) is a computerized information system that collects and analyzes data on injuries to people (mainly children) who are seen at the emergency rooms of the 10 pediatric hospitals and of 4 general hospitals in Canada. CHIRPP is a unique, richly detailed database of "pre-event" injury information obtained by asking: What was the injured person doing when the injury happened? What went wrong? Where did the injury occur?

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For the purpose of this pilot study, we retrieved CHIRPP data for the province of British Columbia for the period 2007-2010 from the Public Health Agency of Canada (PHAC). The data represented child and youth (0-19 years of age) injury cases that visited the BC Children's Hospital emergency department for treatment following an injury. Data was de-identified to preserve patients' privacy and confidentiality, and injury classes with fewer than five cases were not disclosed in the AID dashboard in order to safeguard patients' identities. A "Data confidentiality Agreement" between BCIRPU and PHAC was signed to permit access to the injury database in order to upload the dataset into the designed AID dashboard and pilot test it.

3 RELATED WORK

The use of advanced information technologies has grown within the healthcare system to enable effective collection of health data [Georgiou, 2002]. With this trend, health professionals appreciate the advantage of integrating visualization techniques into the public health workflow to effectively keep track of health issues, facilitate data exploration, monitor health system functioning and support decision-making [Moore et al., 2008]. Previous research has explained how visual analytics addresses the issue of information overload and enables analysts to transform raw data into salient information and knowledge [Cook & Tomas 2005; Keim et al., 2010]. Findings from previous research have revealed that visual analytics facilitates data exploration and knowledge construction and subsequently supports the decision-making process [Keim et al., 2010]. Applying visual analytics to public health problems is vital to convert complex and dynamic health data into salient information and knowledge. Several visual dashboard systems have been used to empower medical and health professionals with advanced visualizations to facilitate detection and investigation of health and medical issues to make timely decisions and interventions [Moore et al., 2008; Cheng et al., 2011; Al-Hajj et al., 2013; Mazzella-Ebstein & Saddul, 2004].

Despite this wide use of visual dashboards within the medical and public health sector, there has been a knowledge gap about the effect of using analytical dashboard on facilitating knowledge discovery and transfer within a real domain application. This paper aims at evaluating the use of visual analytics to support knowledge discovery and transfer in a collaborative visual analytics setting.

4 ANALYTICAL INJURY DASHBOARD (AID)

We borrowed theories and design guidelines from information visualization and visual analytics to design the AID dashboard. We built the dashboard using Tableau Software. Tableau is a commercially available visualization software that uses the Visual Query Language (VisQL) to visually represent large databases through interactive visual interfaces.

The AID dashboard empowers injury stakeholders with a single screen display of multidimensional information including temporality and demographics related to one particular injury issue. Each window view is connected to a full-page visualization with specific functionalities and features to integrate stakeholders' analytical models and facilitate data exploration and knowledge discovery. Every time the stakeholder selects a particular graphical display, a comprehensive visualization will be displayed with advanced analysis capabilities and granularities to enable interaction and in-depth understanding of key injury indicators' performance.

The AID dashboard was built to be intuitive with easily interpreted visualizations that require minimal time and cognitive efforts. The AID's single interface page shows a summary of all

indicators displayed in various graphical representations including stacked bar chart, time trend, and geographic map [Fig.1].

The data analysis component of the AID dashboard enables injury stakeholders to interact with the visual representations at various levels of granularities using advanced visualization techniques (i.e. interactive distortion, zooming, filtering, brushing and linking). This interaction facilitates data exploration while minimizing cognitive load. AID analytical features offer temporal, geospatial and structural data to assist stakeholders in gaining comprehensive knowledge and in-depth understanding of the injury indicators data.

The AID dashboard offers stakeholders the ability to test and manipulate data to understand underpinning leading causes of injuries, identifying areas of alerting health issues and acquire knowledge needed to make informed decisions.

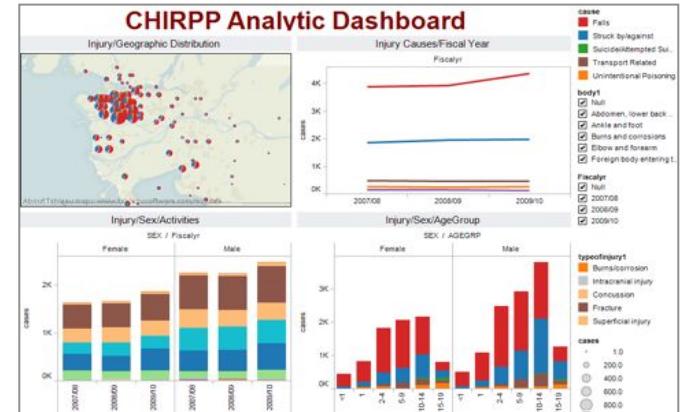


Figure 1: The AID dashboard showing the CHIRPP injury data. It incorporates 4 multiple views: the geospatial visualization, the time trend visualization, and the 2 stacked bar charts visualizations.

5 PROCEDURE

The primary goal of this study was to design a study to pilot test the AID dashboard with real injury stakeholders in a collaborative visual analytics setting. We intended to investigate how the AID dashboard can facilitate multiple injury stakeholders' data exploration as well as enable them to convert complex data into knowledge essential to make informed decisions and take suitable actions.

5.1 Method

Borrowing from the Pair Analytics methodology [Arias-Hernandez et al., 2011], we adopted the Group Analytics (GA) approach to conduct the study. Pair Analytics draws from cognitive science theories [Hutchins, 1995] and the "extreme programming" approach where two programmers collaborate to develop computer software [Beck et al., 2004]. In the Pair Analytics (PA) session, the Subject Matter Experts (SMEs) works collaboratively with the Visual Analytics Expert (VAE) in a one-on-one pair setting to explore the data and solve the analytical problem using the interactive AID dashboard. The VAE is an analyst knowledgeable about the data visualization tools and techniques as well as the design of VA dashboards. SMEs are stakeholders specialized in a specific domain or area. The Group Analytics method extends the PA methodology and synthesizes techniques from the Delphi method [Okoli et al., 2004] to incorporate the co-located collaboration of multiple SMEs with the VAE to solve an analytical problem using the AID dashboard. The Group Analytics gather experts in various fields related injury prevention and focus their skills and expertise on the design and

evaluation of the AID dashboard in a collaborative and social setting. In this study, SMEs are injury stakeholders that possess knowledge, skills and expertise in the field of injury prevention. They have diverse backgrounds ranging from novice public health analysts to senior epidemiologists, and public health medical personnel to public policy specialists. To ensure representativeness and to cover a broad injury prevention audience, injury stakeholders or SMEs were selected from various age groups, gender, academic background, expertise as well as their clinical and research job focus. Each SME was purposely selected to represent a constituent group (e.g. medical officers of health) and to solicit general input from constituents before and after the Group Analytics sessions.

5.2 User Study

We conducted two Group Analytics (GA) sessions, each session lasted approximately 30-minutes. Eight injury stakeholders participated in the two Group Analytics sessions (37% male and 63% female). Participants' ages ranged from 25 to 54. Participants sat around a table, similar to a business meeting setting.

The VAE gave participants an overview tutorial about the AID dashboard and explained its features and functionalities. SMEs were given verbal instructions about the sessions' agenda and expectations. During the GA sessions, SMEs worked together on two scenarios, each describing a specific analytical problem. Group Analytics sessions were audio and video recorded to capture SMEs' interactions with each other and with the VAE. Screenshots were collected to capture VAE's interaction with the AID dashboard as well as to support the data analysis process. All SMEs signed an informed consent form prior to participating in the study.

Immediately following the two Group Analytics sessions, SMEs were asked to fill out a self-reported questionnaire. The response rate of the questionnaire was 87%. To enhance the scale's reliability, the questionnaire adopted a 7-point Likert-type scale (i.e. 1- Strongly Agree, 7- Strongly Disagree). The questionnaire was pilot tested with staff and graduate students from the BCIRPU prior to the Group Analytics sessions in order to ensure its validity and test-retest reliability.

6 RESULTS

Audio and video recording together with computer screenshots provided rich understanding about the usability of the AID dashboard and its role in facilitating SMEs' data exploration and understanding, as well as knowledge transfer. Furthermore, we compiled the questionnaire data and reported the study findings. SMEs rated the AID dashboard in terms of its ability to convert data into useful information, help injury stakeholders brainstorm new ideas, efficiently and effectively complete the assigned analytical task, as well as help injury stakeholders share their ideas with other stakeholders [Table 1].

Metrics	Strongly Agree	Agree	Somehow Agree	No Comments
Useful Information	33%	50%	-	16%
Discussion Stimulating	71%	28%	-	
Task Completion	-	71%	-	-
Ideas Sharing	50%	33%	16%	

Table 1: Compiled data from the questionnaire revealed participants' rating of the 4 main variables following their interactions with the AID dashboard.

The majority of the participants ranked the AID dashboard high in terms of assisting them in converting complex injury data into

useful information that could help them to get insights into the injury data as well as to understand the injury situation.

Fig 2 highlights the study findings and shows a bar chart that illustrates injury stakeholders' high ranking of the AID dashboard in terms of converting data into useful information, brainstorming new ideas and facilitating task completion.

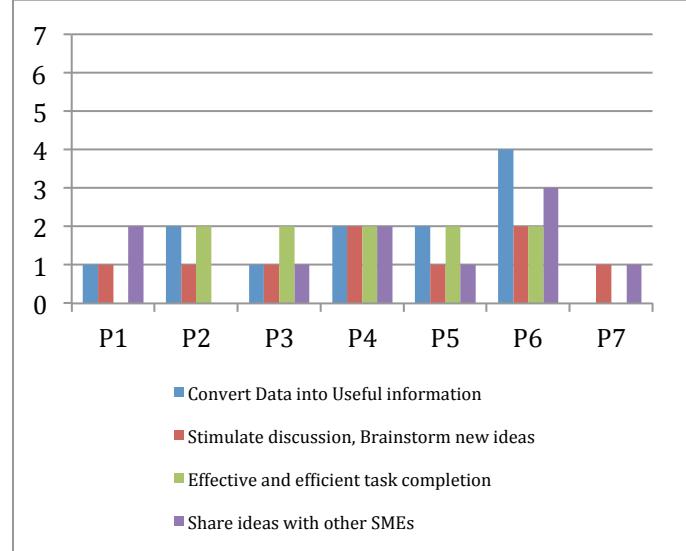


Figure 2. Participants ranked the AID dashboard high in term of information sharing and support for task completion (1-Strongly Agree, 7-Strongly Disagree)

During the collaborative VA sessions, SMEs manipulated the AID visual display and customized the visualizations according to their needs and task requirements. With the assistance of the Visual Analytics Expert (VAE), SMEs interacted with the dashboard to refine the visual representations in a way that enhanced their understanding of the multidimensional injury data and empowered them to converge on a solution and reach a consensus and decide on the best approach to address the injury problem at hand.

7 DISCUSSION

These results confirmed our claim that an interactive and analytical dashboard can enable injury stakeholders to gain insights into the dynamic injury data, generate and test new hypotheses, exchange information and expertise in a collaborative setting, and subsequently build knowledge to make informed decisions.

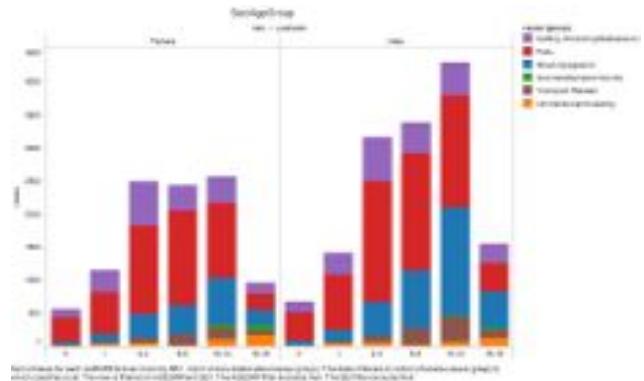


Fig 5. Drill Down of one view of the AID dashboard to discover the leading cause of injury among various age groups.

In order to confirm our study findings and increase the study generalizability, we supplemented the questionnaire data with a qualitative data analysis of the transcripts generated from the Group Analytics video recordings.

SMEs acquired knowledge from the visualization as VAE manipulated the data, refined the visualizations and customized the view according to SMEs needs and preferences. As demonstrated in the study findings, interacting with the AID dashboard visualizations converted the CHIRPP data into useful information and enabled SMEs to discover the leading cause of injury [i.e. "Fall" in Fig.5] among various age groups. Further interaction with the VA dashboard helped injury stakeholders answer their questions and build knowledge about the causes of different injuries. It also enables them to answer questions about the circumstances of the injuries, i.e. was it a "Fall" from furniture or a "Fall" from a high-rise?

The dashboard visualizations enhanced injury stakeholders' knowledge discovery. As one SME explained: "...*You know when we started that project we didn't really know what we would find*". This knowledge discovery encompasses three areas:

1. SMEs increased knowledge about the tool functions and features. They learned how to manipulate the tool to reflect their research needs.
2. SMEs increased knowledge about the CHIRPP data. *SME4: "So what could we learned from the data that would tell us who is falling? Why are they falling? And what can we do to stop them from falling?"*
3. SMEs increased knowledge about the injury situation. *SME1: "they (visual representations) provide a great deal of information very quickly and allow me to understand trends and variation in the injury data.*

Furthermore, the AID dashboard enhanced SMEs exchange and transfer of knowledge. As one SME postulated: "(the visual representation) a good way of sharing findings and presenting the data"

8 CONCLUSION

This study enabled us to empirically evaluate, understand and document injury stakeholders' experience and interaction with the AID dashboard to generate and transfer knowledge and therefore tailor the dashboard to better fit their preferences and needs. Furthermore, it enables us to identify stakeholders' analytical and reasoning processes when exploring complex datasets in order to inform the design of innovative collaborative visual analytics tools and techniques as well as advance the Group Analytics methodologies.

This study incorporated a number of limitations and challenges that we acknowledge. The study sample was relatively small, which may limit the generalizability of the study and its applicability on a larger injury stakeholders' population. However, each SME was purposely selected because of their strong knowledge and expertise in injury prevention and also their credibility and position to represent constituent peers. During the course of the Group Analytics session, it was essential to take into consideration the various challenges including but not limited to the number of stakeholders in each session, the discrepancy in knowledge and expertise among injury stakeholders, SMEs' biases, as well as the levels of authority of participating injury stakeholders. Furthermore, considerations for patients' privacy and confidentiality must be taken into account when designing analytical dashboards to visually depict health data. Protecting patients' privacy and confidentiality is of paramount importance within the healthcare sector. In order to maintain confidentiality and privacy standards and avoid pinpointing patients based on

their geographic locations, the analytical dashboard must be developed and managed so as not to display injury classes with fewer than five cases. Data must be anonymous, removed of any personal identifiers and aggregated so that patient identity and privacy is always protected. Despite these limitations, the study findings clearly reveal the advantages of integrating analytical dashboard as a decision-support tool to synthesize information from multidimensional and dynamic data.

Future research work should take into consideration these limitations and suggest the design of novel group analytics as well as innovative analytical dashboard with advanced visual analytics techniques to support stakeholders' knowledge discovery and transfer. Additional research is needed to explore the implications of integrating visual analytics on health informatics within the healthcare sector.

9 ACKNOWLEDGMENT

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VisXplore: Flexible Visualization System for Analyzing Complex Clinical Datasets

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Abstract:

Assessing, exploring, and analyzing large amount of heterogeneous clinical data are some of the key challenges faced by researchers and clinicians interested in identifying complex clinical patterns. Flexible visualization systems capable of loading different data types and performing individual statistical analysis have the potential of impacting the way clinical datasets are analyzed. This paper introduces VisXplore -- a clinical data visualization system that has been designed to perform group or single-subject analysis of multivariate tabular, hierarchical, or temporal clinical data. The visualization system has been developed as a robust, flexible, and easy-to-use application that can be used by either researchers or clinicians. The framework has been tested with different clinical datasets including a dataset of patients diagnosed with post-traumatic stress disorder (PTSD) and complex comorbid conditions.

I. Introduction

Today, the assessment, evaluation, and treatment of any disease generates a large amount of data that needs to be analyzed. The large number of clinical elements and the vast amount of unstructured information being collected can quickly become overwhelming for clinicians and researchers alike. The complexity of analyzing multiple clinical elements simultaneously often causes that only a small subset of clinical measurements are used to assess the condition of a patient and/or to determine the effectiveness of a particular treatment. In order to successfully analyze a large number of multi-modal clinical variables and integrate different evaluation protocols, new visual analytics techniques and applications are needed.

This paper addresses the clear gap between the acquisition of clinical measurements and the diagnostic step, by providing an intuitive, flexible, and customizable interactive data visualization framework. Current analysis and visualizations techniques do not allow the user to be able to easily navigate through the data. The proposed framework is designed to help clinicians obtain new insights about the underlying conditions of the patients, analyze complex hidden clinical patterns, partition the data into different subgroups, visually explore the correlations between individual assessment techniques, and quickly analyze a particular patient against a specific cohort.

II. Previous Work

Data visualization systems are becoming increasingly important in numerous disciplines for data exploration, data mining, information retrieval, and hypothesis generation [1,2]. The increasing popularity of visual analytic tools has been driven by their effectiveness to enable users to detect patterns, correlations, and anomalies not obvious with other forms of data representations.

Over the last several years, multiple high-dimensional data visualization techniques have been proposed to enable interactive exploration of complex datasets. Generally, three of the main purposes of visual

analytic tools are to find averages of where most of the data lies, to find unique complex patterns, and to better understand outliers. During the last ten years, many graphing and plotting software applications have successfully been used to analyze complex datasets including Excel, SAS, SPSS, Tableau, Spotfire, and QlikView [3,4,5]. However, most of these applications are limited when trying to illustrate the relationship between more than three variables and are not optimized for clinical and healthcare applications. In particular, most of these visualization systems are limited in the amount of data that can be displayed at one time because of the constraints of physical viewing space and the two-dimensional characteristics of the plots.

III. Approach

We recognized that clinical data comes in different types and sources, to guarantee flexibility and acceptance across multiple clinical disciplines, VisXplore supports three of the most widely used types: *tabular*, *hierarchical*, and *temporal*. Once the data has been loaded into the system, the users can perform group or single subject analysis by employing any of the 15+ data visualization techniques and analytical modules that have been implemented. The group analysis focuses on the statistical properties of a specific population or cohort. In this type of analysis, the analytical techniques focus on the descriptive statistics of a data set, such as the average, standard deviation, variance, and correlations. The single-subject analysis focuses on comparing the properties of a particular subject against a particular population or cohort. This type of analysis is done by looking at the values against the z-score or normalized score to be able to see how the subject compares.

Figure 1 shows VisXplore, our visualization system designed to analyze and study complex clinical datasets. The system has been implemented using D3[6] and Extjs to allow the user to have an interactive experience inside of their current web browser without the need of installing any additional application. At the start of the application, the user is presented with a login which supports multiple users so that different researchers can use and analyze their own individual datasets. Upon login the user is presented with the ability to upload their tabular, temporal or hierarchical datasets using common file formats including CSV, Excel, and JSON. Once the dataset is loaded into the system, it becomes a report, allowing the user to have many different datasets / reports. When a specific report is selected, it launches the visualization tool and enables the different modules so the user can dive into exploring their data.

The main window of VisXplore has a section in the left side of the screen with two tabs: *the patients* and *clinical variables* tabs. The user can choose to only see data for certain clinical variables or patients by selecting them in the list. The researcher may see a similarity in certain patients or may want to further investigate a subset of the variables and they are able to do this by forming a group. We have added the functionality for the researcher to be able to create unique labels for their groups, drag and drop the variables/patients into their corresponding groups, and to download the data specific to that group.

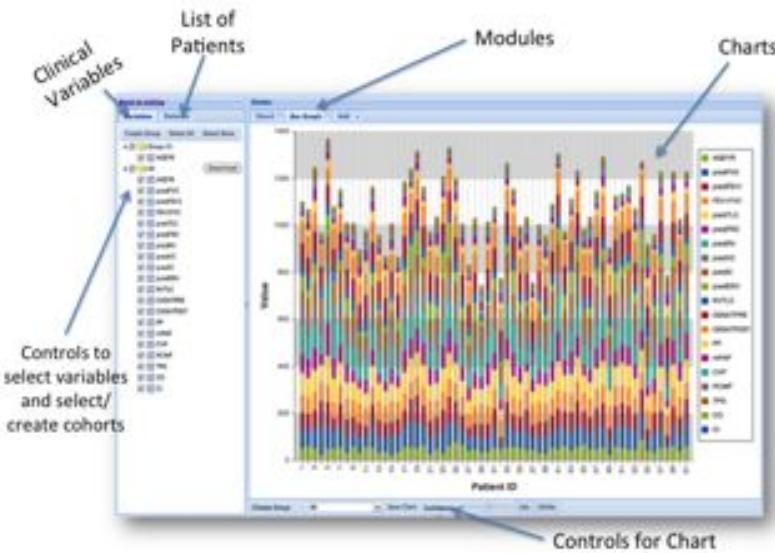


Figure 1: Illustration of the different components and features of VisXplore.

The right hand side of the screen contains the various modules that we have implemented for analyzing data using visualization techniques. To aid in the analysis of clinical data we present the user with many visualization techniques such as area chart, bar graph, chord, co-occurrence matrix, histogram, lines, parallel, and windrose as well as many analytical tools to estimate correlations, averages, standard deviation, t-test, p-values, and many others.

The parallel coordinates visualization (Figure 2(a)) displays all of the patients on a slightly modified line graph. There are M equally spaced vertical axes displayed, each representing a clinical variable. Along these axes N lines are drawn through the axes, where each line contains the data for a patient. Analyzing this visualization helps discover trends in the data such as outliers from the norm or a linear relationship between axes. In addition, the user can interactively define a range within a single or multiple variables (axes), explore the data further, and even create cohorts or subgroups.

The chord visualization (Figure 2(b)) is generated by creating a circular plot consisting of boundaries, where each boundary is a clinical variable. Connections are drawn between boundaries and the thickness of each connection represents the strength of the correlation. Hovering the mouse over a connection displays the corresponding R-value to help the researcher understand the chart. Extra controls are available for the chart, such as only drawing connections above a chosen R-value.

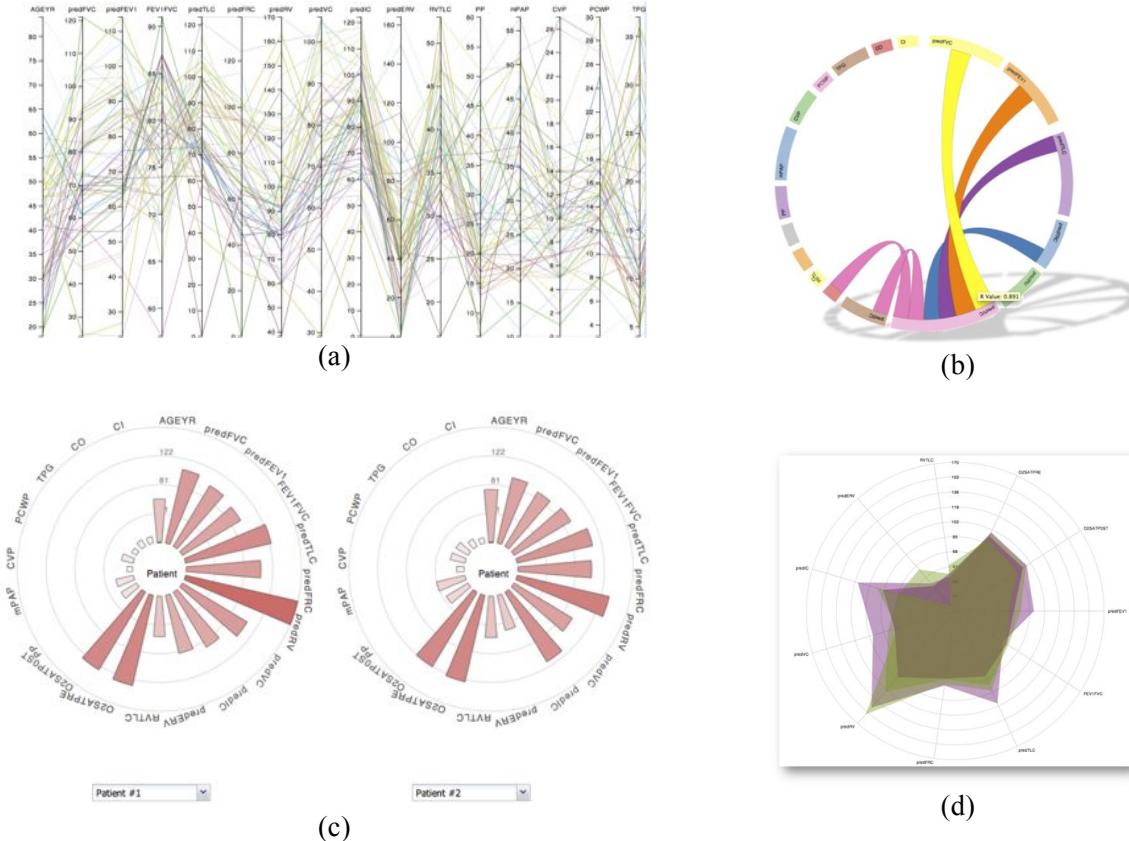


Figure 2: A subset of some of the visualization techniques implemented in VisXplore. (a) Parallel coordinates are used to quickly look at patterns and identify subgroups. (b) The chord visualization is used to study the associations between individual clinical variables. (c) A circular visualization (aka windrose) is used to compare patients. (d) A circular visualization is used to compare patients within a single window.

The windrose visualization (Figure 2(c)) is used to illustrate multiple patients side by side to make comparisons easier. A side-by-side chart is created where the two patients' data is drawn in a circular bar chart rather than a standard bar chart. This enables the researcher to compare the shapes of the patients, as similar patients will have similar shapes.

For navigating hierarchical data, we present the user with two useful visualizations: *hierarchical tree* and *treemap*. The treemap visualization places all of the patients in a grid as individual rectangles. The area of the patient's rectangle corresponds to the amount of data available for that patient, which helps in looking at the overall data. Clicking on a patient's rectangle zooms the user in, displaying another grid of data sub-treemap for the patient and allowing the user to navigate through the hierarchy of data. Figure 3 (b) shows an example of the treemap visualization chart.

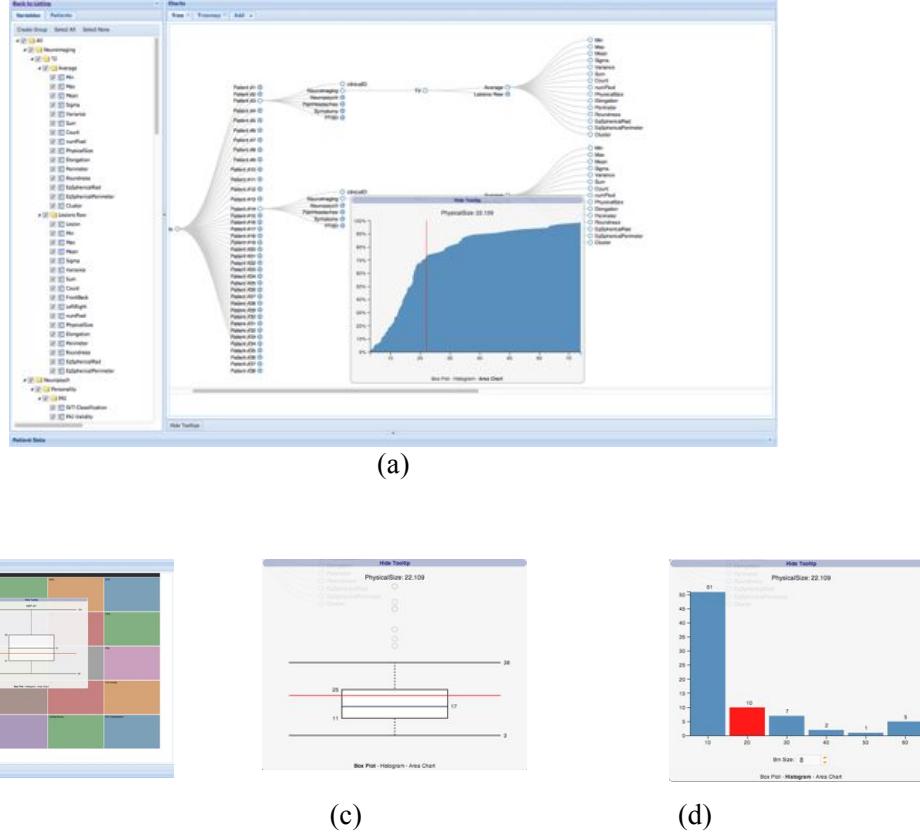


Figure 3: A subset of the hierarchical visualization techniques available within VisXplore. (a) A tree visualization is used to explore hierarchical data. When the user clicks in a leaf node a window appears with a line illustrating the value of subject under consideration against the aggregate results of the group. (b) A treemap visualization used to explore hierarchical data (c-d) When clicking in a leaf node the user can select different ways to compare the current subject against the group under consideration.

The second visualization, displays the data in a tree graph with the data connected by paths. When a node is clicked, an animation takes place to collapse or expand the data in the corresponding node causing the tree to change shape. Figure 3(a) shows an example of the how the user can interactively explore hierarchical data using the tree visualization.

The treemap and tree visualizations both give the user the functionality to navigate through their hierarchical data, but we needed a way for them to be able to analyze the leaf nodes on the graphs. We accomplished this by presenting the user with a boxplot, histogram, and area chart upon clicking on a leaf node. On each of these three graphs the user is shown where the node that they clicked on is in relation to the rest of the data, by means of a red line indicating the position. This enables single-subject analysis when navigating through the hierarchical data. Figures 3a-d show different visualization techniques.

IV. Results and Conclusion

Our visualization system has been tested with multiple clinical datasets, including blood samples, pulmonary datasets, TBI data, and has been shown to display useful visualizations to aid the user in analysis. The analysis of these datasets using our visualization system has provided effective results compared to the standard visualization tools used by clinicians and researchers. Therefore, we have designed and developed a flexible, easy-to-use visualization system capable of handling tabular, hierarchical, and temporal clinical datasets to assist clinicians and researchers in performing single-subject and group analysis on their patients. Future plans include incorporating machine learning techniques to be able to assist the clinician and researcher in looking for patterns in the data.

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Temporal Search and Replace: A Graphic-Based Solution to Temporal Event Data Wrangling and Incremental Querying

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Abstract

Temporal event data is the essence of Electronic Health Records (EHRs), detailing for each patient a history of what happened and when. From this data, clinical researchers try to identify meaningful patterns of events: medication combinations, treatment side effects, disease symptoms, etc. However, these events are rarely recorded to suit the needs of any one study, requiring researchers to modify their datasets to better capture the events of interest. Command-based and spreadsheet-based tools are difficult to learn, and are notoriously ill-suited to manipulating temporal event data. We introduce a graphic-based interface that employs the familiar concept of “search and replace” to help researchers identify and modify event patterns of interest. The Search and Replace interface was used by multiple clinical research groups to facilitate both data wrangling and query construction.

Introduction

Electronic Health Records (EHRs) provide clinical researchers with a detailed history of patient symptoms, treatments, and outcomes. However, a given study is rarely completed using a single, straightforward query against an EHR database. Studies conducted against preexisting records are typically comprised of two phases, which can be done in any order, and repeated as many times as necessary:

- Isolate the subset of patients that is pertinent to the study or the question at hand.
- Transform the events in each patient record to better reflect the perspective of the study.

Both of these steps can require researchers to identify complex patterns of events within a given record. For example, a study might focus on patients who were treated with Medication X for at least 3 months, and then experienced Symptom Y within one month of stopping X. Maybe Medication X is prescribed in month-long intervals, requiring researchers to manually construct the actual duration of exposure by piecing together each prescription. Maybe Symptom Y is not a single event, but two different events that can occur in any order, so long as they occur within a week of each other.

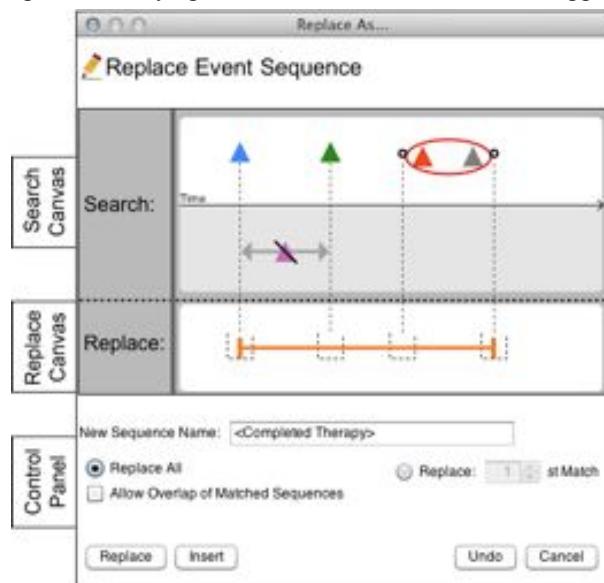


Figure 1: The TSR interface includes a search canvas (top), a replace canvas (middle), and a control panel (bottom). This query is for a blue event, followed by a green event, without an intervening pink event. After that, a red event and a gray event must occur, but in either order. If this sequence is found in a patient record, it is replaced by an orange interval.

Event patterns such as these are usually searched for using command-based and spreadsheet-based tools, which employ query languages that are difficult to learn, are not tailored to temporal event data, and do not provide visual feedback about the impact of the query. In many cases, researchers rely on technical experts to construct their datasets, creating a gap between the data manipulation process and the research domain expertise. To address this problem, we introduce Temporal Search and Replace (TSR), an extension to the advanced search feature of the EventFlow¹ visualization tool that is designed to make querying and modifying temporal event records more accessible and accurate. The interface capitalizes on the fact that most users are familiar with Search and Replace functionality through the use of word processing and spreadsheet applications. We demonstrate its impact on performing common temporal event transformations based on our experience with clinical researchers throughout multiple case studies.



Figure 2: EventFlow’s display of a single patient record. Intervals (such as medication prescriptions) are displayed as a pair of connected bars. Point events (such as diagnoses or reports of symptoms) are displayed as triangles.

Related Work

TSR is based on previous work in both data wrangling and temporal query. Data wrangling is the process of preparing a raw dataset for analysis. This process can be so burdensome and complex that some researchers estimate that it consumes more time than the analysis itself.² Users needing to wrangle temporal event data have two options. The first of these is to master a complex, command-based query language such as SQL or SAS, where data fields can be transformed through creative uses of the “AS” command. The second option is to use prepackaged scripts or stored procedures, which provide shortcuts to common, transformation tasks. However, users in need of transformations that do not exactly conform to these prepackaged scripts are relegated to the first option.

The field of temporal query is comprised of two predominantly disjoint spheres of work, the first of which revolves around incorporating powerful temporal mechanisms into standard, command-based query tools,^{5,6} and the second of which endeavors to make the basic elements of temporal query more accessible to non-technical users.^{3,4} The EventFlow visualization tool bridged this gap with a query system that offered access to a wide range of temporal relationships in an easy-to-learn, usable interface.^{7,9} However, identifying complex temporal patterns still required large and intricately constructed queries. A mistake in one component of such a query would result in a failure of the query as a whole.

The TSR interface and functionality

The TSR interface consists of two canvases, a search canvas and a replace canvas, as well as a small control panel (Figure 1). The search canvas is an exact replica of EventFlow’s advanced search canvas⁷. An event pattern is specified by populating this canvas with event graphics, similar to those used in EventFlow’s individual record display (Figure 2). These graphics are referred to as query elements. Users can click any portion of the search canvas to bring up a short menu where they can specify the details of the query element that they would like to add at that point. They can click on the lower half of the search canvas (in gray) to specify an event that must NOT occur, which are referred to as absence elements. Query elements can be edited or deleted by clicking them.

For each query element that is specified in the search canvas, the replace canvas is populated with a replacement slot, indicated by a dotted line. The replacement slot serves as a placeholder into which users can place one or more replacement events, again by clicking the canvas. Replacement events can be a type of event that already exists in the dataset, or a completely new, TSR-generated marker event type, in which case users can specify both the name of the event, and the color in which it should be displayed. When an event in a patient record is matched to a query element on the search canvas, the timestamp of that event is passed on to any replacement event in that element’s replacement slot. However, there are three types of query elements that require special handling:

- **Absences** – The advanced search allows users to incorporate the absence of an event in their queries (seen in the bottom half of the search canvas). Absences are a semantic requirement that are not matched to any specific event or time, and thus do not provide a timestamp that could be passed on to a replacement event.
- **Permutations** – Users can specify a set of events that can occur in any order. For these query elements, a replacement slot is generated only for the start point and end point of this sequence.
- **Repetitions** – Users can specify that an event or pattern of events must occur a given number of times (e.g. ≤ 3 times). Similar to permutation query elements, replacement slots are generated only for the start point and end point of the repetition sequence.

Once a search pattern and a replacement pattern have been specified, the control panel is used to dictate how the TSR should be executed if the search pattern can be matched to the patient record more than once. Users can specify that a search pattern should be replaced only once, or as many times as possible. If the pattern will only be replaced once, users can choose to replace the first instance of the pattern, or some subsequent instance of the pattern. If the pattern will be replaced multiple times, users can specify whether or not the pattern can overlap with itself. That is, when a replacement pattern is inserted into a record, the search for the next instance of the search pattern can begin either at the beginning of that replacement pattern, or at the end. The former allows patterns to be replaced recursively, with replacement events being matched to elements of the search pattern in subsequent matches. For

example, the interval merging transformation (discussed in the next section) makes use of this option in order to append new intervals to previously merged ones.

In addition to replacements, TSR can be used to delete events entirely, and to insert events into a record without removing anything at all. Event sequences are deleted by simply not specifying a replacement pattern. Insertions can be done by either duplicating elements of the search pattern in the replacement pattern, or by simply using the insert button (Figure 1, lower left). Thus replacement events can be used either to transform data in the patient record, or to generate additional marker events for subsequent analysis, which is discussed in greater detail later. When a TSR is performed, it is added to a stack of TSR modifications. A TSR can be undone only if it appears at the top of this stack. That is, TSR modifications can be undone in the reverse order in which they were performed.

Data wrangling using TSR

With temporal event data, data wrangling can take many forms. Consider the example presented in the introduction where patients are to be selected for a study based on the following event pattern: were treated with Medication X for at least 3 months, then experienced Symptom Y within one month of stopping X. However, Medication X prescriptions appear in the patient records as month-long intervals that can overlap or occur with a gap between them, depending on when the patients happened to pick up their prescription. In this case, the raw data format does not accurately reflect the intention behind this criterion.

To account for this, the first thing a researcher might want to do is to transform those individual prescriptions into new, consolidated intervals that represent the actual exposure time. In fact, this process of interval merging is used by many different research groups as a stored procedure, however these stored procedures are difficult to customize and are limited to this single functionality. Figure 3 demonstrates the use of TSR to perform interval merging and event type merging (combining two different types of events into a single type), two common transformations that, along with countless others, can be customized and executed in a single interface.

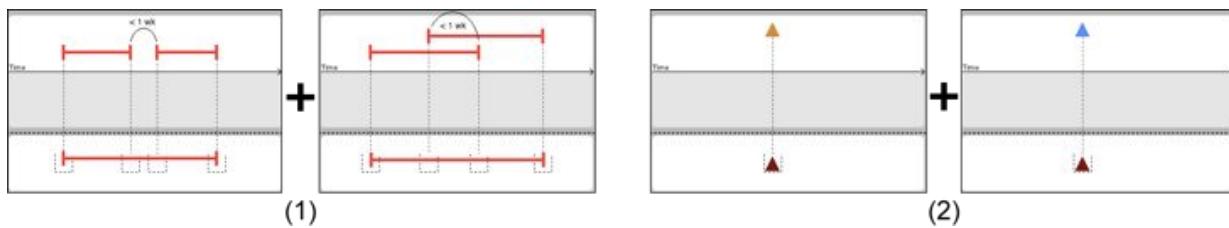


Figure 3: Two common data wrangling transformations are accomplished with two replacements each in TSR. (1) intervals of Medication X that either overlap by less than a week, or are separated by less than a week are merged into a single interval. (2) two different event types (shown in orange and blue), are both replaced by the same event type (shown in dark red).

Incremental temporal query using TSR

Temporal query is critical for isolating sets of patient records that contain a particular event pattern. One of the best strategies for executing these complex queries without making errors is to perform them incrementally, narrowing in on the population of interest step by step. In command-based query tools, this is accomplished using the “AS” statement to save fields and tables as new entities. However, the majority of these command-based tools are designed for relational data structures, and do not provide direct support for temporal event sequences.

TSR allows users to take a similar incremental approach to executing complex queries. Separable components of the query can be executed independently and flagged with TSR-generated marker events. These marker events can then be incorporated into subsequent queries that dictate how the marker events must relate to each other. Returning to our earlier example, consider Symptom Y, which is comprised of two different events that can occur in any order, but must occur within a week of each other. Identifying Symptom Y could begin with a query that replaces any permutation of these two events with a marker interval that spans the duration between them. Records containing a marker interval with duration of less than a week could be queried for and isolated. This marker event, as well as the merged Medication X events discussed in the previous section could then be combined to formulate the final query for qualifying patients. This process, in its entirety, is shown in Figure 4.

This technique of executing queries incrementally using TSR was used substantially in case studies involving researchers at the US Army, Pharmacovigilance Center (PVC), Children’s National Medical Center, and University of Maryland School of Medicine. The TSR interface was also evaluated for learnability and usability with graduate student researchers at the University of Maryland, who ranked the interface with an average score of 5.5 on a 1-7 Likert scale, with a score of 7 representing the best possible experience. The researchers, who were previously limited to only command-based tools, were particularly impressed not just with the ease of use of the TSR interface,

but also with its integration into the EventFlow software. They commented that the interactive visualizations made it extremely easy to see the effects of their TSR modifications as they performed their queries.

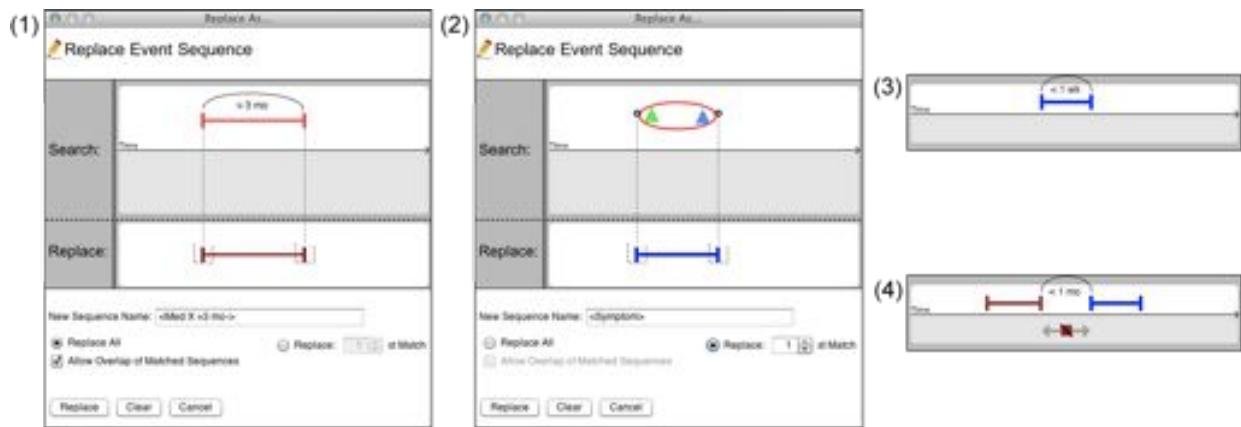


Figure 4: A query is executed incrementally by first replacing Medication X prescriptions exceeding 3 months with a dark red marker intervals (1). Then, both permutations of the two events that comprise Symptom Y are replaced with a blue marker interval (2). Finally, two queries are performed, first to find all the blue marker intervals that do not exceed a week (3), and then to specify the relationship between the dark red and blue marker intervals (4).

Conclusion

Temporal Search and Replace (TSR) provides clinical researchers with expanded capability to transform temporal event data, allowing event sequences to be easily inserted, removed, and modified. The interface greatly facilitates the process of data wrangling, both in performing common operations, as well as complex, customized data alterations. It also allows researchers to break down complex queries into small, manageable increments, making this notoriously difficult and error-prone process more accessible to non-technical experts. Clinical researchers found TSR to be a significant improvement in both usability and capability over standard command-based and spreadsheet-based tools. TSR, and the encapsulating EventFlow application, allowed these researchers to create, explore, and share datasets that better reflected the objectives of their studies.

Acknowledgements

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Dydruma: A Dynamic Drug Map for Exploring the Associations Among Drug Therapeutic Indications and Side-Effects

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Abstract

Inferring potential therapeutic indications and identifying clinically important side-effects are both important and challenging tasks in modern drug development. Previous studies have utilized drug chemical structures and protein targets to construct predictive models for both tasks. According to our study, the drug therapeutic information itself is highly predictive for side-effects, and drug side-effect information highly predictive of therapeutic indication. This confirms that there exist underlying associations among drug therapeutic indications and side-effects. Exploring these associations can lead to better understanding of the drugs as well as more informed hypotheses for drug repositioning and adverse effect monitoring. In practice however, it is impractical to check all possible associations using an exhaustive list. In this study, we present Dydruma, a dynamic drug map which encodes drug therapeutic indications and side-effects as well as their associations. The map can be dynamically adjusted based on a significance value attached to each association, where the significance value is derived from a statistical test such as Fisher's exact test. We describe an optimization-based approach for dynamic bipartite graph layout to ensure visual continuity among successive layouts at different significance thresholds, to help the user maintain a consistent mental map throughout the exploration. We demonstrate the effectiveness of dytruma for exploring the associations among drug indications and side effects and for hypothesis generation using real world data sets.

Introduction

Predictive modeling of therapeutic indications and side-effects of drugs holds is an important computational approach for reducing the drug attrition rate and improving the drug discovery process. In the past many works have been done along this line. For example, prediction with drug chemical structure [1][2], protein target information [3][4], and fusion of multiple information sources [5][6]. In our recent study [7], we developed models to incorporate drug therapeutic indication and side-effect information into the prediction procedure of each other. We showed that drug side-effects are important information for therapeutic indication prediction; and drug therapeutic indications are also predictive for their side-effects. This confirms that there are some underlying associations between them, and understanding those associations can be very helpful to drug development. For example, those discovered associations can provide repositioning hypotheses (e.g., drugs causing postural hypotension are potential candidates for hypertension), as well as adverse-effect watch lists (e.g., drugs for heart failure possibly cause impotence). We also compiled a list of associations among all known drug-disease and drug-side-effect to build disease-side-effect profiles and identified statistically significant associations between drug side-effects and therapeutic indications.

However, because the size of the potential association list is very large, it is exhausting to check the list one by one to identify the interesting ones. Therefore in this study we present *dydruma*, a bi-partite graph representation of the drug therapeutic indication, side-effects and their associations. We will present the details on the visualization design in next section, followed by case study and conclusions.

Visualization Design

On dydruma there are two types of nodes, drug therapeutic indications and side-effects, and the edges correspond to the discovered associations between them. Attached to each association there is a strength (which is represented by the *p*-value of Fisher's exact test, the smaller the value the stronger the association [7]). We do not want to encode those values into the edge colors because that will make the graph messy. Therefore we come up with a dynamic design. We provide a sliding bar which the user can use to adjust the association strength threshold: only the associations whose *p*-value below the threshold will be shown. With the user dragging that bar, the bipartite graph will change and we

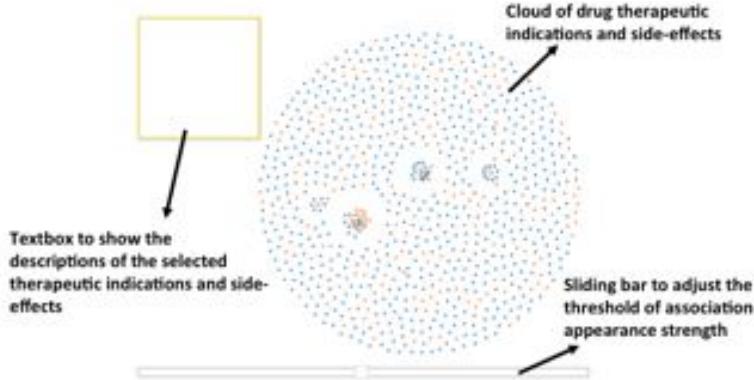


Figure 1: An overview of the *dydruma* system, which consists of three parts: (I) the generated bipartite graph of the drug therapeutic indications (orange) and side-effects (blue); (II) a sliding bar for adjusting the strength threshold (p -value) for showing the discovered associations; (III) a text box displaying the descriptions of the selected nodes (the user can select a bunch of nodes with mouse and their descriptions will be depicted in this box).

need to make that change as smooth as possible for visual pleasure. In the following section we will introduce the details of our visualization design. Before going into that, we give an overview of *dydruma* in Fig. 1.

The dynamic bi-partite graph layout is based on an optimization approach. Specifically, in order to help maintain a user's mental map, successive layouts of similar graphs should have minimal changes (*stability*). Furthermore, each of such layouts should still effectively convey the properties of the underlying graph (*readability*). Thus, our goal is to produce a sequence of graph layouts that optimize both the stability and readability of the resulted visualization. To achieve this goal, we develop a spectral layout algorithm.

Given a dynamic graph $\mathcal{G}_t = \langle \mathcal{V}_t, \mathcal{E}_t \rangle$ at time t , consisting of a set of nodes \mathcal{V}_t and links \mathcal{E}_t , we define an energy function to model the desired graph layout as follows:

$$\min \left[\sum_{i < j} \omega_{ij} \alpha (||X_i - X_j|| - d_{ij})^2 + \sum_{i \in C_k} (1 - \alpha) (X_i - X'_i)^2 \right] \quad (1)$$

Where X'_i and X_i represent the previous and new position of node $v_i \in \mathcal{V}_t$, respectively. The first term of the objective in Eq.(1) is from the Kamada and Kawai method [8], which maximizes the readability of a graph visualization by preserving the pairwise distances, where d_{ij} is the shortest distance between two nodes v_i and v_j . The second item, which we have added, attempts to minimize the changes in successive layouts.

Instead of stabilizing all the unchanged nodes (which consists of a set \mathcal{U}), we extract a representative set of unchanged nodes $C_k \in \mathcal{U}$ to improve the performance of the algorithm. The final layout model is constructed by optimizing Eq.(1) with a spectral method. Here $\alpha \in (0, 1)$ is the weight that is dynamically computed to achieve the desired balance between readability and stability. An online demo of the *dydruma* system can be found on <http://nancao.org/demos/druggraph/>.

Case Study

Data. In the experiment, we analyzed the approved drugs from DrugBank [9], where we collected 1,447 FDA-approved small-molecule drugs. We mapped these drugs to several other key drug resources including PubChem [10] and UMLS [11] in order to extract other drug related information. In the end, we extracted chemical structures of the 1103 drugs from PubChem. To encode the drug chemical structure, we used a fingerprint corresponding to the 881 chemical substructures defined in the PubChem. Each drug was represented by an 881-dimensional binary profile whose elements encode for the presence or absence of each PubChem substructure. There are 132,092 associations between drugs and chemical substructures in the dataset, and each drug has 119.8 substructures on average.

From DrugBank, we also got target information of each drug. To facilitate collecting target protein information, we mapped target proteins to UniProt Knowledgebase [12], a central knowledgebase including most comprehensive and complete information on proteins. In the end, we extracted 3,152 relationships between 1007 drugs and 775 proteins, and each drug has 3.1 protein targets on average. Each drug was represented by a 775-dimensional binary profile whose elements encode for the presence or absence of each target protein by 1 or 0, respectively.

Side-effect keywords were obtained from the SIDER database [13] which contains information about marketed medicines and their recorded adverse drug reactions. This led to a dataset containing 888 small-molecule drugs and 1385 side-effect keywords. Each drug was represented by a 1385-dimensional binary profile whose elements encode for the presence or absence of each of the side-effect keywords by 1 or 0, respectively. Altogether, there are 61,102 associations between drugs and side-effect terms in the dataset, and each drug has 68.8 side-effects on average.

Drugs' known usages were obtained by extracting treatment relationships between drugs and indications from the National Drug File - Reference Terminology (NDF-RT), which is part of the UMLS [11]. This list is also used by Li et al [14] as the standard set for drug repositioning. After normalizing various drug names in NDF-RT to their active ingredients, we were able to extract therapeutic indications for 799 drugs out of the 1103 drugs, which constructed 3250 treatment relationships between 799 drugs and 719 indications. Thus each drug was represented by a 719-dimensional binary profile whose elements encode for the presence or absence of each of the therapeutic indications.

Prediction Results.

As stated in the introduction, the whole motivation of dydruma is the high prediction ability between drug therapeutic indications and side-effects. Based on the approach in [7], we got 167,392 predicted associations between 567 drugs and 1262 side-effect terms, and 22,639 predicted associations between 567 drugs and 612 indications. Then we combine both predicted and ground truth indication-side-effects associations to construct the confusion table for Fisher's exact test [15], from which we can get the strength (*p*-value) of those predicted associations [7].

Example Cliques. We demonstrate those discovered associations in our *dydruma* system and show an example clique in Fig.2, where there are four diseases: *Diabetic Nephropathies*, *Heart Failure*, *Hypertension*, and *Ventricular Dysfunction*. The last three are cardiovascular diseases, and Diabetic Nephropathies is a common comorbidity and one of the causes of cardiovascular diseases. This clique also contains 30 highly correlated side-effects. Some of the side-effects are physiologically linked to the cardiovascular diseases and the mechanism of action (MOA) can be explained. For example, some hypertension drugs may result in a sudden drop in blood pressure when a person stands up, thus the side-effect postural hypotension happens. Some cardiac drugs (e.g., β -blockers) hits α -adrenergic receptors protein target in penile tissue, which will cause side-effect impotence. The decreased blood pressure caused by some cardiac drugs (e.g., β -blockers) also cause side-effects cold extremities, dizziness, vertigo, and weakness. Side-effect pemphigus is related to ACE inhibitors, which is also one kind of cardiac drug. Some popular cardiac medications (e.g., Diuretics) cause human body to lose salt and water, potentially causing side-effect gout.

Conclusions

We present *dydruma*, a dynamic bi-partite graph laying out system for visualizing the predicted associations between drug therapeutic indications and side-effects, which could be potentially very interesting because of their high predictability of each other according to our previous study. We finally present a real world case study to demonstrate its validity.

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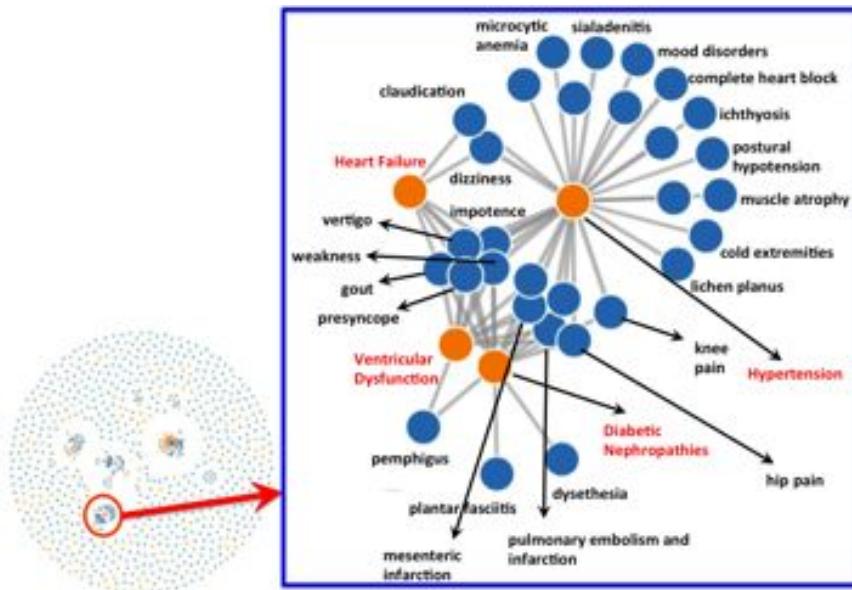


Figure 2: An example clique of drug therapeutic indications and side-effects.

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Visualizing Patterns of Drug Prescriptions with EventFlow: A Pilot Study of Asthma Medications in the Military Health System

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Abstract

The Food and Drug Administration and Department of Defense were interested in detecting sub-optimal use of long-acting beta-agonists (LABAs) in asthmatics within the Military Health System (MHS). Visualizing the patterns of asthma medication use surrounding a LABA prescription is a quick way to detect possible sub-optimal use for further evaluation. Analysis of 100 asthma patients was conducted in EventFlow to display and summarize time-point and interval data. Epidemiologists reported that EventFlow was a powerful tool for rapidly visualizing possible patterns of sub-optimal LABA use that can be targeted for intervention.

Introduction

Electronic health record (EHR) and administrative medical claims databases contain millions of patient records showing medication therapy (e.g., initiation, change of dose, switch to a different medication, augmentation with additional medication for the same condition) for various medical conditions. Clinical researchers and quality improvement analysts have a need to characterize the nature and frequency of such patterns of medication use and, ultimately, to build and test hypotheses regarding the reasons for changes, the benefits and risks of real-world prescribing patterns, and to make recommendations for improved medication management (see ¹ for a survey of tools available). We believe that interactive information visualization tools such as EventFlow² (Figure 1) can lead to a dramatic improvement in a clinical researcher's ability to obtain deep knowledge of the types of medication usage patterns that occur within a medical practice/healthcare system.

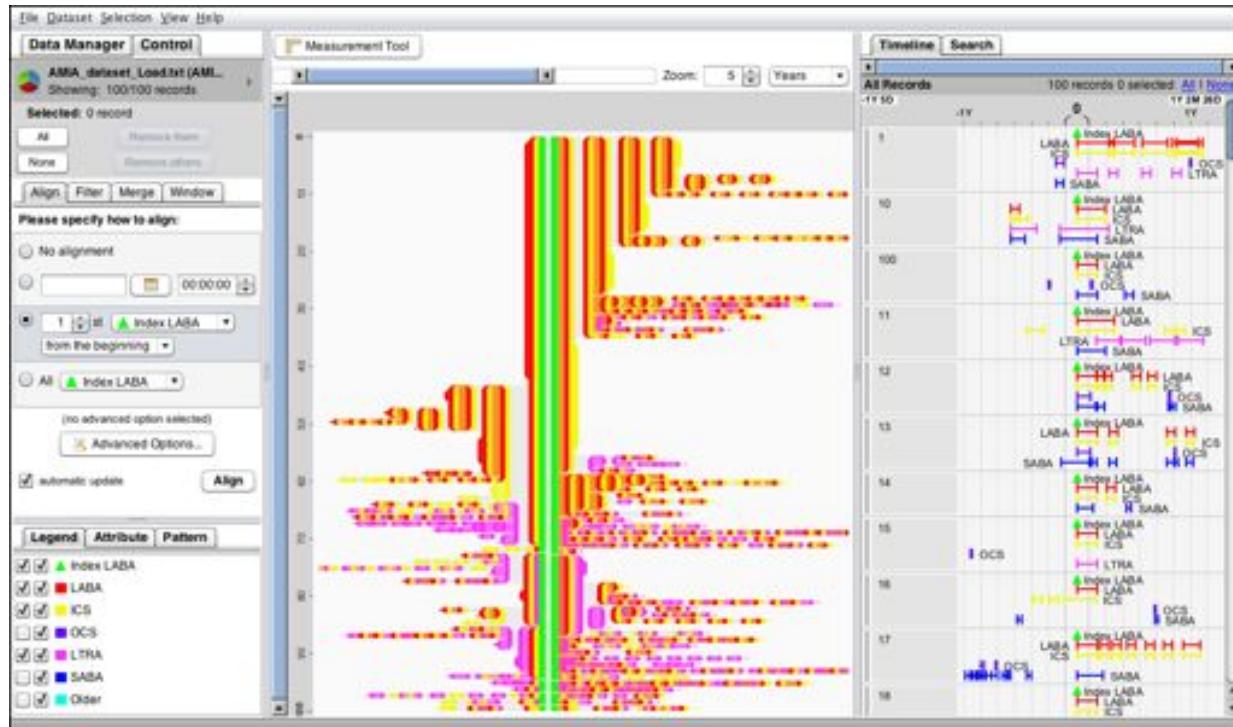


Figure 1: Overview of 100 patients' prescription records. Limiting the display to LABA (long-acting beta-agonist), ICS (inhaled corticosteroid), and LTRA (leukotriene receptor antagonist) simplifies the overview. The data is aligned on the green index LABA (the alignment point is shown as a green vertical line).

This paper summarizes the early stages of a case study being conducted with the US Army, Office of the Surgeon General, Pharmacovigilance Center (PVC) where epidemiologists and clinicians worked with HCIL researchers to understand the prescribing patterns of asthma medications. The PVC is collaborating with the Food and Drug Administration (FDA) and Allergy/Immunology clinicians from the Walter Reed National Military Medical Center to determine if long-acting beta-agonists (LABAs), a type of asthma medication, are being mis-prescribed within the Military Health System (MHS).

Related Work

EventFlow builds on the past research by the HCIL on the visualization of temporal sequences of point events (*i.e.*, events with a single timestamp) LifeLines² and LifeFlow¹. While those tools have been successfully used by clinical researchers and quality assurance administrators to answer many questions, they only operated on point event data (diagnoses, orders, admissions etc.) and therefore had no notion of episodes, partial or complete overlaps, or gaps between events. EventFlow introduces the ability to interactively search and visualize interval data, which is an important step forward. Intervals, such as uninterrupted periods of medication use or episodes of disease, are a central aspect of the analysis of medication use.

In a broader context, temporal database storage, retrieval, interpretation, analysis, and visualization constitute a huge set of research topics. Still the relational database model can be too limiting for many temporal queries. Extensions such as TSQL and other temporal database query languages solve some problems, but the semantics of meaningful temporal queries is difficult or impossible to express in these temporal languages and logics, especially in the presence of interval events³. Data mining strategies that can extract common patterns in baskets of items have been cleverly extended to deal with categorical sequences⁴. However, when events in a sequence have different amounts of time between them, data mining approaches become difficult to apply, leading researchers to adopt more selective approaches that often include “interestingness” measures. Work on extracting common temporal patterns in interval event data is still in its infancy⁵.

EventFlow interface description

The main interface of EventFlow consists of three main components: interactive controls, legend, overview and timeline (Figure 1). On the right the timeline browser shows details of individual records; each patient is shown on a separate timeline. Triangle icons represent point events while connected rectangles represent intervals (and condense to a single rectangle when the interval duration is small). In the center, the overview aggregates all records with the same sequence of events into a single bar. This method was first introduced in LifeFlow⁵ and has now been extended to interval data in EventFlow. The height of a bar is determined by the number of records in the group and the horizontal gap between events is proportional to the mean time between the two events among the records in the group. EventFlow renders overlapping intervals using the combined color of the two overlapping categories. For example, when a red interval intersects a blue interval, the resulting overlap is purple. When two intervals of the same category intersect, the color saturation is increased. While this technique works best when limited to a small number of event categories (*i.e.*, colors) our experience suggests that being able to see overlaps of just two or three event categories is already an important improvement over existing techniques for many users. A basic, menu-based search interface is complemented by an Advanced Search to allow users to specify more complex temporal features such as absolute time constraints and absence of events scenarios⁶. The advanced search interface uses a visual query language to draw the desired sequence of event relationships (see Figure 2). Finally, a set of simplification operations allows users to focus on patterns of interest⁷ (*e.g.* by selecting event categories or applying search and replace operations⁸.)

Ongoing PVC study of long-acting beta-agonist (LABA) therapy

FDA guidelines recommend that patients with asthma who are using LABA therapy also receive a long-term asthma controller medication (LTACM) such as an inhaled corticosteroid (ICS)²²⁻²³. Single-ingredient LABA prescribing has been linked with increased risk of asthma-related hospitalizations, intubations, and death. The FDA has issued drug safety communications and required label changes to all LABA products detailing that, in asthmatics, LABAs should only be prescribed in combination with a LTACM and only after attempts to optimize other LTACM therapies have failed. According to FDA guidelines, LABA therapy should be de-escalated once asthma has been adequately controlled. LABA prescribing patterns in the MHS were unknown, so the PVC and FDA undertook a study to characterize LABA use among asthmatics in the MHS over time. Metrics of interest were the proportion with concomitant LTACM therapies, length of therapy, and escalation/de-escalation practices. The ultimate goal of the study was to understand LABA use in the MHS in order to inform interventions to prevent morbidity and mortality from sub-optimal LABA use.

The PVC performed a retrospective cohort study using administrative health claims from the MHS from January 1, 2006 to March 1, 2010. The study was approved by the US Army Medical Research and Material Command, Office of Research Protections, Institutional Review Board. Eligible patients were identified from the prescription files by

searching for records containing LABA product names. Patients were further limited to asthma patients while excluding COPD patients and limited to patients that did not have LABA in the previous 90 days.

Case study of the use of EventFlow

We randomly selected 100 patients, extracted all of their asthma medication prescriptions for the 365 days surrounding the index LABA prescription date, categorized the asthma medications into useful groups (LABA, ICS, leukotriene receptor antagonists [LTRA], oral corticosteroid bursts [OCS], and short-acting beta-agonists [SABA]) and imported the data into EventFlow. The input file included a de-identified patient identifier, the asthma medication group, the start date of the prescription, and the end date of the prescription derived from the start date plus days supply of the prescription. An indicator to mark the index LABA date was added to each patient's records. We looked for patterns of asthma medication dispensing surrounding the index LABA prescription that suggested good compliance with FDA guidelines²²⁻²³. These patterns included 1) a LABA only in conjunction with an ICS, 2) use of other LTACM such as LTRA or ICS prior to the LABA, and 3) exchange of LABA for other LTACM after the asthma is under control.

We examined patterns surrounding the index LABA using the alignment tool in EventFlow and aligned on the point of interest, the index LABA prescription (Figure 1). To focus on patterns of step-up therapy from a non-LABA LTACM to a LABA and step-down therapy from a LABA to other LTACM, we limited the display to LABA and the other common LTACM: ICS and LTRA. In the absence of significant asthma exacerbations or clinical presentations, we expected to see step up from an ICS or LTRA to a LABA and then step down to an LTRA or ICS alone once the asthma was under control. Using the display, we noted that:

1. About 65% of patients did not have another LTACM before the LABA (*i.e.* started with red LABA or green index LABA) and about half had no evidence of step down to an LTRA or ICS alone. . We were looking for other LTACM like yellow ICS or pink LTRA surrounding the LABA. However, starting on a LABA may be appropriate in the case of a significant asthma exacerbation or symptomatic presentation.
2. We noted that very few LABAs were prescribed without an inhaled corticosteroid (*i.e.* red LABA usually overlaps with the yellow ICS) which is consistent with FDA guidelines.
3. Several patients had a non-index LABA greater than 90 days but less than a year before the index LABA suggesting that a longer washout period may be useful in identifying new (index) LABA prescriptions.

However, we saw that, again, these patterns are not necessarily inconsistent with FDA guidelines²²⁻²³ if asthma symptoms warranted immediate or continued use of LABA. Nevertheless, these patterns do highlight areas for further investigation and possible clinical intervention especially for patients with no evidence of a step-down trial. We are currently working with allergy/immunology specialists at Walter Reed National Military Medical Center, Bethesda, Maryland to evaluate patients who continued on LABA therapy but lacked clinical outpatient follow-up visits after the index LABA.

Finally, we constructed multiple queries to view the patterns that were consistent with FDA guidelines²²⁻²³ by finding patients who were prescribed an ICS, the most common LTACM, within 3 months of both the start and end date of a LABA prescription. We added the additional query to exclude patient therapies that started or ended with a LABA (Figure 2). The query identified five patients that met the FDA guidelines based on prescription patterns of step-up therapy from an ICS to a LABA, use of LABA concomitantly with an ICS, and step-down to an ICS alone. Because the exploration was done on a sample of 100 patients, to confirm these exploratory findings, the entire patient population was evaluated using traditional SQL and SAS queries. These analyses supported the exploratory results. The epidemiologists and clinicians commented that the interface was much easier to learn and use than the command-based, statistical software that they normally employ. Furthermore, these command-based languages offered no simple option of visualizing the patterns in a meaningful way - a feature that is central to the standard search model as well as both of our query interfaces.

Conclusion

EventFlow was effective in uncovering important patterns of LABA use in the data used in this pilot study. Our results provide evidence that secondary use of electronic health records databases could be dramatically expanded if easy-to-use interfaces allowed clinical researchers to specify queries, review results, and find temporal patterns without needing to default to the time-consuming traditional SQL or SAS queries. We believe that the future of user interfaces is moving toward larger, information- abundant interactive visual displays similar to EventFlow, and this will help researchers compare populations, discover relationships, and spot anomalies that are medically-actionable.

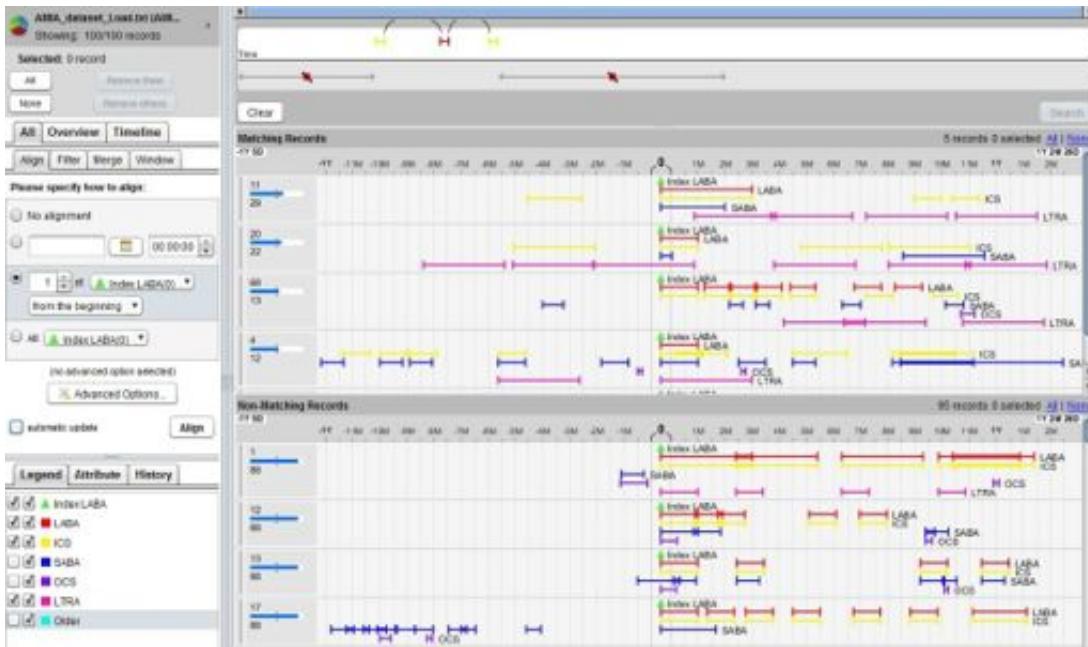


Figure 2: Using the advanced query panel, we searched for patients who received an ICS (yellow) within 3 months of both the start and end date of the LABA (red). We also wanted to ensure that this sequence was neither preceded nor followed by a LABA. Matching records move to the top, but we can also check that the search behaved as expected by looking at the records that did not match.

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*Krist Wongsuphasawat is now at Twitter, but contributed to this work while a PhD student at U. of Maryland.

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POSTER PRESENTATIONS

Interactive visualization for understanding and analyzing biomedical research collaboration networks – a pilot study

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Abstract

A number of social network analysis (SNA) studies have shed light on the characteristics of research collaboration networks (RCNs). In the Clinical Translational Science Award (CTSA) community, SNA provides us a set of effective tools to assess research collaborations and the impact of CTSA. Although quantitative network metrics are valuable, the understanding of these descriptive network statistics is hard to realize by non-experts. Therefore, we aim to create an analytical platform to help network researchers and administration apprehend the network dynamics of research collaborations through interactive visualization. In this study, we present our pilot study in analyzing the biomedical RCNs using visual analytical methods at the University of Arkansas for Medical Sciences – a CTSA institution.

Introduction

The nature of clinical translational science requires inter-disciplinary collaborations. One of the key objectives of the Clinical Translational Science Award (CTSA) is to promote cross-disciplinary collaborations that can accelerate the translation and application of biomedical research discoveries into clinical settings. To better understand, facilitate, and direct clinical translational research efforts, it is essential to analytically assess the quality and efficiency of existing research collaborations in a CTSA institution.

Social network analysis (SNA) methods have been regarded as an effective tool to assess inter- and intra-institution research collaboration networks (RCNs) in the CTSA community¹. Visualization of a RCN is often beneficial to a layperson to understand its topology and dynamics. However, due to the limitation of available tools, researchers in RCN studies often choose to only present static visualizations of the networks, which limits the dissemination of their analyses to non-experts.

In this paper, we present experiences in exploring various network visualization techniques to create an easy-to-use and informative interactive analytical system for studying biomedical RCNs, specifically, analyzing network dynamics and characteristics of the biomedical RCN at the University of Arkansas for Medical Sciences (UAMS) – a CTSA institution. This study serves as the first step towards building a comprehensive visual analytical framework for network science.



Figure 1: The graphic interface of our research collaboration network visual analytics system.

Biomedical Research Collaboration Networks

The biomedical research collaboration networks we study are unique in that those RCNs are formed based on collaborative research grants rather than publication co-authorships^{2,3,4}. Moreover, distinct from existing network analysis studies on scientific collaborations, we abstract RCNs to reflect the degree of collaboration. We formalize a biomedical RCN as an *undirected weighted* graph, i.e., $G = (V, E)$, where each investigator is represented by a vertex or node ($v_i \in V$), and the collaborative relationship between two investigators (v_i and v_j) is evident by an edge or link between the two nodes

$(e_{ij} \in E)$. The weight (w_{ij}) of an edge (e_{ij}) is the *number of research grants* the two investigators have collaborated on during the time period of interest.

An Interactive Visual Analytical System for Research Collaboration Networks

An important goal of our study is to provide analytical tools that can help nontechnical biomedical researchers and administration for understanding the nature and evolution of collaboration. As interactive visualization is much more direct, informative, and appropriate than other forms of data representation for a person to apprehend data and derive accurate observations and useful insights, we started to build a web-based visual analytics system for research collaboration network using a number of cutting-edge Web technologies. Figure 1 illustrates the main interface of our research collaboration network visual analytics (RCN-VA) system. The RCN-VA system is open-source and can be accessed at <http://bianjiang.github.io/rcna/>.

As shown in Figure 1, each circle (node) represents an investigator in the collaboration network, and a curved line connecting two nodes indicates the collaborative relationship between the two investigators. Nodes are colored to distinguish CTSA (green) supported investigators from non-CTSA (gray) supported investigators. The strength of collaboration between two investigators is represented by the thickness of line. To realize vivid, accurate, interactive representation, networks in the RCN-VA system are rendered using a physically-based forced-direct graph layout⁵. The forced-direct graph layout in d3 implements the position Verlet integration to determine moving trajectories of nodes in the network. The physically-based model not only considers repulsive charge forces that spread nodes evenly on the canvas, but also takes into account the gravity forces that keep nodes centered in the visible area and avoid expulsion of isolated components. One immediate benefit of using a forced-direct graph layout for rendering networks is the clustering effect that manifests. A cluster of nodes that are highly connected will naturally be grouped together because of the gravity forces.

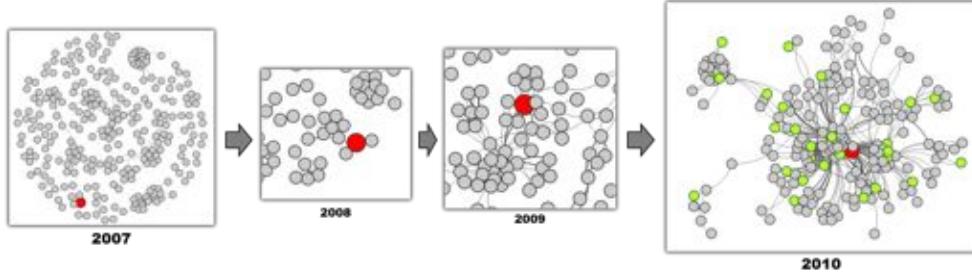


Figure 2: Temporal evolution of an investigator in the research collaboration network at UAMS.

Chronological analysis of network dynamics. The ability to track nodes of interest enables us to study the temporal evolution of individual investigators. For example, as shown in Figure 2, we can track a particular investigator (marked as the red node) in Geriatrics from 2007 to 2010 and observe her collaborative relationships within the network. In 2007, the investigator only collaborated within an isolated small group (four investigators). In 2008, both the size of the group and the number of internal connections increased; however, the group was still disconnected from other parts of the network and the particular investigator still had very few collaborations. In 2009, in preparation of the CTSA program, the group eventually made connections to the largest subgraph of the network. We can easily see in the 2009 graph of Figure 2 that this investigator became a bridge connecting different small clusters. In 2010, the first year after the CTSA, the investigator was drawn towards the center of the network, and her “influence” in the network increased drastically.

Conclusion

In this study, we presented our experiences in exploring various interactive network visualization techniques to facilitate in understanding the network nature and evolution of research collaborations.

Acknowledgments

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Topic Modeling and Network Visualization to Explore Patient Experiences

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Abstract—Online support groups and health-related social networking sites can be powerful ways for patients to connect with each other and seek ways to improve their health. This content can also help clinicians and scientists understand patient experience and unmet needs. However, it can be difficult to navigate and make sense of the large volume of content. This paper proposes and demonstrates techniques that may be used to visualize topics in online health discussions. Topic modeling in conjunction with network visualization can effectively provide overviews and segmenting data. Decisions made during this process affect how content is represented and therefore, interpreted. We present a case study of a lightweight approach to model health discussion content from PatientsLikeMe using open source tools. Implications of differing representations, possibilities for extending this approach, and potential use scenarios are discussed.

Keywords—topic modeling; network visualization; patient experience; online discussion forums; sleep

I. INTRODUCTION

Information interactions in online support forums like PatientsLikeMe (www.patientslikeme.com) assist patient learning about symptoms, treatments, and experiences of others; and may contribute to behavioral changes and outcomes [1]. Visual representations of topics and their relationships in aggregated and segmented text data can provide insight into topics discussed by patients, which offer clinicians, industry, researchers, and patients opportunities to develop new understandings and situate patient behavior in contexts through information not available from other sources such as electronic health records. We present a case study of the use of network visualizations to provide overviews of forum posts, focusing on four sleep aids: Ambien, Lunesta, trazodone and melatonin, discussed in the context of getting an adequate night's sleep.

Challenges to extracting useful information in a dataset could include the quantity of data, perceptions of data quality, data access issues, and questions related to interpretation. Our work contributes to this highly visible though sparse literature with a visually descriptive presentation of forum data, overviews, and filtering and zooming on topics of interest [2].

II. TOPIC MODELING AND NETWORK VISUALIZATION

Topic modeling in conjunction with network visualization is one set of techniques used to make sense of and explore large quantities of text. For example, [3] demonstrated use of

topic modeling and visualization on a set of PhD thesis documents; ReportViz was developed to visualize and explore topics and keywords in public health reports [4]; and Storylines visualizes the latent semantic space of a corpus and coordinate visualizations from the perspectives of people, locations, and events involved in each story line [5].

A. Tools

Two open source packages, the Mallet toolkit [6] and Gephi [7], were utilized for topic modeling and network visualizations. To model topics, we selected a generative probabilistic modeling algorithm, Latent Dirichlet Allocation (LDA). With LDA, documents are described as random mixtures over topics; and a topic is characterized as a distribution of words [8].

B. Overviews: The Composite Network

At the outset, it may be helpful to render an overview of the content. As input, we constructed a corpus comprised of forum posts mentioning the four sleep aids: Ambien, Lunesta, trazodone and melatonin. We trained a model and predicted a set of forty topics using the Mallet toolkit. As output, we have a list of “topics” described by a set of descriptive terms; and a list of documents with estimates of their topic proportions. We manually labeled topics based on examination of term lists and documents containing high topic proportions.

We chose a two-mode network to present the relationships between posts and topics, which allowed us to discover latent topics underlying a set of discussion posts. To prepare data for rendering the network, we created a node list that includes topic and post nodes; and metadata we anticipated we would want to segment data (e.g., condition, self-reported insomnia severity level, and member post authorship experience). The edge list consists of post IDs, the topics they are connected to, and an edge weight representing the proportion of the post that contains the topic in question. The node and edge lists were imported into Gephi, to render a post-topic model (Fig. 1).

There are many ways to render and explore networks in Gephi. Here, we sized topic nodes in proportion to the number of posts to which each is connected, and the text in proportion to node size. Thus, the viewer can quickly discern the prominence of topics in relation to the broader discussion on sleep based on text size. To assist the viewer in distinguishing

This work was completed while the first author was a summer research intern at PatientsLikeMe.

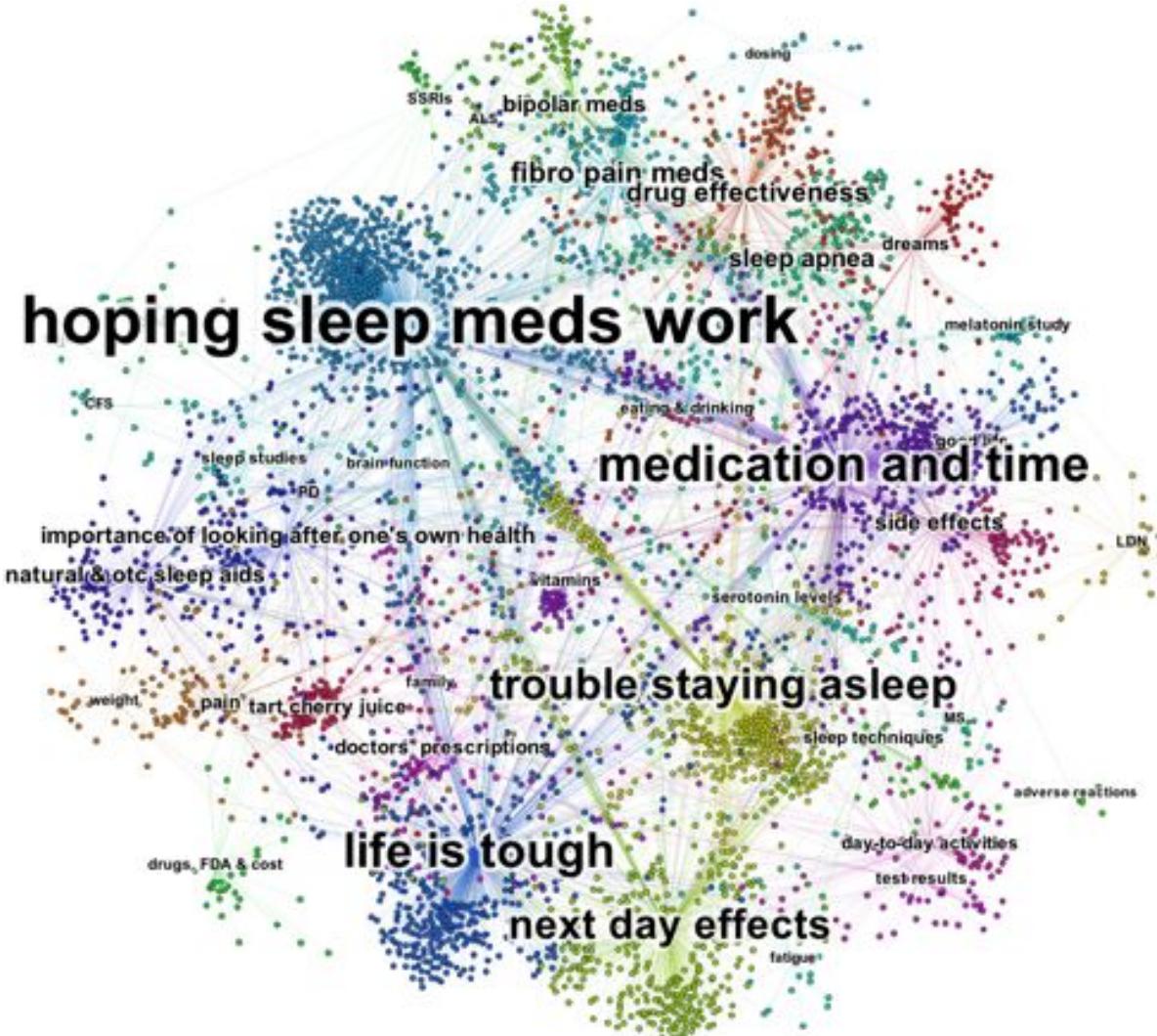


Fig. 1. Composite network of 4,405 posts mentioning four sleep aids (Ambien, Lunesta, trazodone and melatonin). Node colors reflect community membership as determined by the Louvain community detection algorithm [9].

topics, we used a community detection algorithm built in Gephi, which is based on the Louvain modularity method [9]. Node color reflects community membership.

C. Comparing Subsets of Discussion Content

Highlighting subgraphs of a composite network can be a useful approach to research questions that focus on specific subsets of discussion posts that share a common attribute. In this case study, we were interested in exploring how conversations about these four sleep aids differed. Thus, for each sleep aid, we rendered the composite network with the subset of posts that mention the focal treatment highlighted in a distinct color, and other posts in white (at higher resolutions; but which appear gray at lower resolutions, Fig. 2).

Graphs with highlighted subsets expose differences between the highlighted and overall discussion; and when juxtaposed with other subsets, differences between conversations. In our case study, we were able to acquire a sense of the predominant topics of discussion for each sleep aid: concerns of those who talk about Ambien are similar to

those of the composite network. Those who talk about Lunesta are concerned but hopeful about the effectiveness of the sleep aids. Those who discuss trazodone often mention it in the context of timing of medication use, but it also appears often in discussions about mood disorders and fibromyalgia, which makes sense given it is an antidepressant, but often taken for sleep. Melatonin is discussed in terms of its effectiveness; those who take it often find themselves still awake many hours later.

D. Using Patient Data to Explore Associations

Combining post content and attributes of post authors, such as their condition(s), age, and gender, and engaging in comparative evaluation may reveal new insights. In the network presented here, the proportion of patients with Multiple Sclerosis (MS) who post about "Sleep Apnea" (32%) is nearly twice the proportion of MS patients who authored posts in the network overall (18%). This finding is congruent with research that indicates a higher prevalence of sleep apnea among those with MS [10]. This retrospective evidence

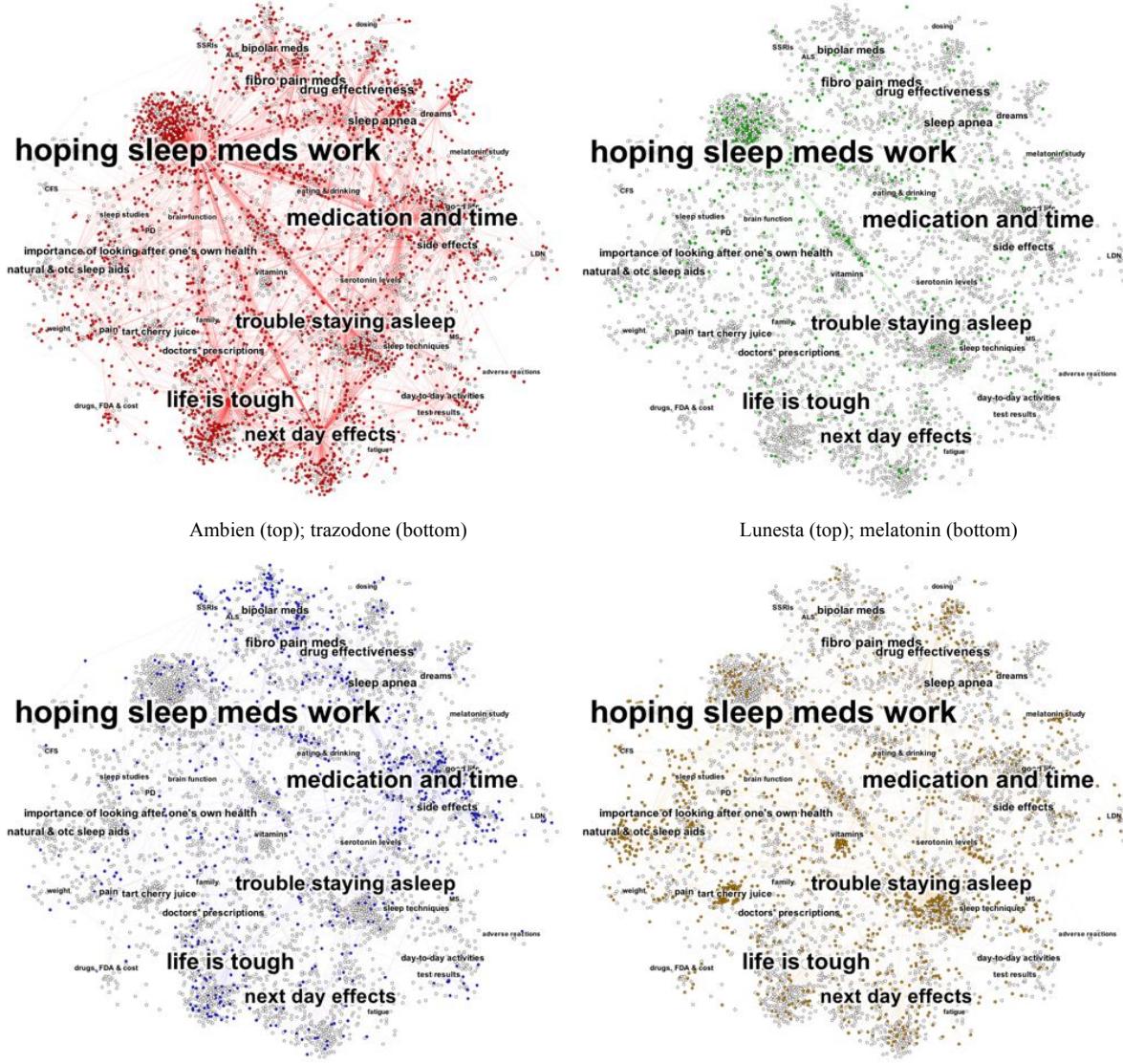


Fig. 2. Subsets illustrate different emphases in discussion across sleep aids.

suggests a role for social health forum data to support knowledge discovery.

E. Applications for Forum Moderation

Semantic network visualizations might be leveraged to aide forum moderation since structured “distant reading” can be accomplished more quickly than close readings of individual posts. Distant reading may enhance comparison across discussions, and identification of unexpected content to review at a detailed level. In our case study, we were surprised to see “Cherry Juice” was an important topic (103 posts). Almost all posts were authored by those with fibromyalgia (91%), and 67% by one person. Examining the posts, we learned about the connection – cherry juice contains melatonin, and about discussion characteristics – this sleep aid has one “champion” who writes about it often, to the point it has become eponymous (e.g., “I am going to try <champion>’s cherry juice”). Fig. 3 illustrates juxtaposing two topic clusters to

highlight differences in post author attributes by topic. As mentioned, the cherry juice topic is primarily discussed by those with fibromyalgia. Trouble remaining asleep is discussed among those with a variety of conditions.

Combining topic modeling with patient condition data can help researchers understand in which subgroups information is being shared. If there is patient knowledge that may be useful to others outside the subgroup, forum moderators may choose to share this information. Examination of such patterns may also result in the discovery of novel information of interest to clinicians and/or researchers.

III. DISCUSSION AND FUTURE DIRECTIONS

Data that is organically created by patients “in the wild” can be invaluable for a wide variety of uses, including research, clinical development, patient education and forum moderation. We have shown how topic modeling and network

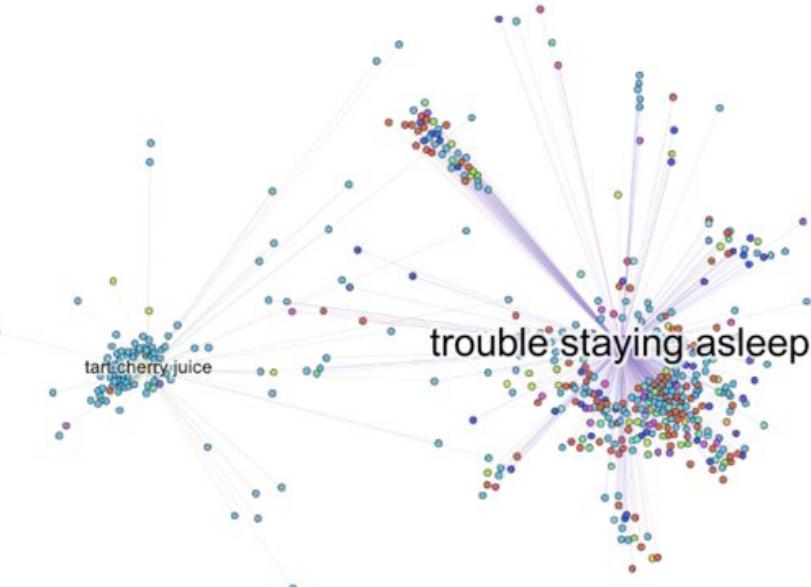


Fig.3. “Cherry juice” and “Trouble staying asleep” topic clusters. Post author conditions are identified by color (■=Fibromyalgia, ■=MS are most prevalent).

visualization might be combined to explore patient experiences. These techniques can lead to novel understandings, including about popular topics of conversation and discussion leaders. Bringing in patient attributes from other data stores can also lead to insights about the experiences of those with certain conditions. Potential uses of health discussion forum data representations are presented in Table 1.

This paper is a brief demonstration of approaches to visual exploration of forum conversations. Other directions include developing timeline visualizations to view trends in topic coverage, varying post selection criteria, aggregations by author rather than post, and connections between forum discussion topics and reports in other media sources.

TABLE I. USE SCENARIOS FOR FORUM ANALYSES

Use segments	Example scenarios
Patient education	Overview of and relationships between topics for navigation and/or education. Simplified and interactive visualizations could be presented online or integrated into PHRs
Informing clinicians	Alert services could provide information on patient concerns (e.g., side effects); and inform physicians about information patients consult online, but are unlikely to share with physicians
Clinical discovery	Discovery of novel associations (e.g., [11]) Illustrative patient experiences could be used to communicate research to broader audiences Less obtrusive data collection may enable greater participation, i.e., Citizen science [12]
Surveillance and monitoring	Overviews enable distant readings of topics associated with drugs and treatments and provide insight into patients perceptions, perhaps suggesting marketing and communication needs Contribute to diffusion analyses of health information across personal and institutional sources

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Data Exploration of a Notifiable Condition Detector System

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Abstract

The Notifiable Condition Detector (NCD) system is an automated electronic lab reporting (ELR) and case-notification system developed by Regenstrief Institute. It has been used in Indiana for over ten years to report laboratory results for the detection of notifiable conditions such as novel H1N1 influenza, sexually transmitted diseases, lead poisoning, and salmonella [1]. In this paper, we discuss ongoing efforts to analyze and visualize dimensions of the NCD data. We identify most common conditions, describe the distribution of the diseases across gender and race, study the co-occurrence of diseases and find the association rules among different diseases.

Introduction

The Regenstrief Institute implemented and has maintained an HIE-based, automated electronic lab reporting (ELR) and case-notification system for over ten years in Indiana. The Notifiable Condition Detector (NCD) uses a standards-based messaging and vocabulary infrastructure that includes Health Level Seven (HL7) and Logical Observation Identifiers Names and Codes (LOINC). The NCD receives real-time HL7 version 2 clinical transactions daily, including diagnoses, laboratory studies, and transcriptions from hospitals, national labs and local ancillary service organizations [1]. The NCD automatically detects positive cases of pre-specified conditions and forwards alerts to local and state health departments for review and possible follow up. These alerts enable public health to conduct more effective and efficient population health monitoring.

The initial analytic dataset contained 833,710 notifiable cases from 543,209 distinct patients. The dataset was deidentified by removing HIPAA identifiers and replacing patient age and zip code columns with pseudonymized values. The dataset contains 22 columns in total, including patient pseudo ID, condition name, test result name, test result value, test normal range, race, and gender, among others. The missing data rate for columns varied substantially from 0% for column Patient Pseudo_ID to over 70% for column Test_Abnormal_Flag.

Data Analysis

We analyzed the condition distribution across genders and the result is shown in figure 1.

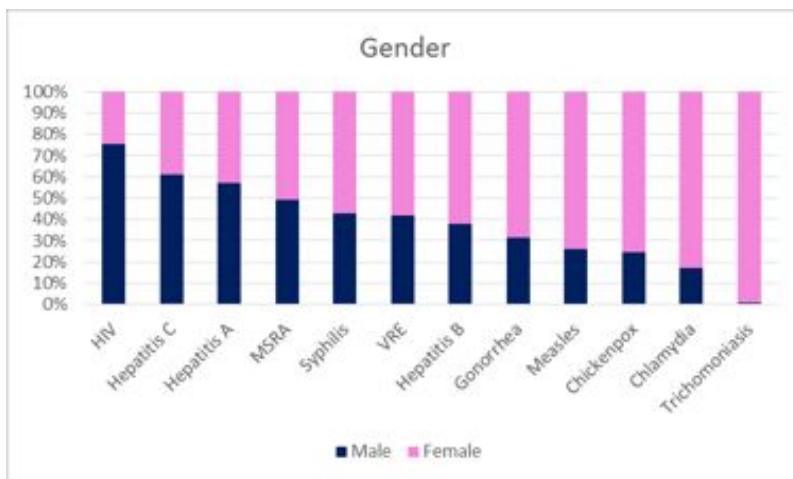


Figure 1: Condition distribution across gender

The conditions in the figure are listed according to male proportion in descending order. It shows that HIV and Hepatitis C are more common in men than in women, while Trichomoniasis , Chlamydia, Chickenpox, Measles, Gonorrhea, and Hepatitis B are more common in women than in men. The conditions that do not show significant gender difference include Hepatitis A, MRSA, Syphilis and VRE.

Disease Association Mining

In the NCD dataset, there are 39,771 patients with two or more diseases. We studied the co-occurrence pattern and derived the association rules between diseases. We generated a graph of associations among conditions using RapidMiner version 5.3, illustrated in Figure 2. It shows 2 clusters among the conditions. One cluster includes Chlamydia/Trachoma, Gonorrhea and Trichomoniasis. The other larger cluster includes Hepatitis A, Hepatitis B, Hepatitis C, HIV, Syphilis, Measles, Mumps, and Chickenpox. The figure also suggests an association between MRSA and VRE. The reason behind the associations has yet to be studied with domain experts.

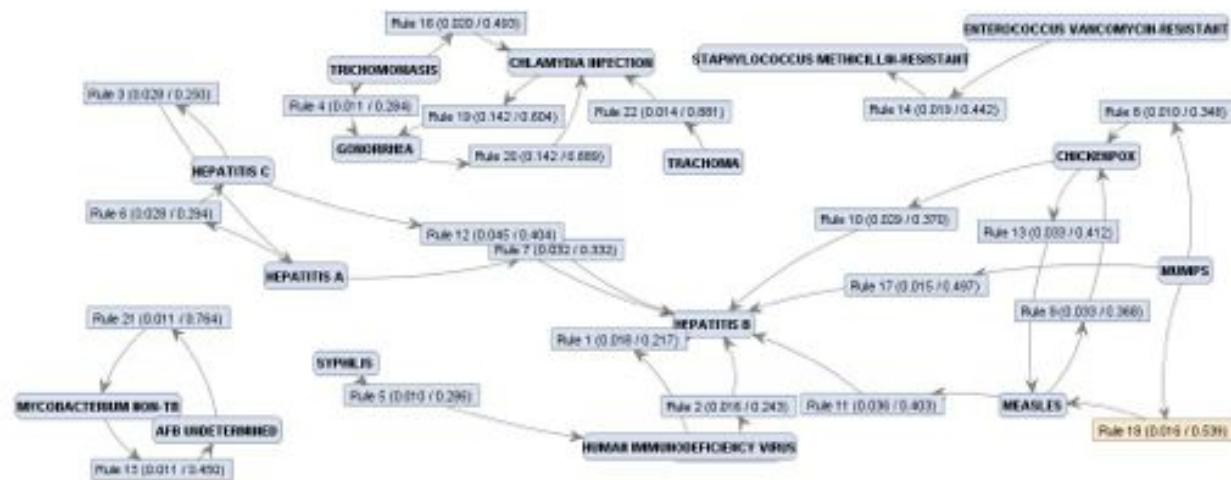


Figure 2: Diseases Associations

Table 1 shows a portion of the association rules in tabular format. The premise and conclusion of the rule is shown in the table, with the quality measures of each rule including the Support, Confidence, Laplace, Gain, p-s, Lift and Conviction. The rules are sorted according to the Confidence in ascending order. The higher the Confidence, the stronger the association is. A complete explanation of all the quality measures can be found in [2]. We are working with domain experts to evaluate the association rules and tuning the parameters to produce optimum results.

No.	Premises	Conclusion	Support	Confid.	Laplace	Gain	p-s	Lift	Convic.
5	SYPHILIS	HUMAN IMMUNODEFICIENCY VIRUS	0.010	0.298	0.976	-0.060	0.007	3.468	1.285
6	HEPATITIS A	HEPATITIS C	0.020	0.294	0.939	-0.162	0.017	2.628	1.258
7	HEPATITIS A	HEPATITIS B	0.012	0.332	0.942	-0.159	0.009	1.423	1.148
8	MUMPS	CHICKENPOX	0.010	0.348	0.981	-0.050	0.008	4.377	1.413
9	MEASLES	CHICKENPOX	0.013	0.368	0.948	-0.145	0.026	4.628	1.457
10	CHICKENPOX	HEPATITIS B	0.019	0.378	0.964	-0.130	0.011	1.588	1.298
11	MEASLES	HEPATITIS B	0.016	0.403	0.951	-0.142	0.015	1.726	1.284
12	HEPATITIS C	HEPATITIS B	0.045	0.404	0.940	-0.179	0.019	1.732	1.287
13	CHICKENPOX	MEASLES	0.013	0.412	0.957	-0.126	0.026	4.628	1.543
14	ENTEROCOCCUS VANCOMYCIN-RESISTANT	STAPHYLOCOCCUS METHICILLIN-RESISTANT	0.019	0.442	0.977	-0.067	0.014	3.647	1.586
15	MYCOBACTERIUM NON-TB	AFB UNDETERMINED	0.011	0.450	0.987	-0.038	0.011	31.475	1.783
16	TRICHOMONIASIS	CHLAMYDIA INFECTION	0.010	0.493	0.981	-0.060	0.010	2.098	1.509
17	MUMPS	HEPATITIS B	0.015	0.497	0.985	-0.045	0.008	2.128	1.523
18	MUMPS	MEASLES	0.016	0.538	0.987	-0.044	0.014	6.065	1.978
19	CHLAMYDIA INFECTION	GONORRHEA	0.042	0.604	0.925	-0.328	0.094	2.932	2.007
20	GONORRHEA	CHLAMYDIA INFECTION	0.042	0.688	0.947	-0.270	0.094	2.932	2.480
21	AFB UNDETERMINED	MYCOBACTERIUM NON-TB	0.011	0.764	0.997	-0.018	0.011	31.475	4.143
22	TRACHOMA	CHLAMYDIA INFECTION	0.014	0.881	0.998	-0.018	0.010	3.748	8.436

Table 1: Association rules among conditions

Acknowledgement

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StickWRLD : Interactive Visualization of massive parallel contingency data for Personalized Analysis to facilitate Precision Medicine

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Christopher W. Bartlett[§]

ABSTRACT

The coming promise of precision medicine suggests that medical practice will tailor treatment to each individual, rather than assuming that what works best for the largest number of people, will be appropriate for the patient at hand. To accomplish this goal, clinicians will need tools to comprehensively examine many variables across a population, and to project an individual into this data to see where they match, and where they differ from whole-population trends. Tools to support this type of comprehensive view are nascent, and primarily involve dimensional reduction, identifying through statistical means, a few features on which an individual is outstandingly different than the population, and focusing attention on just these facts. We sought to design a tool to enable clinicians to explore the data and to interactively determine whether the statistical choices for the “significant” features are appropriate for an individual. Patients will benefit from personalized analyses of their data, as well as personalized treatment of their conditions. In this manuscript we present a method for simultaneously and interactively visualizing and comparing thousands of patient-data contingency tables. An individual’s data can be projected into this visualization, enabling the user to verify automatically-chosen significant features, or to explore the existence and consequence of interactions between features that might be missed by arbitrary statistical thresholds. We apply this tool to a large expression Quantitative Trait Locus data set, as this type of *genotype* → *phenotype* ↔ *phenotype* data is an ideal proxy for the richness of personalized medical data where biomarkers are instrumental in guiding medical treatments.

Keywords: Precision Medicine, Personalized Medicine, Visual Analytics

Index Terms: I.6.8 [Computing Methodologies]: Simulation and Modeling—Types of Simulation; Visual; J.3 [Computer Applications]: Life and Medical Sciences—Medical Information Systems

1 INTRODUCTION

The quest for truly personalized medical treatment will eventually involve not only consideration of the myriad of biometric details that can be determined about a patient at the time of treatment, from their temperature to their treatment history, to their genome, but also the inclusion of as many of these details as can be acquired over the patient’s history. It will also involve comparing this data to amassed biometric and treatment data from the population, and identifying on which features the patient is similar to the population, and on which they are different. Unfortunately, for developing Visual Analytics tools to deal with this data, current patient and population data is insufficient for developing and testing scalable

solutions. In one of the few attempts to use Visual Analytics to build statistically predictive models for healthcare data, the system is limited to a few dozen features[4], while realistic systems in the future will be required to deal with tens of thousands.

To meet this need, we present StickWRLD, a tool that enables the simultaneous visualization of every possible *feature* × *feature* contingency table based on the all the observed features of a population. StickWRLD presents an interactive view of every marginal, and every per-cell residual, and is interactively filterable to focus attention on interesting, interconnected networks of residuals. In addition, an individual can be projected into this visualization, showing where they fall on the marginals, and which residuals are pertinent to understanding their features. By using visual exploration and interactive filtering, the user can either explore and gain knowledge about the individual from the visualization, or, use the exploratory process to build a statistical model of the population and individual features that are of interest, enabling simulation of the effect of changing features (altering treatment options) in the population and in the individual.

To demonstrate this system with data of adequate size, we have used expression Quantitative Trait Locus (eQTL) as a proxy data type. In using eQTL data as a proxy for developing tools for personalized medicine, our goal was twofold: 1st, to develop a tool by which the properties of the population - that is, the typical “feature A influences outcome B, except in the presence of feature C” characteristics of the population can be explored, modeled and understood; and 2nd to enable the projection of an individual into the visualization so that where they match, and where they differ from the population expectations can be identified.

2 DISCUSSION

eQTL projects are generating massive data sets that correlate Single Nucleotide Polymorphism (SNP) genotypes with gene expression phenotypes. This data is a good mimic for personalized medicine data. SNPs are like treatments, or observations about a patient, while expression levels are like outcomes. Some SNPs may predispose an individual towards certain expression levels, just as some treatments may predispose a person towards certain outcomes. The reliability of SNP A, predicting expression level B, may depend on other SNPs (just as the outcome of a treatment, may depend on other treatments the patient has already had), and it may depend on other expression levels, influenced by other SNPs (just as treatment outcomes may depend both on the treatment, and on other unrelated conditions in the patient).

The SNP and expression data for an individual involves millions of SNP genotype data points, and tens of thousands of expression levels, making it an ideal launching point for personalized medicine analytics, as it mimics the type of data envisioned for personalized medicine, and because eQTL data itself will eventually be part of the portfolio of information available for diagnosis and treatment of individual patients.

In an attempt to create sufficient data that useful tools of this scale can be developed, numerous projects are cataloging eQTL data. The GTEx project, for example, aims to quantify whole-transcriptome expression levels in up to 70 tissues across their entire subject population[5].

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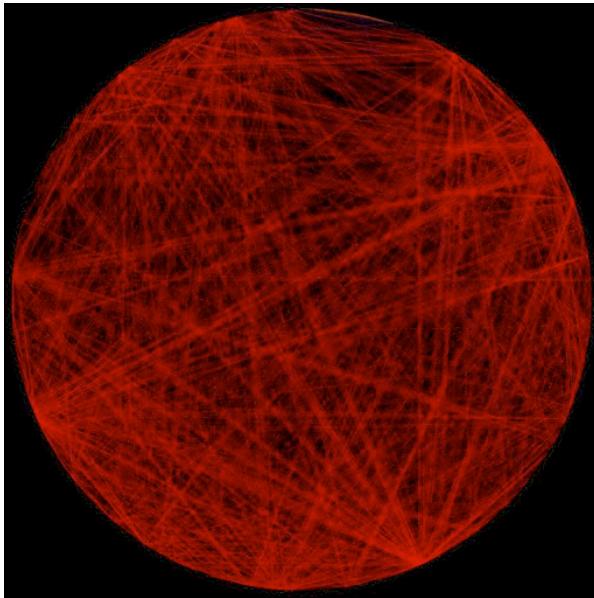


Figure 1: The full eQTL data from [6] prior to user-guided filtering and zooming in StickWRLD. **This is the starting, rather than ending point, of StickWRLD analytics.** This image shows thousands of contingency tables, each represented by a line between points on the periphery. A large residual creates a brighter line. In use this figure is interactive and is not restricted to an “overhead” view of the contingency tables based on just their strongest residual. By interacting with the visualization, the individual cell contents from each contingency table can be simultaneously viewed, and the visualization can be dramatically simplified to focus on just those features of interest for an individual.

A staggering 3.4Gb of results are generated when using state-of-the-art analysis tools for eQTL data, and analyzing only 1% of the genome in a single human tissue. Even if this data represented nothing more than discrete, independent SNP effects with no interdependencies, understanding the results would still be daunting. Without tools to further summarize and represent the analysis results in a form that facilitates end-user understanding, the most likely result of such an analysis would be the identification of a handful of especially tractable features, and the relegation of the remainder of the results to storage without further examination. This is the situation in which Personalized Medicine finds itself today, in the absence of useful exploratory Visual Analytics tools that enable personalized analysis and interpretation of personal data.

As a concrete example : We created a primary analysis from the eQTL study of [6]. This data set consisted of 193 postmortem brain samples where RNA and DNA were extracted for gene expression analysis and genotyping. We focused on the 101 cadherin superfamily genes, with B3GTL included as a positive control. SNPs within +/-50kb of each cadherin gene which passed quality-control were tested for phenotype-SNP association using standard linear regression (of allelic dose on expression) in PLINK. We additionally analyzed every possible $SNP \times SNP \times phenotype$ combination. To ascertain whether our approach produced reproducible results with disjoint but similar data, a replication data set from [2] consisting of 93 postmortem brain samples were used for an experiment analogous to the primary data set. Additional features of this analysis can be found in [1]. Sorting all results based on p -value revealed many statistically significant “hits” scattered across various combinations of expression phenotypes and SNP (or SNP-pair) combinations. While it is possible to visualize this network using force-directed graphs, this commonly used format is visually unstable and denies the user a familiar “landscape” in which to make observations. In the case of eQTL data, genetic variants are located in a specific lin-

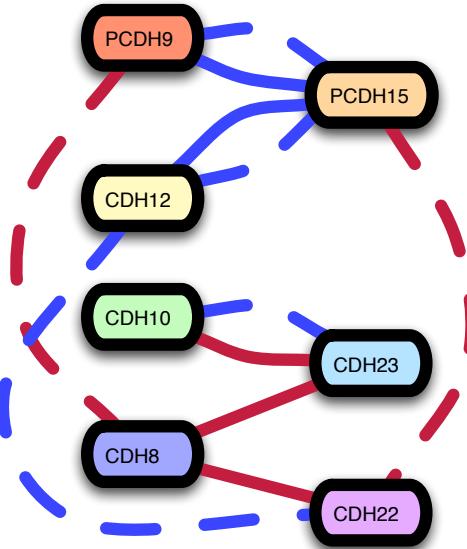


Figure 2: A schematic representation of the gene network extracted from Figure 1 as shown in Figure 3. Solid lines indicate positive correlations between expression levels under some genotypes, while dashed lines indicate negative correlations under different genotypes. Red lines connect pairs of SNPs associated with altered **CDH23** expression and blue lines connect pairs associated with altered **PCDH7** expression. If presented with an individual showing decreased **CDH12**, and desiring to correct this through modification of **PCDH15** levels, it is necessary to know whether their genotype corresponds to the positive or negative correlation edge of the network.

ear order across the genome and this order cannot be easily imposed on standard network graphs. In personalized medicine, a similar phenomenon will hold, in that it will be beneficial to visually group related observations, and to deterministically order the groups.

This eQTL analysis forms a massive collection of 2-dimensional ($SNP \times phenotype$ and $phenotype \times phenotype$, we ignore immutable $SNP \times SNP$ interactions called linkage disequilibrium in the genetics literature), and 3-dimensional ($SNP \times SNP \times phenotype$) contingency tables. Understanding where the observed characteristics of the population differ from the expectation based on the marginals (where any cell has a large residual), and how an individual’s observations fit, or differ from this pattern (even, in the case of small marginals, if the individual’s residual is small), is critical to understanding how the population, or the individual will respond to perturbing their state by changing some feature.

Applying StickWRLD makes interpreting this massive collection of contingency tables reasonably straightforward. The data is arranged around a cylinder, with each SNP genotype locus, or phenotype expression level given an equiangular “slot” around the surface of the cylinder. At each angular position, the vertical stripe of the cylinder is used to encode the categories (SNP genotype or binned expression level) for that feature. The population marginal for each category of each feature, is encoded by a scaled sphere, with radius proportional to the marginal percentage.

Per-cell residuals (interesting relationships between features) are shown within the cylinder by drawing “sticks” connecting the related observations - genotype to genotype and genotype to phenotype. The diameters of the sticks are scaled to the magnitude of the residual between those categories of the particular features, thereby representing the strength of the relationship.

The user is initially presented with a visualization similar to what appears in Figure 1, though the actual interface is live, interactive, and exploratory in three dimensions. By interactive exploration and adjusting thresholds, this view of “all the data” can be reduced to just the most interesting features, as shown in Figures 3 and 4,

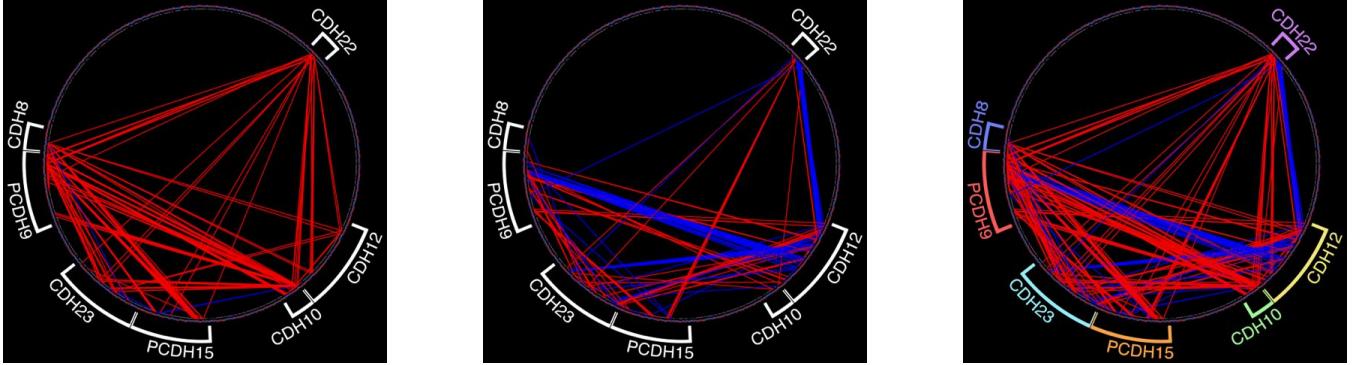


Figure 3: Substantive genetic interactions mapped by *StickWRLD*: The primary, replication and merged datasets presented in *StickWRLD*. We show only the most significant findings from the primary data set and the significant replications using only the same expression phenotypes. Colors added to the gene labels correspond to the schematic colors in Figure 2.

eventually enabling the identification of salient networks of relationships, such as shown in Figure 2. A more thorough description of this visualization technique is available in [8, 9, 7].

Readers familiar with the Circos[3] data visualization package will recognize that the *StickWRLD* display is related. However, while the static overhead view appears to be a simple locus-to-locus relationship graph, the actual live diagrams are 3-dimensional and interactive. In addition, other methods are limited to representing relationships between loci (data columns) within the data, and do not enable the exploration of features within the loci. In a live *StickWRLD* view, each apparent point around the circular periphery is actually a data column showing all observed values in it, and by interactively reorienting the view and exploring the data, the user can identify conditional interactions within the data in particular columns, rather than just the existence of column-column interactions.

To illustrate the representational power and potential for knowledge discovery that is supported by our system for presenting relationships, we focus on a very limited subset of the eQTL analysis shown in Figure 3. A walkthrough of the relationship features that can be visualized, is presented in Figures 4 and 5.

Figure 4(a) shows an “unrolled” *StickWRLD* for the data subset. This is a portion of the cylinder from Figure 3, viewed from the side. On-screen it is an interactive, visually-represented propensity matrix. That is, each column represents an observation and each row in each column represents a possible value for the observation. What appears as a point on the cylinder periphery in Figure 3, appears as a column here. On the left are columns of spheres representing ordinally-categorized expression levels for gene probes (represented as unchanged, or significantly changed +/-). On the right are SNP locus genotypes (represented in terms of the bases of the allele pair for that locus). This representation contains the complete discrete information from the subset of the [6] data set, as well as useful summary statistics, all compacted into an interface that requires only minimal training for the user to attain fluency. In a typical *StickWRLD* display, the propensity matrix from Figure 4(a) is rolled around a cylinder, as shown in Figure 4(b). Interaction with and exploration of the cylindrical form is straightforward in the live interface, and the arrangement as a cylinder allows relationships to be displayed in an intuitive manner – by simply drawing lines between the related items. Figure 4(c) shows the same view of the cylindrical propensity matrix, with interesting relationships discovered within the data added. Because of the cylindrical organization, every possible pairwise relationship can be displayed in the figure without occluding any other relationship. Metadata regarding the relationships can be added to the lines’ textures, colors and other features, such as positive versus negative correlation, which

are encoded in solid, versus dashed line textures respectively.

Focusing on the area representing the expression profiles for CDH9 and CDH12 (Figure 5(a)), we see that individuals with CDH9 levels near the mean, also have CDH12 levels near the mean. The converse of this relationship, CDH12 near the mean implies CDH9 near the mean, is also true. Similarly, we see that decreased levels of CDH9 imply decreased levels of CDH12. Normal levels of expression of CDH12 are negatively associated with reduced expression of CDH9, while the apparent contrapositive is not supported by the data – normal expression of CDH9 is not negatively associated with reduced expression of CDH12. The apparent contradiction is explained by the full distribution of expression values in the entire 193-subject data set, where the differing numbers of subjects with reduced expression in CDH9 versus reduced expression in CDH12, leads to different marginal distributions when conditioned on one reduced level versus the other reduced level.

Associations between expression level and genotype are also represented. Looking at the SNP associations for B3GTL (Figure 5(b)), we see that reduced expression for B3GTL is positively associated with two neighboring SNP minor alleles and negatively associated with the SNP major alleles at the same locations.

None of these relationships can be identified in systems that visualize only feature-to-feature relationships. By discretely classifying, and appropriately representing features and categories of the data, as well as relationships between the categories, we enable the user to directly assay the cause of a feature-to-feature interaction, without requiring a secondary analysis.

3 CONCLUSION

The tool we present here, *StickWRLD*, designed to visualize massive collections of contingency tables, is immediately amenable to understanding personalized medicine data where the features and their interactions can be described with nominal values (e.g. “affected”, “unaffected”, SNP genotypes, sex, presence or absence of treatment, etc.). It is applicable to ordinal data with little loss of generality, and can be applied to continuous data with appropriate binning. Higher order, $observation \times observation \times outcome$ contingency tables can also be simultaneously displayed. By projecting an individual into this display, users can discover where an individual is likely to respond similarly to the population, and where they are likely to respond differently, based on their unique features. Interactive exploration and filtering of the entire collection of contingency tables enables personalized analysis, and individualized reduction of the data to the most salient features, from which a predictive statistical model can be constructed. Work is ongoing in better adaptations for continuous data, as well as automated development of statistical simulations from the data.

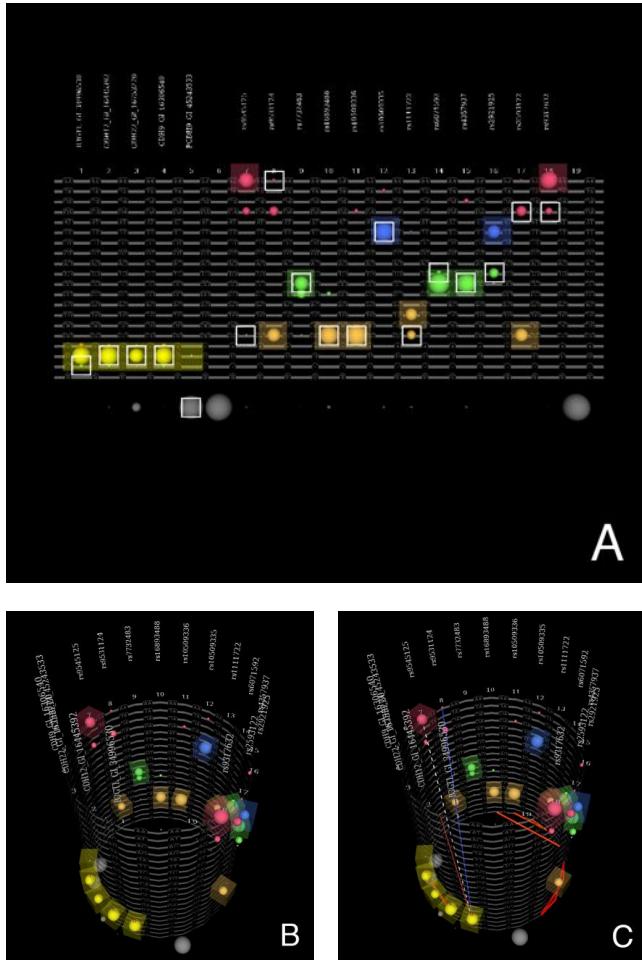


Figure 4: How *StickWRLD* works. **a)** Categorical and quantitative information contained in a table can be summarized visually. A subset of the [6] eQTL data is shown here. The visual “rows” indicate particular categories contained in the table, and the visual “columns” correspond to the table columns. The radius of each ball scales with the percentage population of the column in that category. The live version also contains the discrete data in the table, as well as summary statistics. The transparent cubes trace the “consensus” categories for each column. The gray spheres indicate the proportion of missing values in a column. The white squares trace the data from an individual subject’s row. **b)** The utility of the visualization in **a** is increased by wrapping it around a cylinder. **c)** To indicate relationships, we add lines between the related positions in the cylindrical table visualization. The diameter, color, texture and opacity of the lines can be used to encode information about the relationship.

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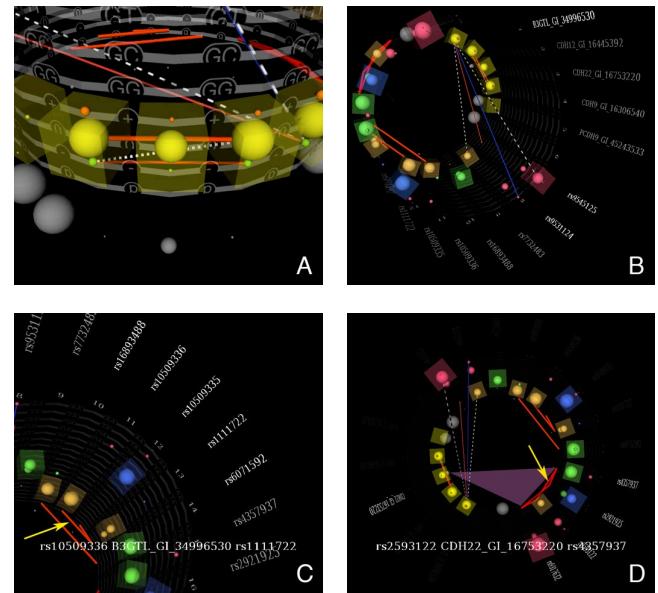


Figure 5: *StickWRLD* used to dissect details from an eQTL network. **a)** The live interface is interactively explorable. The user can move fluidly between a top-down overview that is similar to traditional graph layouts, and arbitrary exploration in the data “world” to examine relationships in fine detail. Zooming in on the expression levels of CDH9 and CDH12, we see that these share positive relationships between both normal, and reduced expression, and a negative relationship between normal CDH12 expression and reduced CDH9 expression. **b)** Examining the relationships between SNP genotypes and B3GTL expression levels, we find that reduced expression of B3GTL has a cluster of relationships with two different SNP loci: a positive relationship with the minor variant at both rs9545125 and rs9531124, and a negative relationship with the major variant at these positions. Relationships between entire columns can also be conveyed, as shown in **c**). This region of the visualization captures SNP-SNP interaction data as calculated by PLINK. Here we see that rs1111722 and rs10509335, as well as rs1111722 and rs10509336, when modulated in tandem, are associated with changes in B3GTL expression. Textual metadata is displayed in response to user cursor interaction (indicated here with a yellow arrow). rs16893488 and rs6071592 also interact and modulate expression of B3GTL, independently of the rs1111722, rs10509335, rs10509336 trio. Additional visual aids assist in understanding the combinations of interactions. In **d**) the interactions between SNPs rs9317632, rs2593122, rs2921925, and rs4357937 all affect expression of CDH22, and this relationship is conveyed both textually and by a dynamic visual pointer (pink triangle) which appears in response to the user interaction with components of the network.

A research pipeline of information extraction for visualization of narrative clinical reports on a timeline

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Abstract

Selecting adequate information to be visualized is essential for clinical information visualization design. Through this preliminary study, we propose a research pipeline that could be feasible to identify the most useful information from clinical notes for display on a timeline.

Background

Previous clinical information visualization studies focus on the visual styles and the interactive interfaces to represent information. They have made great contributions to solve the question about "how" to visualize clinical information. However, another related question that has not been fully addressed is "what" to visualize. With dozens or even hundreds of clinical events described in narrative clinical reports, the question of what to visualize is critical when designing a timeline view of the patient's record. Wang, et al. [1] suggest a detailed description of records, because physicians like to check all details. However, few studies discussed how detailed a representation is needed when visualizing clinical information over time. Hsu et al. [2] point out the importance of characterizing the information that physicians need when implementing the "details on command" function.

In this paper, we propose a feasible pipeline that could be used to untangle the "what" question. Further application of this pipeline would support future research and increase the usability of clinical information visualization systems.

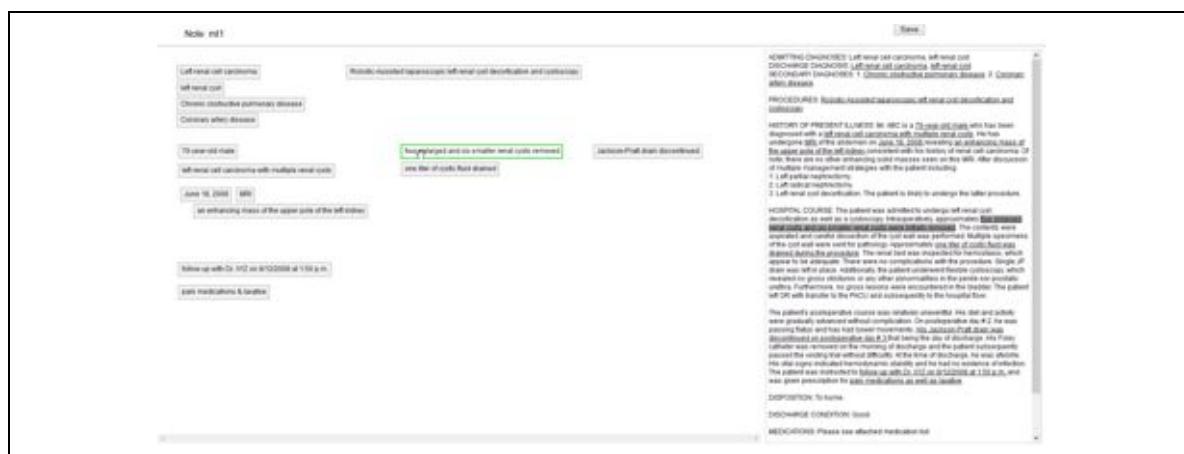


Figure 1. A screenshot of the selection tool (The left side is the whiteboard. The original note is displayed on the right. This screen shot is for demonstration purpose. This note is adopted from www.mtsamples.com instead of I2B2 [3], due to the constraints of the Data Use and Confidentiality Agreement).

Methodology

1. Data collection

Because this is a pilot study, our aim is not to find out an actual solution of the research question but the way to solve it. We included 6 people (3 physicians and 3 informaticists). We selected 10 discharge notes from the I2B2 dataset [3] as the sample clinical data and asked participants to mark which information they would like to visualize on a timeline when seeing a single narrative patient report, such as a discharge summary. Knowing that the same information may be valued differently in different clinical scenarios, we simply select a follow-up scenario in this preliminary study.

We developed a selection tool to help participants express their opinions about what information to place on a timeline. This tool can generate a labelled symbol on a whiteboard when participants highlight words or phrases from the discharge summary (Fig. 1). Participants can also reword the labels of the symbols and rearrange the symbols on the whiteboard. With this tool, we can obtain the users' input pertaining to questions such as "What information in the report is important enough to view on the timeline," "What labels best represent the information in the report that are placed on the timeline," and "What information from the report should be grouped together on the timeline."

2. Data Analysis

We merge the data from the whiteboards into one table per note. In each table we record whether each word in the note is selected by participants and how the words are grouped together to represent a single clinical event or concept. Through comparison of selected and grouped words in the table, we make a variety of quantitative comparison:

Analysis 1: Through inter-annotator agreement statistics such as kappa, we can quantitatively compare user selections against I2B2 annotation of clinical events to learn how well user needs align with ideal NLP output.

Analysis 2: In addition to annotations of clinical events, I2B2 annotations include attributes of the events such as "modality" and "polarity." We are adding additional manual annotations on top of the I2B2 annotations, including attributes such as "duration" and "change" that may be relevant to temporal visualization. Through attribute annotations, we can explicitly describe in detail the concepts users place on the whiteboard and the labels they select (e.g., users may use the "change" attribute in a concept label).

Analysis 3: Through interpreting participants' selection using clinical knowledge, we derive patterns in what concepts are included on the whiteboard, which are not included, how they are grouped, and how they are labeled. For instance, a participant annotated "abdominal pain" in a statement: "Mr. Strength is a 40 year old man with a history of GERD, who presents with abdominal pain of seven days duration". A possible pattern is "the chief complaint need to be visualized on the timeline", because "abdominal pain" is the chief complaint. As more users participate in this user-driven design study, we will expand and quantify the observed patterns based on their frequency of use. These patterns can be used to automate instantiation of information on the timeline and can be evaluated in future user evaluations of timeline visualization from clinical reports.

Preliminary findings

We have collected data from six users on one report and have preliminary findings related to the following:

1. What concepts/events should or should not be viewed on the timeline: We have found that only a portion of the annotations in the I2B2 dataset are desired for visualization by users (approximately 38% of I2B2 events). If counting the word-to-word agreement, the Cohen's kappa is around 0.19.
2. Which concepts should be grouped together on the timeline: We have found several patterns of grouping in our initial assessment: 1. Symptoms that occur at the same time; 2. Treatments received in one location; 3. Treatments for a single symptom; 4. A test and its result; 5. A medication and its usage; 6. a physical measurement and its value; 7. A problem and a possible diagnosis describing the problem.
3. How preferred labels correspond to words in the reports: We have found that participants are more likely to label positive problems, positive findings in tests, and treatments (especially related to chief complaint). They seem to omit the predicates in a sentence unless it indicates patient's condition changes. For instance, to visualize the statement "The ultrasound showed biliary sludge", one participant labeled this statement as "ultrasound: biliary sludge".

All these preliminary findings need to be further refined after more data are collected.

Future research

We will set up this tool on an online server, integrating with a database on the backend, so that data can be collected in an automatic manner. After collecting data from more participants and more notes, in addition to refining our derived patterns, we will analyze the data quantitatively by comparing events and concepts preferred to be visualized by users against those annotated in the I2B2 dataset and by comparing preferences among users. Informed by these research results, future visualization designers will understand what information is expected to be visualized in a certain clinical scenario.

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Detecting Comorbidity of Chlamydia from Clinical Reports

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Abstract

Using a standards-based messaging and vocabulary infrastructure, the Regenstrief Institute implemented and has maintained an unparalleled automated electronic laboratory reporting and noticeable condition detection (NCD) system for over 11 years [1]. The NCD automatically detects positive cases of pre-specified conditions and forwards alerts to local and state health departments for review and possible follow up. In this paper, we discuss ongoing efforts to analyze the clinical reports of one specific NCD condition, Chlamydia. Our goal is to identify the presence of any comorbidities of Chlamydia across 6238 patient records and integrate this finding along with our health analytics and visualization system that we are developing.

Introduction

The participants of this project are working on a Health Terrain visualization system centered on an innovative concept-based knowledge discovery and visualization. In this approach, raw health data are first processed, mined and transformed to an information-rich Health Concept Space, where attribute values, association relationships and other partial knowledge are extracted from patient data to form a more structured multi-dimensional data space. The concept space is built on a controlled vocabulary (concepts) that can be pre-defined based on application needs, and therefore is a scalable framework that can be expanded progressively as the applications and use cases expand. For building the concept space, we utilize the structured data as well as unstructured clinical reports from the EHR data. One piece of knowledge that can be extracted from the clinical notes is comorbidity and this can be discovered using Natural language processing (NLP). The text in medical records (e.g. radiology reports, pathology reports, clinical notes, and discharge summaries) includes a wealth of information about patients. NLP can be very useful in extracting information from these free text documents and creating structured information that can be used for further knowledge extraction.

Data

The dataset consists of 6238 de-identified clinical notes that include discharge summary, laboratory reports, etc. Since the clinical records are de-identified, the patient specific information is lacking in the clinical reports.

Method

Natural language processing (NLP) techniques are carried to detect comorbidities that co-occur with chlamydia. In this case, the NLP process is composed of low-level and high level task. Low level tasks consist of sentence splitting, tokenization, stemming, part of speech (POS) tagging and phrase chunking (identifying phrases from POS tagged tokens) and the higher level tasks consists of named entity recognition (NER) of co-occurring diseases. Once the NER process is complete, we use the *tf-idf* vector space model [1] (term frequency * inverse document frequency model) to identify significant co-occurring diseases along with chlamydia. The *tf-idf* is recognized as one of the more effective text mining models compared to Log Level Likelihood and Odds ratio models, amongst the various other models. The *tf-idf* model uses the concept of relevance and co-occurrence of terms. The relevance of a term j w.r.t. a document i is given as,

$$w_{ij} = t_{ij} * \lg\left(\frac{N}{N_j}\right) \quad (1)$$

w_{ij} = relevance of term j in the patient record i ; t_{ij} = term frequency of term j in in the patient record i ; N_j = frequency of records for term j ; N = total number of records ($N=6238$). A particular term is more relevant w.r.t. a record if it appears more frequently in the record and appears in fewer numbers of records in the total records set. An association weight is attached with every association between a pair of terms [3]. This is given by A_{jk}

$$A_{jk} = \sum_{i=1}^N t_{ij} * \lg\left(\frac{N}{N_j}\right) * t_{ik} * \lg\left(\frac{N}{N_k}\right) \quad (2)$$

This is essentially a product of the relevance of each of the pair of terms over the entire records set N . If the terms do not co-occur in any of the N records, then the association is 0. We will be interested mainly in non-zero associations.

Results

After applying the low-level NLP steps, the resulting terms were subjected to named entity recognition (NER). The UMLS [4] database was used for NER to identify diseases that are present in the 6238 discharge summaries. A total of 1337 possible disease conditions were identified that can be roughly considered as comorbidities with Chlamydia. Figure 1 show the most commonly occurring diseases along with the number of reports in which they occur. The co-occurring diseases with Chlamydia were further analyzed using the $tf\text{-}idf$ model to understand the significance of these diseases across all the 6238 records. For this analysis, $tf\text{-}idf$ score was calculated for the diseases using the Equation 1.

Comorbidity with Chlamydia

The final analysis and the goal of this work are to identify comorbidity with Chlamydia. To accomplish this, we calculated the pair-wise significance of each disease with Chlamydia using Equation 2. Figure 2 shows all the diseases those are found to be comorbid with Chlamydia. This graph shows some of the expected diseases such as hepatitis, gonorrhea, etc., along few other health conditions such as Bacterial vaginosis, obesity, and so on. The accuracy of these findings has to be validated by the experts. In addition to the comorbidity, the NLP analysis also revealed symptoms, risky behaviors, and mental behaviors those are associated with chlamydia as shown in Figure 3.

Conclusions

We have developed an NLP method to identify comorbidity of Chlamydia from the discharge summary of 6238 clinical records. This information, once validated by the experts, will be incorporated in to our Health Terrain visualization system that is currently under development.

Acknowledgement

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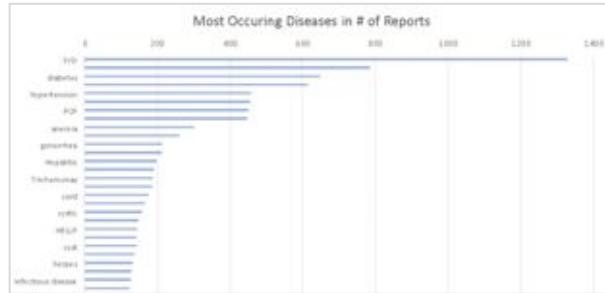


Figure 1: Top diseases with the corresponding number of reports

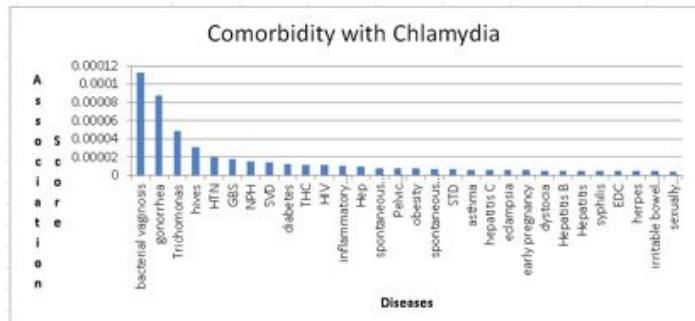


Figure 2: Top scoring comorbidity with Chlamydia

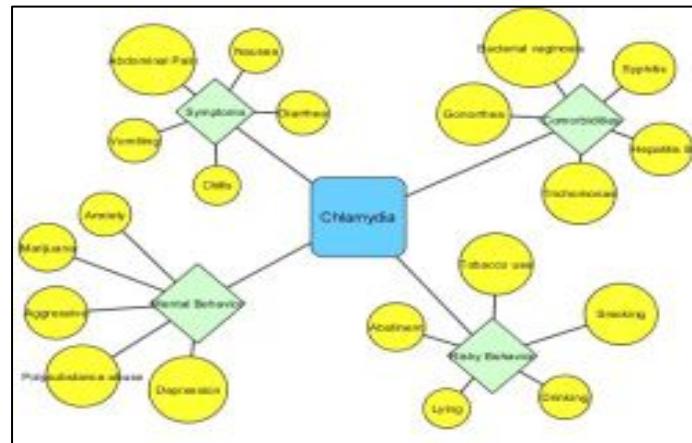


Figure 3: Symptoms and risky behaviors associated with Chlamydia detected using NLP

Use Cases for Public Health Data Visualization

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Abstract

Epidemiologists in Marion County, Indiana, use massive amounts of public health data to provide insight to previous and current disease outbreaks. Typically, they use statistical analysis and simple charts to convey information in public reports, but the work is tedious and difficult without contextual knowledge from years of investigation. Use cases highlighting potential disease outbreaks and research topics, provided by these epidemiologists, will inform a new interactive health data visualization system designed to facilitate and enhance the discovery and strategic intervention.

Introduction

Epidemiologists and other public health officials need to contain the spread, and identify and reduce exposure to disease. We intend to provide a visualization engine to facilitate discovery of these outbreaks. The following factors contribute to a useful public health dataset, and can be used as variables in visualizations:

- Age
- Gender
- Geographic Location
- Race
- Social Networks

Existing visualizations are limited to heat maps or simple overlays, typically simplified to charts and tables for communicating the most essential data to describe the spread or impact of a disease. A useful interface will allow for rendering these reduced views for use in reports. Data analytics can provide insight to what might be the most interesting data, with the final decision of relevance in the hands of the user.

Interviews with Dr. Joseph Gibson, MPH, PhD, Director of Epidemiology at the Center for Urban Health in the Marion County Public Health Department, and Dr. Roland Gamache, PhD, Affiliate Research Scientist with Regenstrief Institute, inform the use cases in this presentation. Some use cases are specific to Indiana or the Indianapolis area.

Use Case: Histoplasmosis

A rare disease, affecting only 20-25 people yearly in Marion county, histoplasmosis outbreaks should be easy to detect locally. Excavation that disturbs ground where mold spores have settled typically predicates an outbreak of this disease. Indiana has a long history with histoplasmosis due to a high concentration of relevant spores throughout the state; the largest outbreak in the country occurred in Indianapolis in September 1978 and again in August 1979 [1]. Public health officials need to see each diagnosis, with multiple occurrences in a similar location prioritized over others, alongside relevant excavation data. Visualization techniques can highlight geographic proximity to potential causes.

Major Visualization Factors	Visualization Traversal Vectors
Occurrence density in geographic locations Nearby potential causes (e.g. construction, tree removal, or demolition)	Chronological time Proximity to causal events

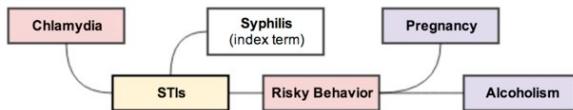
Use Case: Gonorrhea

When researching gonorrhea, epidemiologists are interested in co-morbidities and other related diseases. They also want to know who is repeatedly infected after treatment. Gonorrhea is a social disease, transmitted sexually, and a proper visualization will highlight these connections. Social networks, both online (e.g. Facebook and Twitter) and traditional (e.g. high schools, colleges, neighborhoods, and workplaces), become the most important correlation factor. Intervening with super-spreaders, people who may be unknowingly giving gonorrhea or related diseases to several others, can help contain the impact and prevent recurrence. Social data may require approval by individuals, but would facilitate better care.

Major Visualization Factors	Visualization Traversal Vectors
Frequency of recurrence in individuals	Chronological time
Comorbidities (e.g. other sexually transmitted diseases)	Social distance from a super-spreader

Use Case: Risky Health Behavior

Some diseases are indicative of risky health behavior, and epidemiologists need to know when an individual has a higher potential for infecting others in the community. Visualizing layers of an index term against related diseases and risky behavior can show unexpected correlations. The example below shows first, second, and third relations.



Major Visualization Factors	Visualization Traversal Vectors
Cumulative occurrences of risky behavior Time range between occurrence (e.g. a spike on multiple short deltas)	Time deltas (e.g. daily, one week, two weeks, months) Age ranges Relatedness of other diseases or categories

Use Case: Influenza Pandemic

Influenza is the type of disease that appears seasonally, as a response to airborne allergens. Strategies for a breakout of influenza vary depending on the current state of the pandemic. When integrated with a monitoring system, a visualization engine could highlight a grouping of recent diagnoses and assist in intervention and containment. If the pandemic has already breached a certain threshold, the system would switch to a different visualization useful for monitoring and forecasting spread. It is important in such a breakout to identify the first cases, to understand how the disease is progressing and spreading from the index patients. This information should be presented visually to help decide the best strategy.

Major Visualization Factors	Visualization Traversal Vectors
Earlier occurrences highlighted for easy identification Occurrence density in geographic locations	Amount of time since infection Social or geographic location links

Future Research

Each use case above demonstrates problems in public healthcare that cannot be easily interpreted without a series of statistical charts and tables, and the knowledge to recognize trends and similarities. We will use these scenarios as starting points to inform the design of a visualization engine with an interactive interface, primarily useful to the epidemiologists. We expect this system to make the discovery and research of outbreaks and pandemics easier, faster, and more effective.

Acknowledgements

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Perceived Usefulness and Usability of a Visual Analytical System for Toxic Chemical Identification: Results from a National Survey of First Responders

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Abstract

Despite the critical importance of decision-support tools used by first responders during toxic chemical emergencies, little is known about the usage and design requirements for such tools. Guided by the results from a qualitative study of 20 first responders from 2 states, we conducted a nation-wide survey of first responders to analyze how current decision-support technologies are being used, and to solicit perceptions for the usefulness and usability of a prototypical visual analytical system for toxic chemical identification. The results ($n=139$) revealed that while respondents from regional jurisdictions had significantly different profiles for tool usage compared to single and countywide jurisdictions, there were uniformly high ratings for the perceived usability and usefulness of the prototypical visual analytical system across all jurisdictions. A closer inspection revealed a significant difference in perceived usefulness versus usability across all jurisdictions, with the textual comments providing clues for that difference. These results extend our prior understanding of technology use by first responders, and help to identify the critical features necessary for the wide adoption of future systems.

Introduction

Although the rapid identification of toxic chemicals during chemical incidents is a nation-wide imperative, few studies have analyzed technology usage nation-wide. Here we report preliminary results from a nation-wide survey of first responders designed to address the research question “How do first responders use technology during a toxic chemical incident, and what are their perceptions regarding a prototypical visual analytical system designed for toxic chemical identification?”

Method

Guided by a qualitative study¹ of technology usage by 20 first responders in 2 states, we conducted a nation-wide online survey consisting of 36 questions related to: (1) **demographics** (e.g., location and jurisdiction), (2) **tool usage** (e.g., frequency and type of tools used), and (3) **perceptions of the usefulness and usability** of a prototypical visual analytical system, using a validated instrument based on the technology acceptance model. The visual analytical system called Mining And Interpretation of Diagnostic Networks (MAIDN)² was demonstrated through an online video provided as part of the survey.

As shown in Figure 1, MAIDN integrates search and visual analytics in a single interface. The usefulness and usability of this design was iteratively refined through consultation with an expert first responder, and through the application of ten heuristics³ for designing general-purpose graphical user interfaces, and seven heuristics⁴ that are specific to the interaction design of visual analytical systems. Furthermore, the contextual appropriateness of the design was verified through qualitative interviews⁵ with first responders in two states. The interface was designed to have few menu selections, appropriate for use in stressful and time critical situations. The top left pane provides a dynamically generated list of symptoms ranked by their ability to eliminate close to half of the remaining chemicals. For example, the top-ranked symptom (*Dizziness*) in the figure will eliminate 47% of the chemicals (as shown by the pop-up box) if its yes option (“Y”) is selected, and about the same if the (“N”) option is chosen.

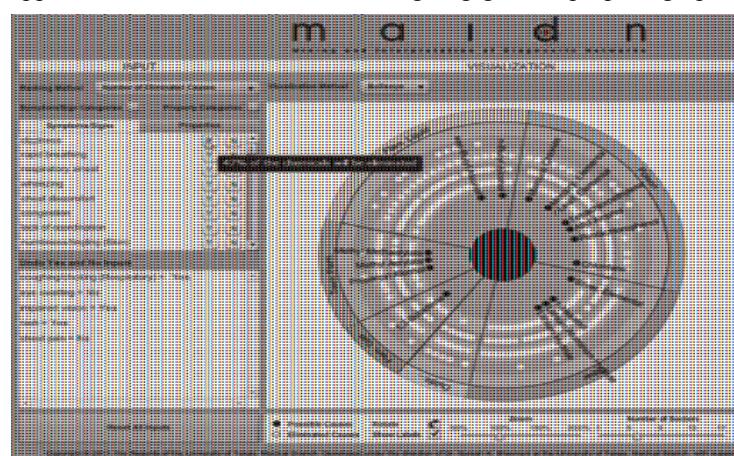


Figure 1. The MAIDN prototype integrates an algorithm which guides users to consider the most discriminating symptoms (upper left pane), and a visualization (center) that provides “at-a-glance” how the symptom selections reduce the candidate chemicals (black dots moving to the center), which are categorized by their chemical properties (sectors).

In the middle pane, the visualization provides “at-a-glance” the chemicals that are eliminated (white dots), and candidate chemicals (black dots with labels) which progressively move into smaller rings

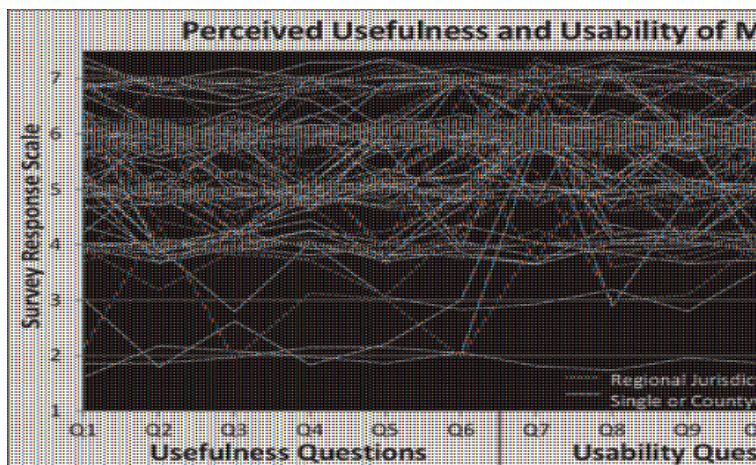


Figure 2. How 139 first responders across regional versus smaller jurisdictions perceived the usefulness and usability of MAIDN.

Results

The survey yielded 191 responses (24% response rate) from 27 states, with 139 who completed all questions, and who were chosen for the current analysis. The analysis revealed a significant stratification of tool usage based on jurisdiction (response coverage). Compared to respondents from jurisdictions with smaller coverage combined (single and countywide), respondents from regional jurisdictions used significantly more ($U=843.5$, $p<.001$, two-tailed test) detection technologies (e.g., radiation detectors), and used WISER¹ (a decision-support system) significantly more often ($U=1185.0$, $p<.01$, two-tailed test). This difference in WISER use is important because there was no significant difference in the number of chemicals identified by respondents in regional jurisdictions compared to the rest. However, as shown in Figure 2, despite the above differences in tool use, there were no significant differences between the two jurisdiction groups in the 12 questions about the perceived usefulness and usability of MAIDN. Finally, while the overall ratings were mostly positive (higher score=more positive), the usefulness scores were significantly lower compared to usability across all jurisdictions.

Discussion and Conclusions

The results were presented to an expert first responder for interpretation. The discussion revealed that: (1) the difference in tool usage reflects the extra federal funding received by regional jurisdictions, and their increased usage of WISER suggests that they will be more frequent users of MAIDN, and (2) the absence of differences related to perceived usefulness and usability to the prototypical system suggests that the proposed design has the potential to be widely adopted. Furthermore, textual comments suggest that MAIDN could benefit from additional functionality such as inter-operability with other technologies used during chemical identification.

The combined results from the prior qualitative study, and the current quantitative survey therefore deepened and broadened our understanding for designing future tools for first responders.

Acknowledgements. Funded by CDC/NIOSH #R21OH009441-01A2.

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towards the inner red circle. When no more symptoms are available to distinguish between chemicals, the final candidate chemicals move into the inner red circle (the “bull’s eye”). The system therefore guides the user towards considering symptoms that eliminate many chemicals, and simultaneously provides visual feedback on the effects of different inputs to help make a rapid decision.

The survey, which included a video of MAIDN, was sent to 795 email addresses of first responders obtained from an organization that trains HAZMAT teams nation-wide in partnership with federal agencies, and therefore represented a wide cross-section of first responders.

How Graphical Visualization can Aid in Understanding and Developing Clinical Ontologies: Exploring the Overlap Between ICD and SNOMED

Evan Minty MD MSc, Marco Cusumano-Towner, Dean Yergens, Bill Ghali MD MSc

Abstract

Finding overlap between existing controlled terminologies might be seen to represent a different knowledge curation problem relative to others in the ontology creation space, one which might be amenable to the use of a graphical interface in the modeling process. Humans are highly visual and spatial in their reasoning, and the user may have a better intuition about the structure and content of the model they are building if it is laid out visually, instead of hidden in a series of annotation fields. In this project, we examine the conceptual overlap within the cardiovascular disease chapter of The International Classification of Diseases (ICD), and a sub section of SNOMED Clinical Terms (SNOMED-CT) relating to myocardial disease, through a visualization oriented paradigm. This exercise is not designed to suggest a replacement for existing ontology editing systems, but as an environment through which requirements for possible ontology GUI editors can be conceived. These requirements are subsequently discussed.

Introduction

The International Classification of Diseases (ICD) has long had use cases within healthcare administration and health services research, and will remain a de facto standard terminology in medical practice. The ICD has always had considerable clinical input into the development of the taxonomy, however the classification logic is not always made explicit. SNOMED-CT, meanwhile, has evolved to a level of remarkable level of specificity that reflect both its origins as pathological descriptors, but also its evolution in an environment where there were less constraints restricting the addition or modification of terms. Interoperability between these two systems is essential, so finding a common taxonomic (and ontological) underpinning of SNOMED and ICD is of interest with interoperability as an ultimate aim. Although mappings between the two exist [1], the conceptual overlap between the two, or a unifying content model, is not made explicit. As importantly, both may need to be mapped to clinical terminologies used locally in EMRs [2], mappings which would likewise benefit from defining the space of terminological overlap and common model underpinnings.

A project that aims to find overlap between existing terminologies might be seen to represent a different knowledge curation problem relative to others in the ontology creation space. For well defined systems, a decomposition into ontological classes can be relatively easily accomplished within existing editors. Even when systems are large, if the inherent concepts are well defined, the problem might be amenable to an approach wherein a large number of the 'actors' in a system can be defined early in the modeling process – akin to a computer programmer's decomposition and upfront declaration of classes in an object oriented paradigm.

In this instance however, the task is to take an established hierarchy, examine it for classification logic, and find overlap between it and other terminologies that aim to describe the same domain. In this use case, structure that defines overlap and common underpinnings is an emergent property, not a declared one. Therefore a platform that allows conceptual groupings to be formed, examined, and annotated would be helpful, and a graphical user interface (GUI) that might enable such a process would be ideal. This would allow the visualization of pattern emergence in two dimensions, and aid in the communication of the model with other user groups.

Methods

It was felt that such an endeavor uncovered a gap in the tool set currently available for this type of knowledge work. A workflow that enabled an 'ontology creation GUI' was envisioned, such that annotations created in a graphical representation of relationships might be encoded for subsequent export to another editor for further model refinement. The tool of choice was a repurposing of Tinderbox (www.eastgate.com), which adopts an XML based, object oriented approach to note taking.

Existing graphical ontology editors (Owlged, Ontotrack) allow the user to produce and examine Web Ontology Language (OWL) ontologies through UML-style diagrams. Tinderbox allows on-the-fly annotations to be applied based on the visual arrangement of items, allowing for a more rapid and experimental data exploration process. In particular, overlapping an item with an "adornment" in a concept map can be made to automatically apply a specific set of annotations. This allows for greater expressiveness than a simple annotation alone (for example, the amount of overlap or spatial relationships can be used as a visual guide for the user to arrange their mental model of the concepts).

As a proof of concept, the ICD 10 cardiovascular chapter was downloaded from the ICD alpha browser (February 2012), and a splice of the SNOMED ontology, about 'myocardial disease' was created via export to OWL and manual curation (credit: Vincenzo Della Mea). Both were exported into an XML format that was able to preserve a mono-hierarchy, and could subsequently be input into Tinderbox (Outline Processing Markup Language, OPML). This splicing preserves some, but not all, of the *is_a* relationships within SNOMED, although mapping back to a fully specified SNOMED ontology could conceivably re-establish them.

Results

The use case is best illustrated by considering an example after organization and addition of adornments in a graphical view. The view of the top level of ICD 10 after such a process is shown in figure 1.

As 'aggregating' concepts are identified, prototype adornments are created such that they set user defined attributes of the individual notes. Thus, in figure 1 the centre 'container' (which is simply a parent concept) highlighted in blue represents the ICD concept "Congenital malformations of peripheral vascular system". Its position in the map is reflected by the metadata that is subsequently set by the adornments it contacts. The effect on the metadata of this concept can be seen along with the list of defined user attributes, in figure 2.

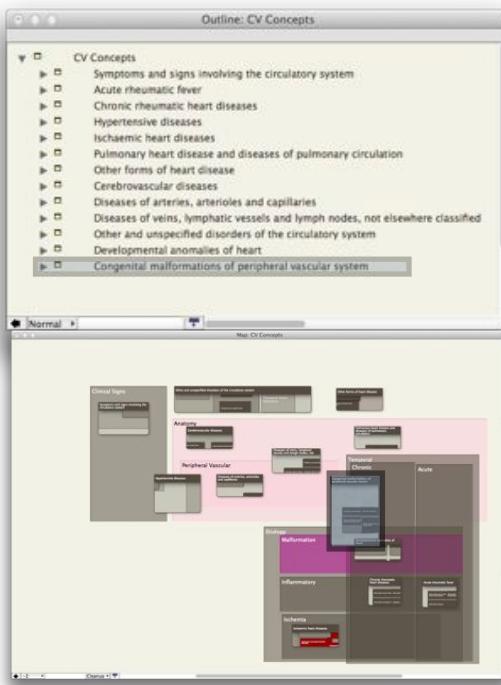


Figure 1. Top view of the ICD cardiovascular chapter in Outline Form, and Map form.

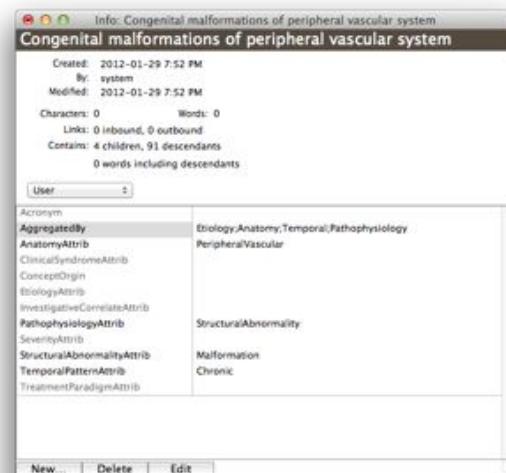


Figure 2. Attributes added to the ICD concept 'Congenital malformations of the peripheral vascular system' due to its physical position on the concept Map and contact with content model adornments.

The GUI functionality is especially useful in cases where a large collection of concepts is relatively unstructured, as in, for example, children of the ICD parent concept 'Other Forms of Heart Disease'. A rendition highlighting the knowledge structure at an intermediate stage of development is shown in figure 3.

An advantage of GUI organization is that it allows a spatial mental model of concepts to be arranged, amenable to annotation at increasing levels of specificity. For instance, closer examination of the arrangements of concepts in figure 3 suggests aggregating concepts specifying groupings of infectious agents shown in figure 4. Infectious agents are organized, then captured by adornments reflecting bacterial, mycobacterial, and viral causes (greens). If additional aggregation specificity is desired, the mental model in this case has been organized such that organisms that are commonly transmitted sexually could be captured as shown in the blue highlight, with diseases caused by syphilis in the red highlight.

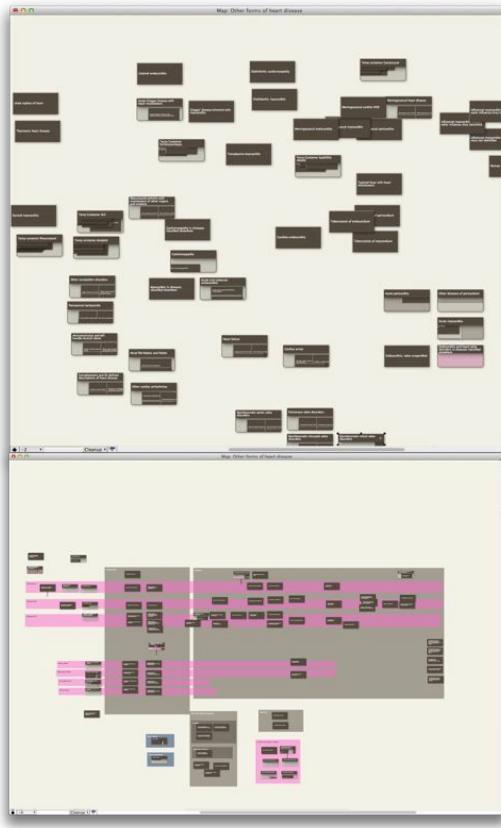


Figure 3. Map of concepts within the ICD parent “Other Forms of Heart Disease” at stages of organization through aggregating adornments.



Figure 4. The spatial mental model of concepts can be captured with adornments of increasing conceptual specificity.

The process of finding overlap between the ICD cardiovascular chapter and SNOMED myocardial disease concepts can then be modeled through the introduction of SNOMED concepts into the formed ICD maps, as shown in figure 5.

Once the modeling process is complete, the model created via the GUI interface is accessible in XML. In our case, the XML file was parsed using the Java Document Object Model (DOM) parser into a Java object model, and subsequently used in the development of a Reasoner that operates on top of the model, to map between ICD and SNOMED concepts.

Discussion

This exercise in the use of GUI approach to ontology analysis and development was not designed to suggest a replacement for existing systems, but as an environment through which to conceive requirements for a possible ontology GUI editors. Ontology creation is hard, both in terms of developing a concept model for a domain, and communicating requirements for its logical assertion. The process involves considerable interaction between developers and domain experts, who may not initially conceptualize their domain in a decomposition that can be logically asserted.

Humans are highly visual and spatial in their reasoning, and the user may have a better intuition about the structure and content of the model they are building if it is laid out visually, instead of hidden in a series of annotation fields. Existing modelers allow layout on the two-dimensional plane for purposes of the user organizing their mental model, but the layout and the annotation itself are generally separated. Treating the physical layout itself as the control for actually applying annotations reduces the workload of having to go through and manually add each annotation.

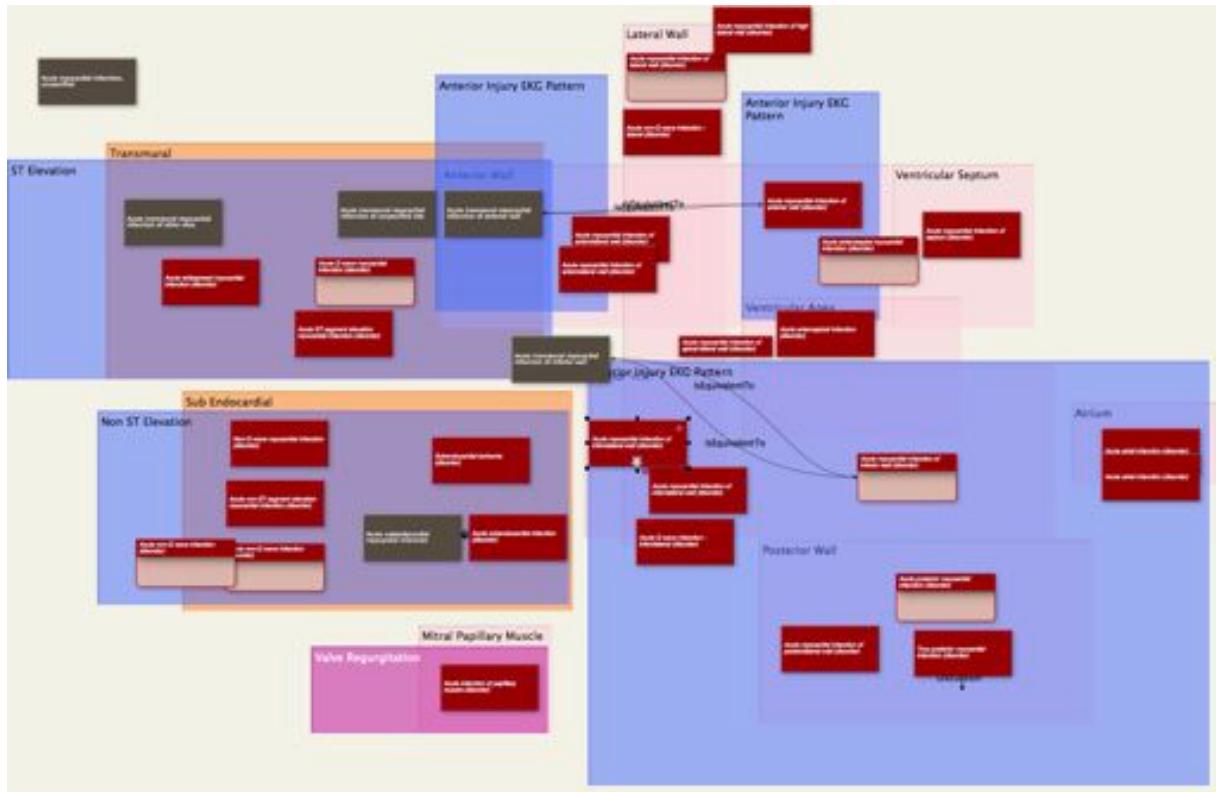


Figure 5. Introduction of SNOMED terms (red) into the ICD map view of Acute myocardial infarction. Orange adornments reflect injury extent (transmural, subendocardial), peach adornments reflect anatomic references, blue reflect injury currents seen on EKG.

Some requirements for a GUI editor, based on this experience, would be:

- 1) The ability to arrange concepts in 2D, to aid in the formation of a spatial mental model.
- 2) The ability to capture this mental model through the addition of adornments to the 2D space that would annotate the concepts. Allowing different degrees of overlap, can help with the arrangement of a mental model, but doesn't need to affect the application of annotations. Having a concept touch multiple adornments allows each annotation associated with the adornment to be applied.
- 3) The ability to create prototypical (or class) adornments to speed the annotation process by allowing subsequent instantiation.
- 4) The ability to create these adornments in an inheritance chain, such that children adornments inherit transitive attributes of their parents.
- 5) Forcing the annotations to be inferred from overlap on a two-dimensional plane imposes constraints on the set of possible graphs that can be represented. A solution to this problem is to allow for multiple fields of view (and multiple working copies of the concepts) in which concepts and adornments can be overlapped. Logically, these are different projections of the user's mental model onto different modeling dimensions.
- 6) A data model that is amenable for transition to RDF, and subsequent completion (entailments, closure) in an reasoner environment if a true Ontology is desired or felt possible as an end product.

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COPTADS: Clinical Online PTSD and TBI Analysis and Detection System

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Abstract—Thousands of US soldiers returning from the long wars in Iraq and Afghanistan have been diagnosed with symptoms of Post Traumatic Stress Disorder (PTSD) and Traumatic Brain Injury (TBI). Family members of many of these vets (or the vets themselves) post blogs of varying length on online web sites intended to support them. In this paper, we ask ourselves the question: Is it possible to perform a detailed analysis of the emotions expressed in the text so that subjects of such blog posts suffering from either PTSD or TBI can be identified accurately. We developed algorithms to extract emotional signals from text and algorithms to predict whether a person with a given set of emotion signal intensities has PTSD or not. Our PTSD predictions algorithms are about 80% accurate while our TBI prediction algorithms are over 90% accurate. In this paper, we describe the COPTADS system that incorporates these algorithms.

I. INTRODUCTION

According to a 2008 report by the Rand Corporation [5] (available at <http://www.rand.org/news/press/2008/04/17.html>), 20% of US veterans returning from service in Iraq and Afghanistan suffer from Post Traumatic Stress Disorder. Leading military figures consider PTSD to be one of the biggest threats to the US military — for instance, President Obama declared that “We’re working aggressively to address another signature wound of this war, which has led too many fine troops and veterans to take their own lives—Post Traumatic Stress Disorder.” [3] (available at http://www.cbsnews.com/8301-503544_162-20099337-503544.html) Returning military personnel and/or their families often blog about their experiences via a wide variety of web sites such as healmyptsd.com, ptsdwayout.com and Facebook’s Battling Bare group. In this paper, we ask ourselves the question *Is it possible to predict whether a person has PTSD or TBI by a computational analysis of the text in their posts?* If this can be achieved, then this may serve as an early warning system for vets and thus enable early interventions which in turn result in an earlier rehabilitation of these wounded warriors. In order to achieve this task, we have developed the COPTADS (Clinical Online PTSD and TBI Analysis and Detection System). Figure 1 shows the architecture of COPTADS which consists of the following components:

(1) A text stream (e.g. blogs) is fed into an **symptom extraction engine** which automatically extracts from the text, information about the intensity of various psychological signals (e.g. fear, anger, depression). We used the US Army’s PTSD Checklist to identify PTSD symptoms and the Neurobehavioral Symptom Inventory (NSI) to identify symptoms for PTSD.

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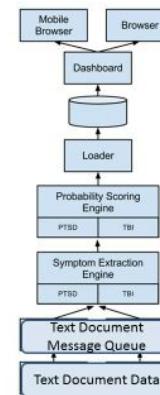


Fig. 1. COPTADS Architecture

(2) Using a body of training data, we developed some **probabilistic scoring algorithms** which includes both algorithms to score the probability that a particular document describes a subject having PTSD/TBI as well as some known classification algorithms to distinguish between blogs where psychologists Ed Rossini and Jeri Morris said symptoms of PTSD/TBI were present. We tested these algorithms against a separate validation data set and found the accuracy of COPTADS in predicting PTSD and TBI to be around 80% for the best algorithms.

(3) COPTADS has both a desktop and a mobile enable version that clinicians can use in order to track the status of their patients.

II. COPTADS ARCHITECTURE

In COPTADS, a collection of documents (e.g. from posts on a military blogging site or elsewhere) can feed documents into a message queue. COPTADS is designed to explicitly support parallelism as the documents in this message queue can be processed by any number of CPUs.

A. Symptom Extraction Engine

A CPU implementing COPTADS’ *symptom extraction engine* can select a document from the queue for processing. Each document is processed for the presence of 14 symptoms for PTSD and 14 symptoms for TBI. These do not implement all of the 17 symptoms in DHCC’s OTSD Checklist or the

21 symptoms in the National Symptom Inventory checklist. Similar checklists have been described in [2], [6], [1]. For example, consider a blog post such as:

Blog Post B1: I'm recently married to an incredible Iraq combat veteran since I've known him the only thing we have dealt with ptsd related is his inability to get a honest hood night normal sleep... Until recently it's all falling apart, he's always angry short tempered doesn't remember things and idk what's going on! He wants to have children and thinks things are fine and he's slowly decreasing in happiness and liveliness I feel like he's falling back into major PTSD symptoms how do you deal with your spouse with PTSD??

Blog post B1 given above is a real blog post with both spelling and grammatical errors. For each symptom s , COPTADS maintains a *positive* word list (PWL) and a *negative* word list (NWL). The PWL list consists of words which, when they occur positively in a sentence (i.e. not negated) support the hypothesis that the symptom exists in the document. For example, in Blog Post 1, the occurrence of “angry” in the post is also in the positive word list for “anger.” On the other hand, “sleep” is in the negative word list for insomnia, meaning that if the post says the person sleeps a lot or sleeps well (i.e. sleep is not negated) then the word “sleep” contra-indicated insomnia. However, in Blog Post 1, “sleep” is negated, so it actually indicates insomnia. COPTADS uses a sophisticated parsing and scoring algorithm to identify positive/negative occurrences of words as well as any adjectives, verbs, and adverbs that may apply to words in the PWL/NWL. These are then carefully combined together. For instance, consider three categories:

The “anger” category. We see that the phrase “...always angry short tempered...” occurs in this blog post. COPTADS searches for words in the “anger” category that appear (in stemmed form) in the above blog post. In the above article, the words stems “anger” (from “angry”) and “short temper” (from “short tempered”) appear in the word list associated with “angry”. Moreover, the polarity of the occurrences of these words is positive (i.e. the sentence does not negate them). COPTADS’s word list assigns a score to the word “angry” (or rather to its stem, “anger”) and to the word “short temper”. Suppose these scores are 0.5 and 0.6, respectively, indicating that the strength of these words implies a degree of belief that a subject being described in blog post B is angry with probability 0.6 (we take the maximum of the two scores). **The “insomnia” category.** If we also consider the “insomnia” category (similarly stemmed), we see that the words “inability to get a honest hood night normal sleep” appear in this blog post – presumably the “hood” in this sentence is mis-spelled and should have been “good”. We do not correct spellings of mis-spelled words in COPTADS. In this sentence “honest hood night sleep” references the word “sleep” which is associated with insomnia when negated. The word inability that precedes sleep in this sentence negates the occurrence of the word sleep. The negated form of sleep may have a score of 0.4, for instance, denoting a 40% probability that this article references lack of sleep in the subject being discussed. **The “memory loss” category** In the same vein, we see the phrase “doesn’t remember” in the blog post, indicating a lack of memory. The word stem “remember” is negated and as a consequence, may have a score of 0.3.



Fig. 2. COPTADS Screenshot showing Symptoms identified in a Blog Post

We do not go through the detailed scoring algorithm for the algorithm used by COPTADS to score emotions - but the above three examples should provide some insight into how this occurs. The emotion scoring algorithms parses the sentences, handles negations in the sentences, and also uses combinations of adverbs, verbs, and adjectives[4] in order to score the intensity of a symptom. For instance, COPTADS would process *I can hardly sleep* using the adverbial minimizer “hardly” to infer lack of sleep. Likewise, *He gets really, really, mad* would compute a score for anger by taking the strong intensifier adverb “really” into account. Thus, the Symptom Extraction Engine uses a sophisticated scoring algorithm to score intensity of a symptom in a sentence. Figure 2 shows a screenshot of how COPTADS identifies symptoms (and their intensity) within a document. A snippet of this blog post shows depression in the very first sentence as well as fear in the sentence starting with “I dread the wrapping process ...”.

The Symptom Extraction Engine populates symptoms into a database called *Sym_DB* with schema (*DocID, Patient, Symptom, Score*) describing the intensity of each symptom. We use *Tuples(p)* to describe the set of tuples in *Sym_DB* with *Patient = p*; *Tuples(d)* denotes the set of tuples in *Sym_DB* with *DocID = d*.

B. Probability Scoring Engine (PSE)

The data contained in the *Sym_DB* contains all symptoms in a document, irrespective of whether those symptoms are indicative of PTSD or TBI. *Sym_DB* is processed on a document by document basis by PSE which populates a database called *Result_DB* having schema (*DocID, Patient, Disease, Score*) where *Disease* is either PTSD or TBI and *Score* is a number between 0 and 1. Each tuple of the *Result_DB* database has the form $(d, p, disease, s)$ saying that the document d about patient p receives a score of s for disease dis . In order to calculate s from d , we must consider *Tuples(d, dis)* which denotes the set of all tuples in the symptom database *Sym_DB* pertinent to disease dis (i.e. referencing symptoms relevant for disease dis).

COPTADS contains 8 different methods to compute s for a given document d and a given disease dis . Due to space constraints, 6 of these methods are briefly described in this section. PSE uses a training set TS of blogs, each of which was read and independently evaluated by two clinical psychologists, Ed Rossini at Roosevelt University and Jeri Morris at Northwestern University. About half the data set was annotated as being positive for PTSD and half was not.

The proportions for TBI were more skewed - a relatively small proportion of blog posts were marked as being indicative of TBI. A separate validation set VS consisted of a set of posts that have also been annotated. In VS , the annotations were unknown to the COPTADS scoring engine which was then used to gauge the accuracy of the PSE. It is important to note that the validation set constitutes a blind sample on which COPTADS' accuracy can be objectively evaluated. The training set included 360 open source documents including blogs, newsgroups and forums known to be popular with US Army personnel and family members. Standard cleanup procedures were applied to remove personal identifying information. Our clinical psychologist members then graded each document as positive or negative for PTSD and TBI. The annotated data set was divided into two equal subsets, with one half being used for training of the models described above, and the other one serving as a validation set.

Messages as Vectors We first note that a message or post m can be considered to be a vector $ptsd(m) = \langle v_1, \dots, v_n \rangle$ where v_i denotes the intensity of PTSD symptom s_i returned by the Symptom Extraction Engine. For the training set TS , let $POS_PTSD(TS) = \{vec(m) | m \in TS \wedge m.ptsd = true\}$ — this is the set of all messages or posts which are marked as being positive for PTSD. In the same vein, let $NEG_PTSD(TS) = \{vec(m) | m \in TS \wedge m.ptsd = false\}$ — this is the set of messages marked as being negative for PTSD. We can define similar sets for TBI. Due to space constraints, we will only present the algorithms for PTSD — the algorithms for TBI are identical, but use symptoms for TBI instead of PTSD.

1) SVM-Based Algorithm: Each message m is a point in an n -dimensional space. A separator line L is a linear (or nonlinear) line that minimizes error, separating the set of n -dimensional points in $POS_PTSD(TS)$ from those in $NEG_PTSD(TS)$. L can be computed using a standard linear or non-linear support vector machine. We assume the line learned by SVM is always an equation of the form $f(s_1, \dots, s_n) = c$ where the s_i 's denote the various symptoms and c is a constant. In the SVM implementation, the set $POS_PTSD(TS)$ mostly lies to one side of the line, i.e. most points in $POS_PTSD(TS)$ will satisfy exactly one of the two constraints: $f(s_1, \dots, s_n) \leq c$ or $f(s_1, \dots, s_n) \geq c$. Without loss of generality, we will assume the former — but the treatment is exactly mirrored if the other case is true. The probability that a message m in the validation set has PTSD is now defined as follows. $\mathbb{P}(m \text{ has PTSD}) =$

$$= \begin{cases} \min(1, \frac{d(vec(m), L)}{\max_{d' \in POS_PTSD(TS)} d(vec(m'), L)}) & \text{if } f(vec(m)) \leq c; \\ 0 & \text{otherwise.} \end{cases}$$

What this says is that if the vector $vec(m)$ associated with the message m falls on the same side of the separator line as the positive instances in the training set, then the probability that a subject (patient) described in message m has PTSD increases linearly with the distance of the person from the separating line. If message m falls on the other side of the line, then the probability is set to 0.

2) KNN-Based Scoring: A second method does not use scoring at all, but uses a k -nearest neighbor style clustering method. Given an integer $k > 0$, we use the following notation:

$$\begin{aligned} NN_1(m) &= \{m' \in TS | (\exists m'' \in TS) \\ &\quad d(vec(m), vec(m'')) < d(vec(m), vec(m'))\}. \end{aligned}$$

Thus, $NN_1(m)$ denotes the set of all immediate nearest neighbors of m . We can inductively define sets:

$$\begin{aligned} NN_j(m) &= \{m' \in TS | (\exists m'' \in TS - \bigcup_{i < j} NN_i(m)) \\ &\quad d(vec(m), vec(m'')) < d(vec(m), vec(m'))\}. \end{aligned}$$

We use the notion of a cumulative nearest neighbor to denote the sets:

$$CNN_j(m) = \bigcup_{i=1}^j NN_i(m).$$

According to the KNN scoring method,

$$\mathbb{P}(m \text{ has PTSD}) = \frac{|CNN_k(m) \cap POS_PTSD(TS)|}{|CNN_k(m)|}$$

3) Weighted Symptom Centered Scoring: A third mechanism to score associates a weight w_i with each symptom s_i . The probability that a message m reflects a subject with PTSD is now computed as follows.

$$\mathbb{P}(m \text{ has PTSD}) = \frac{\sum_{i=1}^n w_i * v_i}{\sum_{i=1}^n w_i}$$

where v_i is the intensity of symptom s_i in message m as described above. Recall that each v_i is a real number in the $[0, 1]$ interval, so this ratio gives us a probability. This raises the question: how can we get these weights. We offer two implementations of this scoring method. (i) *Expert weighting*. In this paradigm, an expert gives us the weight for each symptom. Or alternatively, a set of experts give us weights and the selected weight is either the mean or the median.

(ii) *Learning the weights*. A better approach is to learn the weights from the training set itself as follows by setting

$$w_i = \frac{|\{m \in POS_PTSD(TS) | v_i \geq \mu_i + \sigma_i\}|}{|\{m \in TS | v_i \geq \mu_i + \sigma_i\}|}$$

where μ_i, σ_i respectively denote the mean and standard deviation of the value of symptom s_i computed across all people in the training set. A person is deemed to have the symptom if the intensity he exhibits for that symptom is more than one standard deviation away from the mean. The above weight merely computes the percentage of the population in the training set exhibiting a symptom who have PTSD.

4) 2,3 Symptom Scoring: The 2-symptom scoring method assigns 1 to a document a score if at least two symptoms with a score of 0.6 or more were detected in the document. 3-symptom Similarly, 3-symptom scoring is similarly defined with 3 symptoms.

C. Experiments

We evaluated all 8 of our methods on the validation data set VS . The accuracy of the 4 scoring algorithms shown above is given in the table below using two scoring measures. Let $ALG = \{m | m \in VS \text{ has PTSD according to the algorithm}\}$, $BOTH = \{m | m \text{ has PTSD according to both experts}\}$ and $ONE = \{m | \text{at least one expert says } m \text{ has PTSD}\}$.

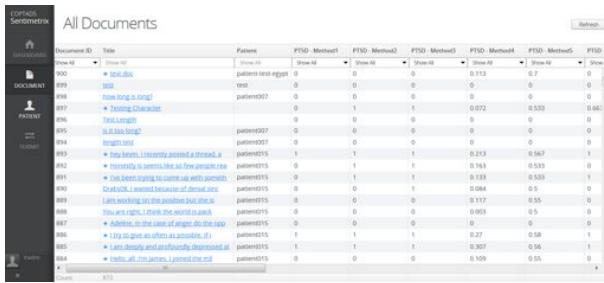


Fig. 3. Main Document Screen (desktop)

$$\begin{aligned}
 Acc1 &= \frac{|ALG \cap BOTH|}{|BOTH|} \\
 Acc2 &= \frac{|ALG \cap ONE|}{|ONE|} \\
 Acc3 &= \frac{TP_1 + TN_1}{P_1 + N_1} \\
 Acc4 &= \frac{TP_2 + TN_2}{P_2 + N_2}
 \end{aligned}$$

where $TP_{i,i}$, P_i , N_i for $i = 1, 2$ denote the number of true positives/negatives when agreement with one or both annotators is considered and P_i, N_i shows total positives/negatives.

The table below shows the accuracy results of our algorithm with respect to both measures for PTSD only – the corresponding numbers for TBI are higher and generally in the 0.90s..

Algorithm	PTSD Acc1	PTSD Acc2	PTSD Acc3	PTSD Acc4
SVM	0.75	0.8	0.75	0.67
KNN	0.72	0.77	0.73	0.65
Equal Wts	0.75	0.73	0.75	0.67
Learned Wts	0.75	0.80	0.75	0.67
2-Symptoms	0.76	0.80	0.76	0.68
3-Symptoms	0.73	0.78	0.73	0.65

These scores show that the SVM based method, the k -nearest neighbor method, and the Weighted Symptom Center Scoring Methods with both equal and learned weights perform very well. While the 2-Symptom and 3-Symptom approaches work well for PTSD, they were less effective in predicting TBI (not shown in table) — but these three algorithms were able to return over 90% accuracy according to these four measures on TBI.

III. DASHBOARD

The COPTADS dashboard supports both desktop and mobile access from smartphones. Figure 3 shows a screenshot of the “Document View” of the main screen showing the title and patient associated with the document. In addition, there is one column for each of the 8 scoring methods implemented in COPTADS for PTSD and 8 columns for TBI.

Figure 4 shows some screenshots of the COPTADS mobile dashboard. Using the COPTADS mobile dashboard, users of smartphones can access COPTADS from their devices (iPAD, iPhone). The dashboard allows clinicians and/or authorized researchers to see blog posts/messages, see information about



Fig. 4. Mobile Dashboard Screens

word usage statistics, view predictions made by COPTADS about whether the person has PTSD or not, and so forth.

IV. CONCLUSION

In this paper, we have presented preliminary results establishing that the automated analysis of emotions expressed in text documents can accurately predict whether the subject of such a message has PTSD/TBI by comparing the predictions with ground truth provided by clinical psychologists. COPTADS is the first system with high accuracy scores (consistently in the 75-80% for PTSD, over 90% for TBI). We have developed multiple algorithms for these predictions, evaluated these algorithms, and determined that 4 of our algorithms - the SVM-based algorithm, the k -nearest neighbor algorithm, and the Weighted Symptom Scoring algorithm all provide highly accurate predictions. Much work remains to be done. For instance, we need to implement all 17 of the symptoms of PTSD on the Army’s PTSD checklist (3 are currently not implemented) and all 21 of the symptoms for TBI on the Neurobehavioral Symptom Inventory for TBI (14 are currently implemented). We expect the implementation of these additional symptoms to lead to greater accuracy.

Acknowledgement. This work was supported by the US Army Medical Research and Materiel Command (USAMRMC) under Grant No. W81XWH-13-C-0030. The views, opinions and/or findings contained in the report or interview are those of Sentimetric and should not be construed as an official Department of the Army position, policy or decision. V.S. Subrahmanian’s work was done as a consultant to Sentimetric.

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LIVE DEMONSTRATIONS

Harnessing patient-reported data to project and visualize disease course

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Abstract

Multiple sclerosis (MS) is a progressive neurological condition with a high degree of variability in presentation. PatientsLikeMe, a patient-powered research network, collects and analyzes patient-reported data from over 220,000 patients, including tens of thousands of MS patients. We aim to help patients understand their condition in the context of their fellow patients. Here we present a prototype online tool for projecting the progression of an individual MS patient, against a backdrop of the PatientsLikeMe MS community.

Introduction

Multiple sclerosis (MS) is a neurological condition caused by inflammatory damage to myelin sheaths encapsulating neurons in the brain, optic nerves, and spinal cord. The disease affects patients in both observable symptoms like walking impairment, which can be measured with timed walking tests, as well as subjective ways like cognitive impairment that are difficult to measure accurately. The most accurate objective measurements of disease involve the quantification of brains lesions using magnetic resonance imaging, but these require extensive resources, are available infrequently, and are often only weakly correlated with patients' experience of the disease. For patients, clinicians, and researchers, measuring MS is a significant challenge.

To cast a different light on this measurement challenge, PatientsLikeMe, an online health platform and forum, developed and validated a Multiple Sclerosis Rating Scale (MSRS)¹, a clinically validated² patient-reported outcome. The aims of this outcome are to allow patients to quantify their level of disability over time in order to facilitate discussions with their healthcare team, identify trends in their progression, and connect with other patients like them to better manage their care.

Measurement and visualization of disease course

Since 2007, PatientsLikeMe has collected over 100,000 MSRS data points from over 20,000 MS patients. In previous work in another neurological disease (amyotrophic lateral sclerosis, ALS), we used a large dataset to build models comparing patients' disease progressions, to assess the impact of putative drug effects³. Here, we present the continuation and expansion of this work to develop an interactive tool to help MS patients understand their disease progression and its variability, in the context of their fellow patients' experience. Figure 1 shows a snapshot of the prototype visualization.



Figure 1. Visualization of the disease course of a de-identified multiple sclerosis patient.

The model underlying the visualization is a linear regression with explanatory variables: gender, time since disease onset, latest MSRS score, age at disease onset, and disease subtype. While the predictive power of the model (or really any current model of MS) is limited, the framework nonetheless provides a concrete basis for helping patients, clinicians, and researchers quantify the uncertainty of disease progression.

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Introduction

The widespread introduction of Electronic Health Record (EHR) systems has revolutionized the ability of clinicians, support staff, healthcare payers, and managers to track, understand, and act on patient and clinical conditions and outcomes. However, healthcare outcomes and the success of initiatives meant to improve them remain inextricably bound to the adoption of effective clinical workflows and the proper use of electronic tools, both of which are difficult to measure using standard EHR indicators. Arcadia Healthcare Solutions has added a visualization to its analytics suite that will permit clinicians, administrators, and managers to easily view and investigate clinical workflows and behaviors using HIPAA-mandated audit tracking built into their EHR systems. And, because Arcadia's Analytic Platform already integrates multiple healthcare systems, activity can be visualized along multiple dimensions, allowing viewers to directly infer clinical workflows and practices, and to associate clinical activity with patient outcomes and operational indicators. With this information, participants in the healthcare ecosystem at all levels can play a role in improving clinical effectiveness, increasing patient and provider satisfaction, reducing medical costs, and improving patient outcomes.

Visualization

A Day in the Life was born from a simple request our clinical consultants heard from a physician in a large hospital system: "If only management could spend a day in my shoes, and see what I have to go through..." By tapping deep into the EHR systems, we can come pretty close.

Arcadia developed a tool to present a "day in the life" for providers and care teams, visualizing even the smallest activities captured in the EHR into an easily consumable timeline. The tool permits the user to flip quickly through multiple providers and compare their workflows, EHR usage habits, and support staff role alignment, answering the following questions:

- Which care teams are not distributing work to support staff?
- Who is staying up late documenting the day's visits?
- Which providers are consistently falling behind on their schedules?

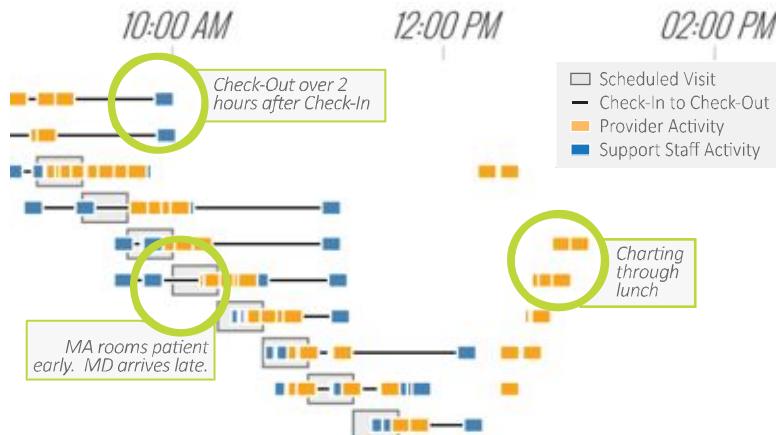


Figure 1: Detailed View of Provider/Care Team EHR Activity

A Day In The Life: Visualizing Clinical Workflows

2013 Workshop on Visual Analytics in Healthcare

For example, a view of our physician's day (**Figure 2**) reveals some obvious and not-so-obvious features of Dr. X's workflow. Let's map it out:

1. On January 24, 2013, Dr. X has 19 scheduled appointments; the user can learn about specific patients and encounters simply by hovering over an appointment (**Figure 3**).
2. Dr. X's care team uses a morning huddle to prospectively plan for the day's patients
3. After 11am, Dr. X begins to fall behind, with appointments starting after the designated windows
4. By working through the lunch break, Dr. X is able to catch up
5. Dr. X spends 2½ hours after dinner closing out charts



Figure 2: A Full-Day View for a specific provider

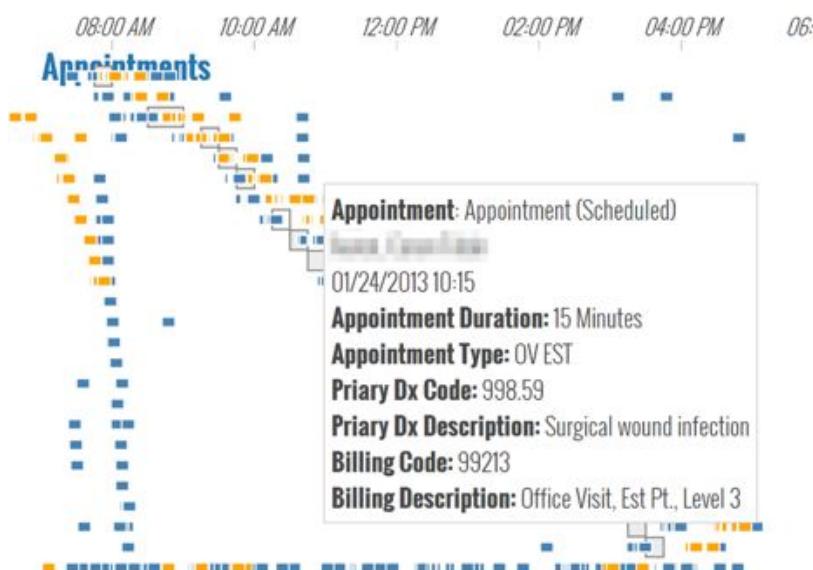


Figure 3: Hovering over an appointment reveals more details about the visit and documentation activities.

A second view that emphasizes specific workflow elements (**Figure 4**) reveals additional insights. We see that Dr. X is personally performing many EHR actions that could be performed by another care team member. By transferring these responsibilities to a medical assistant, Dr. X would gain precious additional minutes, which could be used to expand patient interactions, improve inter-appointment preparations, or reduce appointment delays. Such information may also reveal use (or lack thereof) of EHR resources. Dr. X had recently participated in a retraining on using medical history information. We can confirm that Dr. X is using these skills in the clinical setting, repeatedly employing medical history resources within the EHR.



Figure 4: EHR Activity for a Single Physician and Associated Support Staff

Conclusions

Effective visualization of clinical activity through EHR systems can provide useful insights into clinical workflows as they actually happen. This visual information is easy to interpret and can be used at multiple levels of practice to identify best practices and opportunities for improvement. Integration of EHR audit tracking with other systems – clinical measures, claims, prescriptions, HR, etc. – allows users to explore a day in the healthcare setting from any number of perspectives, and spend a virtual day in the clinician's shoes.

Presenters

- **Nick Stepro** – Product Manager, Analytics, Arcadia Healthcare Solutions, Burlington, MA
- **Michael Simon** – Principal Data Scientist, Analytics, Arcadia Healthcare Solutions, Burlington, MA

Demonstration of Visualization of EHR and Health Related Data for Information Discovery

David Borland¹

Vivian West²

W. Ed Hammond²

¹ Renaissance Computing Institute, The University of North Carolina at Chapel Hill

²Duke Center for Health Informatics, Duke University

Introduction

In this demonstration we present research we are conducting in response to a program announcement solicited by the Assistant Secretary of Defense for Health Affairs, Defense Health Program. We have developed visualization prototypes for multivariate heterogeneous data along with visualizations of retrospective data queries from DEDUCE, an electronic health record (EHR) query tool developed at Duke University.

Our current approach involves incorporating data queries of Duke's EHR system to help identify what data elements are used in queries and classify them according to what types of information users were seeking (e.g. queries searching for outcomes, or outliers of treatment methods). Eventually groups of related data elements will be incorporated into a visualization that allows a quick comparison of the data from a large population with the ability to view trends over time within a chosen measure.

Methods

We have developed two interactive visualization prototypes, one a radial coordinates visualization (Figure 1, left) based on parallel coordinates techniques, and one a force-directed node-and-link network visualization (Figure 1, right). Our radial coordinates visualization is a multivariate visualization suitable for heterogeneous data that incorporates multiple supplemental scatterplots, direct visualization of axis correlations, and a novel technique for spreading lines to enable improved visualization of individual lines and line clusters. Our force-directed network visualization enables the interactive selection of nodes to see relationships between groups of nodes.

In our demonstration we will show how various relationships in the data are reinforced between the two views, and how different visualizations can be more adept at showing different relationships in the data. We will also apply these visualization techniques to publicly available EHR data from the NHS.

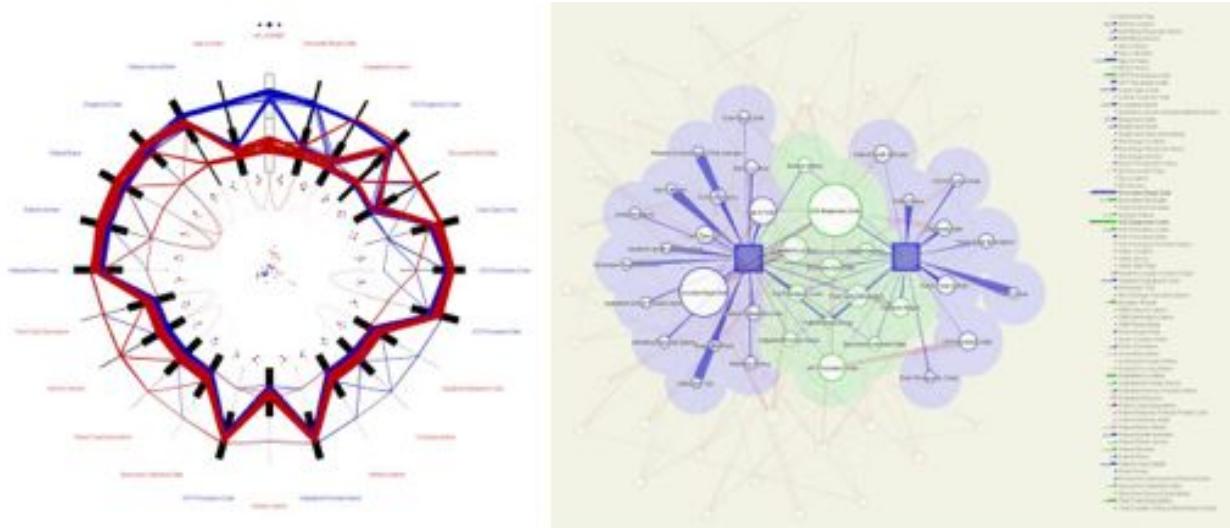


Figure 1: Radial coordinates (left) and force-directed network (right) visualizations of the same EHR query data

Acknowledgements

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Demonstration #4

Visualizing the Overview of Temporal Patterns of Patients' Activities

Kazuo Misue, Yuta Kanai, and Hideaki Takagi University of Tsukuba, Tsukuba, Japan

Abstract:

It is necessary to determine patients' activities for effective management in hospitals and affiliated regional medical institutions. The purpose of this study is to support the identification of features from temporal patterns of patients' activities using information visualization. This paper introduces a technique called "ChronoView" for visualizing temporal patterns. ChronoView provides an overview of many temporal patterns and enables us to easily determine the similarity and anomaly of temporal patterns. In order to illustrate a use case, temporal patterns of patients' activities were extracted from an actual data set of patients of the University of Tsukuba Hospital. This paper reports some features of the temporal patterns identified using ChronoView.

Demonstration #5

Visual Exploration of Common Behaviors for Developmental Health

Yi Han, Agata Rozga, John Stasko and Gregory D. Abowd

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Abstract:

Detecting early signs of developmental issues in a child is critical for successful interventions. Using behavior capture technologies such as video cameras, microphones and wearable sensors, it is increasingly possible to record and analyze human behavior in unprecedented detail. However, the analysis of such rich and complex dataset poses new challenges for developmental psychologists. We present the initial design of a visualization tool aimed at supporting the exploration of digitally captured behavioral data for studying developmental health.

Demonstration #6

Visualizing Patterns of Social and Communicative Behavior in Children Using Plexlines

John Lee, Sanny Lin, Karrie Karahalios

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Abstract:

We present a system to visualize the annotations of videos of children engaged in a 3–5 minute interactive protocol that assesses communicative behavior, the Rapid ABC. Rapid ABC session videos are annotated to capture the child’s gestures, gaze, and vocalization — important developmental indicators for a young child. From these annotations, we create a graphical fingerprint for each session. In doing so, we introduce Plexlines, a technique for visualizing multiple types of information layered compactly as timelines. Our tool highlights points of interest to probe Rapid ABC sessions that require more attention. Early feedback suggests this system has potential as a tool for communicating developmental concerns to parents and as a training tool for clinicians.

Demonstration #7

VisXplore: Flexible Visualization System for Analyzing Complex Clinical Datasets

Filip Dabek¹ and Jesus J Caban²

¹ University of Maryland, UMBC ²National Intrepid Center of Excellence (NICoE),
Walter Reed Bethesda

Abstract:

Assessing, exploring, and analyzing large amount of heterogeneous clinical data are some of the key challenges faced by researchers and clinicians interested in identifying complex clinical patterns. Flexible visualization systems capable of loading different data types and performing individual statistical analysis have the potential of impacting the way clinical datasets are analyzed. This paper introduces VisXplore -- a clinical data visualization system that has been designed to perform group or single-subject analysis of multivariate tabular, hierarchical, or temporal clinical data. The visualization system has been developed as a robust, flexible, and easy-to-use application that can be used by either researchers or clinicians. The framework has been tested with different clinical datasets including a dataset of patients diagnosed with post-traumatic stress disorder (PTSD) and complex comorbid conditions.

Demonstration #8

Temporal Search and Replace: A Graphic-Based Solution to Temporal Event Data Wrangling and Incremental Querying

Megan Monroe, Rongjian Lan, Hanseung Lee, Allan Fong, Catherine Plaisant, PhD, Seth Powsner, MD, Ben Shneiderman, PhD

University of Maryland, College Park, MD

Abstract:

Temporal event data is the essence of Electronic Health Records (EHRs), detailing for each patient a history of what happened and when. From this data, clinical researchers try to identify meaningful patterns of events: medication combinations, treatment side effects, disease symptoms, etc. However, these events are rarely recorded to suit the needs of any one study, requiring researchers to modify their datasets to better capture the events of interest. Command-based and spreadsheet-based tools are difficult to learn, and are notoriously ill-suited to manipulating temporal event data. We introduce a graphic-based interface that employs the familiar concept of “search and replace” to help researchers identify and modify event patterns of interest. The Search and Replace interface was used by multiple clinical research groups to facilitate both data wrangling and query construction.

Demonstration #9

Visualizing Patterns of Drug Prescriptions with EventFlow: A Pilot Study of Asthma Medications in the Military Health System

Tamra E Meyer¹, PhD, Megan Monroe², Catherine Plaisant, PhD², Rongjian Lan², Krist Wongsuphasawat², PhD; Col. Trinka S Coster, MD¹, Sigfried Gold³, Jeff Millstein⁴, PhD, Ben Shneiderman, PhD²

¹ US Army, Office of the Surgeon General, Pharmacovigilance Center, Falls Church, VA;

² University of Maryland, College Park, MD; ³ Social & Scientific Systems, Silver Spring, MD, ⁴ Oracle Health Sciences, Burlington, MA

Abstract:

The Food and Drug Administration and Department of Defense were interested in detecting sub-optimal use of long-acting beta-agonists (LABAs) in asthmatics within the Military Health System (MHS). Visualizing the patterns of asthma medication use surrounding a LABA prescription is a quick way to detect possible sub-optimal use for further evaluation. Analysis of 100 asthma patients was conducted in EventFlow to display and summarize time- point and interval data. Epidemiologists reported that EventFlow was a powerful tool for rapidly visualizing possible patterns of sub-optimal LABA use that can be targeted for intervention.

Demonstration #10

Topic Modeling and Network Visualization to Explore Patient Experiences

Annie T. Chen and Laura Sheble

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Abstract:

Online support groups and health-related social networking sites can be powerful ways for patients to connect with each other and seek ways to improve their health. This content can also help clinicians and scientists understand patient experience and unmet needs. However, it can be difficult to navigate and make sense of the large volume of content. This paper proposes and demonstrates techniques that may be used to visualize topics in online health discussions. Topic modeling in conjunction with network visualization can effectively provide overviews and segmenting data. Decisions made during this process affect how content is represented and therefore, interpreted. We present a case study of a lightweight approach to model health discussion content from PatientsLikeMe using open source tools. Implications of differing representations, possibilities for extending this approach, and potential use scenarios are discussed.

Keywords—topic modeling; network visualization; patient experience; online discussion forums; sleep

Demonstration #11

A research pipeline of information extraction for visualization of narrative clinical reports on a timeline

Jianlin Shi, MD¹, Ruth Reeves, PhD², Edna Shenvi, MD³, Melissa Sharp, BA⁴, Robert El-Kareh, MD, MS, MPH³, Zia Agha, MD, MS^{3,5}, Yunan Chen, MD, PhD⁶, Wendy W. Chapman, PhD¹

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Abstract:

Selecting adequate information to be visualized is essential for clinical information visualization design. Through this preliminary study, we propose a research pipeline that could be feasible to identify the most useful information from clinical notes for display on a timeline.

Demonstration #12

COPTADS: Clinical Online PTSD and TBI Analysis and Detection System

Steven Banaszak, Vadim Kagan, Andrew Stevens, and V.S. Subrahmanian

Sentimetric, Inc.
Bethesda, MD

Abstract:

housands of US soldiers returning from the long wars in Iraq and Afghanistan have been diagnosed with symptoms of Post Traumatic Stress Disorder (PTSD) and Traumatic Brain Injury (TBI). Family members of many of these vets (or the vets themselves) post blogs of varying length on online web sites intended to support them. In this paper, we ask ourselves the question: Is it possible to perform a detailed analysis of the emotions expressed in the text so that subjects of such blog posts suffering from either PTSD or TBI can be identified accurately. We developed algorithms to extract emotional signals from text and algorithms to predict whether a person with a given set of emotion signal intensities has PTSD or not. Our PTSD prediction algorithms are about 80% accurate while our TBI prediction algorithms are over 90% accurate. In this paper, we describe the COPTADS system that incorporates these algorithms.

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Gamache, Roland	Indiana University - Purdue University Indianapolis	66,75,77
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Han, Yi	Georgia Institute of Technology	15,98
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Krishnan, Anand	Indiana University - Purdue University Indianapolis	66,75,77
Lan, Rongjian	University of Maryland	47,55,101,102
Lee, Hanseung	University of Maryland	47,101
Lee, John	University of Illinois at Urbana Champaign	28,99
Li, Ning	the Research Institute at Nationwide Children's Hospital	68
Lin, Sanny	University of Illinois at Urbana Champaign	28,99
Mane, Ketan	Renaissance Computing Institute (RENCI), University of North Carolina, Chapel Hill, NC	19
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Minty, Evan	University of Calgary, Stanford University	82
Misue, Kazuo	University of Tsukuba	11,97
Monroe, Megan	University of Maryland	47,55,101,102
Mostafa, Javed	School of Information and Library Science, University of North Carolina, Chapel Hill, NC	19
Nguyen, Thanh	Indiana University	66,75,77
Palakal, Mathew	Indiana University - Purdue University Indianapolis	66,75,77
Pietrowicz, Mary	University of Illinois at Urbana-Champaign	23
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Plaisant, Catherine	University of Maryland	47,55,101,102
Powsner, Seth	Yale Medical School	47,101
Ray, William	the Research Institute at Nationwide Children's Hospital	68
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Rozga, Agata	Georgia Institute of Technology	15,98
Sharp, Melissa	Tharp Consulting, Pittsburgh	72,104
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Shenvi, Edna	Division of Biomedical Informatics, UCSD	72,104
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Stevens, Andrew	SentiMetrix, Inc	86,105
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Takagi, Hideaki	University of Tsukuba	11,97
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West, Vivian	Duke University	33,96
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Wongsuphasawat, Krist	University of Maryland	55,102
Xia, Yuni	Indiana University - Purdue University Indianapolis	66,75,77
Xie, Mengjun	University of Arkansas at Little Rock	60
Yergens, Dean	University of Calgary	82
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