Directional Scan Path Characterization of Eye Tracking Sequences: A Multi-Scale Approach

Michael P. McGuire
Department of Computer and
Information Sciences
Towson University
Towson, Maryland 21252
Email: mmcguire@towson.edu

Joyram Chakraborty
Department of Computer and
Information Sciences
Towson University
Towson, Maryland 21252
Email: jchakraborty@towson.edu

***Abstract*—Historically, eye tracking systems have been a very useful tool for finding salient regions in interfaces that naturally attract the visual attention of users. Scan paths are created as the eye moves from one salient region to another. Research has shown that a relationship exists between scan path direction and cognitive load when navigating a user interface. The analysis of scan paths during interface navigation can therefore indicate specific user tendences that could give insight into the cognitive load required to navigate an interface. Thus far, the analysis of the scan paths has largely focused on measuring scan path similarity or analyzing scan paths and their relationship to a predetermined AOI sequence. The focus of this paper is the characterization of eye tracking results based on the analysis of scan path sequences. The proposed approach summarizes scan paths at a macroscale associated with the overall navigation of an interface and a microscale paths associated with saccades that occur within fixations. The approach uses nearest neighbor search and density-based clustering to differentiate between the macroscale and microscale. A directional sequence encoding technique based on the saccade angle is then applied at each level. Finally, frequent sequence mining is used to find frequent scan paths at both scales. Empirical results show that the resulting set of frequent sequences offer an interesting summary of summarize the users scan path for an eye tracking session and can be used to indicate information seeking tendencies of users and characterizes visual search patterns.**

Keywords*—*eye tracking; scan path characterization; sequence mining; multi-scale

I. Introduction

The analysis of eye tracking data has been widely used to understand how users visually process information [1]. Advances in eye tracking technology and reduced equipment costs have made eye tracking data more ubiquitous in marketing and HCI research. As a result, the volume of eye tracking data has increased significantly. Current methods of analyzing gaze patterns in eye tracking data either require visual analysis or are not scalable to large datasets. As a result, there is a growing need for methods that offer a summary of a set of user's gaze patterns during an eye tracking session.

It has long been known that a relationship exists between eye movements and the internal processing of a visual scene [2]. Furthermore, the pattern of fixation locations directly reflect the visual scene [3]. The analysis of scan path sequences has yielded interesting results where frequent scan path patterns are found over a known set of areas of interest (AOIs) showing similarities in user's visual processing of a computer interface [4], [5], [6], [7]. These studies largely focus on eye movements between fixations where the sequence labels represent a particular AOI. Because of this, the resulting sequences account for large eye movements between fixation locations. Scan patterns can occur at smaller scales. For example, it has been suggested that microsaccades, or small eye movements within a fixation, are important factors in visual processing [8]. Thus, there is a need to analyze scan paths at multiple scales. Furthermore, recent findings suggest that there is a relationship between scan path direction and increased cognitive processing when the scan path is to the right [9]. With this in mind, summarizing scan path direction can offer interesting insights regarding the cognitive load for a given visualization task.

The objective of this paper is to develop a method to automatically characterize frequent scan path sequences at multiple scales based on the direction of eye movements. In this approach, the data is divided into two scales including the macroscale, which encompasses the entire viewing area of an interface, and the microscale, which incorporates eye movements within individual fixations. The approach first separates movements between fixation points into the macro and micro scales using density-based clustering. Then each eye movement is encoded based on the saccade angle which is the angle on the Euclidean plane between two gaze points. Movements between fixation points are then given a sequence code based on the four cardinal directions. Finally, frequent sequence mining is used to find interesting patterns in the resulting macro and microsequences. The approach is then tested on data from an eye tracking experiment focused on the analysis of information foraging behaviors using two news web interfaces. Interesting patterns were found at both the macro and micro scales. The rest of the paper is ordered as follows: In Section II literature related to this research is presented. Section III formally presents the approach. Section IV presents the experimental results. Finally, Section V discusses the results and offers some concluding remarks including a discussion of future research directions.

II. Related Work

The literature most related to this paper focuses on applying sequence analysis methods to a series of fixations. For example, time delay embedding and recurrence analysis have been used to provide quantification and visualization of frequent fixation sequences [5]. Transitions between fixation AOIs have been modeled as Markov chains where Shannon's entropy is computed to quantify the distribution of attention across a set of AOIs [6]. This measurement is then used to analyze differences of individuals viewing a set of classical art paintings. Finally, frequent pattern analysis has been used to find frequent sequences of eye tracking data as related to predetermined AOIs in interactive visualizations [7]. In this approach, AOIs are given labels that represent their location on the screen. Then, sequences are create based on the order of fixations on each AOI and a statistical analysis of sequence frequency metrics showed significant differences in gaze behavior based on the visualization task.

Significant research has been carried out in scan path comparison which is typically based on a string representation of a scan path over a series of fixations. Proposed methods largely vary in a number of ways including, how fixations are identified, the method used for creating a string representation of the scan path, the method used for measuring scan path similarity, and the method for presenting the results. Some approaches automatically generate a set of AOIs for comparison. For example, image analysis techniques have been used to automatically identify regions of interest AOIs in a set images. Then, k-means clustering was used to identify AOIs in eye tracking results based on the same set of images. Sequences were then created based on the set of generated AOIs and string editing was used to analyze similarity between the automatically generated AOIs and AOIs generated from eye tracking results [10]. West et al. [2006] also focus on comparing scan paths across a sequence of fixation locations. They present a software system that is designed to identify patterns and similarity in saccade sequences. Instead fo string editing, they use the Needleman-Wunsch algorithm which is used in gene sequence alignment [11]. In Duchowski et al. [2010] the mean shift algorithm is used to automatically generate fixations from eye tracking data. Elipses of the clusters were then created using PCA. The resulting elipses were then intersected to find spatial overlap in cluster locations. A kd-tree was built to provide fast nearest neighbor search. Scan paths were then labeled based on cluster overlap and a temporal overlap parameter. Then Levenshtein's string similarity metric and Y matrices were used to analyze scan path similarity [12].

Scan path comparison is also useful when analyzing user's scan paths over a known set of AOIs. For this purpose, string edit similarity has been combined with linear distance to compare scan paths[13]. Cristino et al. [2010] also focused on fixations across a known set of AOIs. This approach included temporal binning in the generation of fixation sequences where the sequence label for a fixation was repeated in the resulting sequence based the length of time spent at the fixation and used the Needleman-Wunsch algorithm for scan path alignment [14]. The idea of sequence similarity has also been used to test the similarity between a known sequence pattern based on a series of AOIs to estimate the effectiveness of interactive mapping interfaces [4]. In this research both transition probabilities are used to quantify the transition from one AOI to the next by different types of users. Also, the Needleman-Wunch sequence alignment and Levenshtein distance were used to analyze scan path similarity between users. MultiMatch [15] uses a number of dimensions including shape, length, direction, position, and duration to compare scan paths. The work presented in this paper is motivated by this approach where we focus on the dimensions of scan path distance and scan path direction to summarize a sequence of scan paths exhibited during an information foraging task.

Scan path comparison has been extended to handle dynamic scenes by combining image analysis, object tracking, and sequence comparison [16]. Then, in a follow up paper, Kübler, Kasneci, and Rosenstiel [2014] propose the SubsMatch algorithm where the SAX algorithm is used to encode sequences based on fixation distance. Substrings are stored in a hash table and the difference between the substring tables is used to calculate sequence similarity [17].

Another related field of research to this paper is the use of visual analytics techniques to analyze eye tracking data. Using visual analytics allows the user to interact with the eye tracking results while applying various machine learning algorithms and visualization techniques. One such approach uses the space-time cube to visualize the spatio-temporal pattern of gaze data to visually compare the similarity of scan paths[18]. Eye tracking analysis has also been decomposed into a number of visualization tasks and visualization tools have been recommended to support each task [19]. This work is extended by using a prototype system that allows users to efficiently visually analyze eye tracking data [20]. Finally, saccade plots can be used for visualizing heat maps and saccades over time [21]

The approach proposed in this paper builds on the existing literature and offers a number of unique contributions. First, many of the above approaches use distance-based clustering to identify fixation locations. In this paper, density-based clustering is used where time is included as a dimension in the clustering so that fixation locations are time dependent. Thus far research in scan path sequence analysis has created sequences using labels associated with fixations or AOIs. In this approach, the saccade angle is used to encode sequences that are based on the direction of the scan path. Another novel contribution of this paper is the analysis of scan paths at the macroscale and microscale where we can summarize scan paths that encompass an entire scene or interface as well as scan paths that occur within an individual fixation. Finally, we offer two approaches for mining frequent sequences where for macrosequences we propose an algorithm that finds the top-k frequent subsequences and for mining frequent microsequences we use a modified algorithm that is based on general sequential pattern (GSP)[22].

III. Methods

A. Preliminaries and Problem Statement

Given an ordered set of gaze points $P = \{p_1, p_2, ..., p_n\}$ where each $p_i \in P$ consists of a tuple (x_i, y_i, t_i) where x and y are coordinates in Euclidean space that represent the spatial location of the gaze point on the computer screen and t_i is a time stamp where each gaze point is in sequential order such that $t_1 < t_2 < \cdots < t_n$.

The spatial coordinates of two sequential gaze points form a line that represents the movement of the eyes from one area of the screen to another. This movement from one gaze point to another is typically referred to as a saccade. More formally, a saccade can be defined as follows:

Definition 1 (saccade): Given an ordered set of gaze points $P = \{p_1, p_2, ..., p_n\}$ a saccade between any two sequential gaze points p_q and p_r is defined by the line connecting the spatial coordinates (x_p, y_p) and (x_q, y_q) for each gaze point.

Therefore, a saccade exists between each adjacent gaze point in P forming a set of saccades $S = \{s_1, s_2, ..., s_m\}$. For the purposes of this paper, each saccade is characterized by the saccade distance and saccade angle. The saccade distance is the spatial distance between two sequential gaze points defined as follows:

Definition 2 (saccade distance): Given a saccade consisting of the line connecting the spatial coordinates, (x_p, y_p) and (x_q, y_q), of two sequential gaze points p_q and p_r the saccade distance sd is the Euclidean distance between p_q and p_r given by the following equation:

$$sd = \sqrt{(x_p - x_q)^2 + (y_p - y_q)^2} \qquad (1)$$

The saccade angle is the angle of the straight line formed by a saccade between two gaze points and is defined as follows:

Definition 3 (saccade angle): Given a saccade consisting of the line connecting the spatial coordinates, (x_p, y_p) and (x_q, y_q), of two sequential gaze points p_q and p_r the saccade angle sa is the angle of the straight line between p_q and p_r. The angle is calculated as the arc tangent between the difference of the spatial coordinates (x_p, y_p) and (x_q, y_q) and is given by the following function:

$$sa = \arctan(x_p - x_q, y_p - y_q) \qquad (2)$$

The resulting value for sa is thus a value between -180° and 180°

Problem Statement: Given the above measurements of human eye movements, the overall objective of this approach is to determine the saccade patterns that exist at two spatial scales. The first of which, consists of holistic patterns resulting from cognitive processing of an interface. The second consits of eye movement patterns within local salient regions of an interface. To do this, a method is needed to distill the spatial characteristics of each saccade including the sd and sa measurements into meaningful sequences at the two previously mentioned spatial scales. Then, the objective is to find frequent sequences at each spatial scale and to relate the frequent saccade patterns to user tendencies and interface design.

B. ~~*Approach and Algorithms*~~

An overview of the approach is presented in Figure 1. In the first two steps of the approach, k-nearest neighbor search and density-based clustering are used to differentiate between macro points which represent scan paths that are used to navigate the interface and micro points which represent scan paths within salient regions of the interface. Then directional sequence encoding is applied where the saccades between micro and macro points are converted to a character string sequence based on their saccade angle measurement. The resulting macrosequence and microsequences are then mined for frequent patterns. A top-k approach is used to find frequent macrosequences where candidate subsequences are drawn from the macrosequence itself. Each candidate is then counted and the top-k sequences are selected for inspection. Frequent microsequences are then mined using an apriori-like algorithm that treats each microsequence as a transaction and each subsequence as a possible item. The rest of this section formally explains the approach where Section III-B2 presents the directional sequence encoding algorithm, Section, III-B3 presents the mining of top-k frequent macrosequences, and Section III-C1 presents the mining of frequent microsequences.

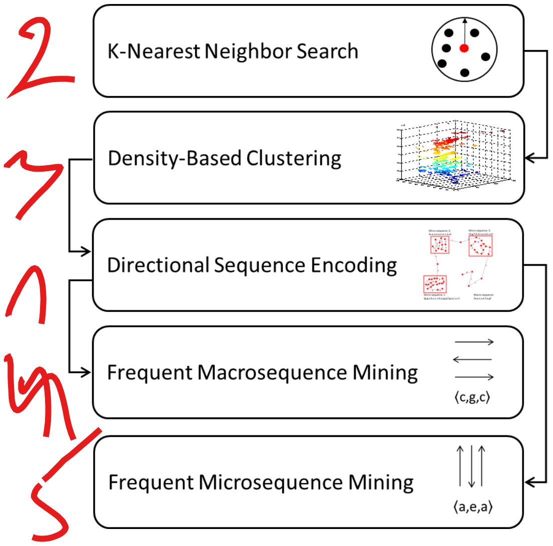

2
K-Nearest Neighbor Search
3
Density-Based Clustering
7
Directional Sequence Encoding
4
Frequent Macrosequence Mining
⟨c,g,c⟩
5
Frequent Microsequence Mining
⟨a,e,a⟩

Fig. 1. Overview of Approach

1) Creation of Macro Gaze Points and Micro Gaze Points: The first step in the approach is to divide gaze points into macro gaze points and micro gaze points. Macro gaze points are associated with a more general scanning of the interface to look for areas that deserve closer inspection to solve a given information seeking task. Micro gaze points represent fixations where a user focuses on an individual object such as a piece of text or a component of a visualization.

The well-known density-based clustering algorithm DBSCAN [23] is used to determine dense areas of gaze points in time. Because we are concerned with the sequence of saccades over time, density-based clustering is applied on the values $(x_i, y_i, t_i) \forall p_i \in P$. The time stamps are included in the clustering so that we can differentiate between spatially overlapping sets of points that may be separated by a considerable amount of time. Because of this, we first normalize P using min-max normalization. The DBSCAN algorithm partitions points based on their density in space using two parameters. The first, ϵ,represents distance within which a set of points is considered to be within the same neighborhood and the second, $minpts$, represents the minimum number of gaze points to create a density based cluster. Micro gaze points P_{micro} are then the gaze points that belong to the density-based clusters C. This results in a set of micro gaze points $P^C_{micro} = \{P^{c1}_{micro}, ..., P^{ck}_{micro}\}$. Macro gaze points P_{macro} are then formed by calculating the spatio-temporal center C_{center} of each density-based cluster $c_k \in C$.

It is conceivable that saliency might vary across interfaces and therefore, to make the algorithm generalizable, the ϵ parameter value might vary between different interfaces. Because of this, ϵ is estimated by using k-nearest neighbor search to calculate the average distance between adjacent points. In this step, a kd-tree [24] is built, then using the kd-tree the average distance between each point and it's k-nearest neighbors is calculated. A histogram is created over the resulting distance values and ϵ is set to the center value of the largest histogram bin.

2) Directional Sequence Encoding: The first objective of the approach is to distill the spatial characteristics of each saccade into a set of discrete values to represent the movement patterns represented by each saccade. To do this, a directional sequence encoding scheme was divised based on the sa measurement for each saccade. Each saccade is classified based on its sa measurement and each saccade is assigned an alphabetic character from a - d. A more formal definition of the directional sequence encoding is as follows:

Definition 4 (directional sequence encoding): Given a set of saccades $S = \{s_1, s_2, ..., s_m\}$ where each $s_j \in S$ is characterized by a saccade angle sa and a saccade distance sd, the directional sequence encoding (dse) is based on a threshold function applied on the sa values for each $s_j \in S$ such that:

$$dse(sa) = \begin{cases} a, & if \quad 135^\circ > sa >= 45^\circ \\ b, & if \quad 45^\circ > sa >= -45^\circ \\ c, & if \quad -135^\circ > sa >= -45^\circ \\ d, & if \quad 135^\circ > sa >= -135^\circ \end{cases}$$

An illustration of this classification scheme is shown in Figure 2. A parallel can be drawn between the directional sequence encoding and the four cardinal directions where ”‘a”’ corresponds to north, ”‘b”’ corresponds to east, ”‘c”’ south, and ”‘d”’ corresponds to south.

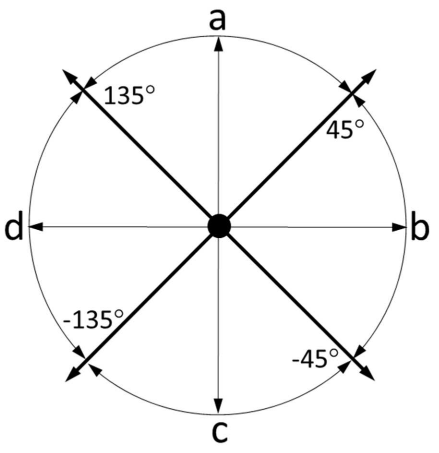


Fig. 2. Directional sequence encoding of eye tracking saccades

The directional sequence encoding is the basis for encoding sequences and finding patterns at both the interface-wide and local scales. Interface-wide sequences or macrosequences are saccades that are typically associated with more a more general scanning of the interface to look for areas that deserve closer inspection to solve a given information seeking task. Local sequences or microsequences correspond to small areas of interest where a user focuses on an individual object such as a piece of text or a component of a visualization. To distinguish between saccades associated with macrosequences and saccades associated with microsequences, a threshold λ is applied to the saccade distance sd for each $s_j \in S$. With this in mind, a macrosequence is formally defined as follows:

Definition 5 (Macrosequence): Given a set of saccades $S = \{s_1, s_2, ..., s_m\}$ where each $s_j \in S$ is characterized by a saccade angle sa, a saccade distance sd, and a directional sequence encoding dse, a macrosequence $\mathcal{MA} \subset S$ is composed of dse values $\forall s_j \in S$ where $sd >= \lambda$ such that $\mathcal{MA} = \{dse_1^{ma}, dse_2^{ma}, ..., dse_r^{ma}\}$.

Given this definition, a macrosequence is then defined as follows:

Definition 6 (Microsequence): Given a set of saccades $S = \{s_1, s_2, ..., s_m\}$ where each $s_j \in S$ is characterized by a saccade angle sa, a saccade distance sd, and a directional sequence encoding dse, a microsequence $\mathcal{MI} \subset S$ is composed of dse values $\forall s_j \in S$ where $sd < \lambda$ such that $\mathcal{MI} = \left\{dse_1^{mi}, dse_2^{mi}, ..., dse_s^{mi}\right\}$ and any set of gaze points can contain a set of microsequences $\mathcal{MP}$ such that $\mathcal{MP} = \{\mathcal{MI}_1, \mathcal{MI}_2, ..., \mathcal{MI}_t\}$.

Figure 3 depicts an example of a set of saccades that are characterized by a single macrosequence and three microsequences. In this example, each microsequence exhibits a different saccade pattern. For example, microsequence 1 exhibits a vertical saccade pattern and consists of the sequence ⟨c, a, c, a, a, c, c, b, a, a⟩. In this sequence we can see that sequence ⟨a, a⟩ and sequence ⟨c, a⟩ repeat twice. microsequence 2 consists of the sequence ⟨b, d, c, c, c, b, a, a, c, c, c⟩ and shows a more vertical saccade pattern. Then, microsequence 3 consisting of the sequence ⟨b, b, b, a, d, d, d, d, a, b ,b, b, b, b, b, d, d⟩ shows a saccade pattern that is circular in nature. The three microsequences are nested in a macrosequence ⟨b, c⟩ which also shows a more circular saccade pattern.

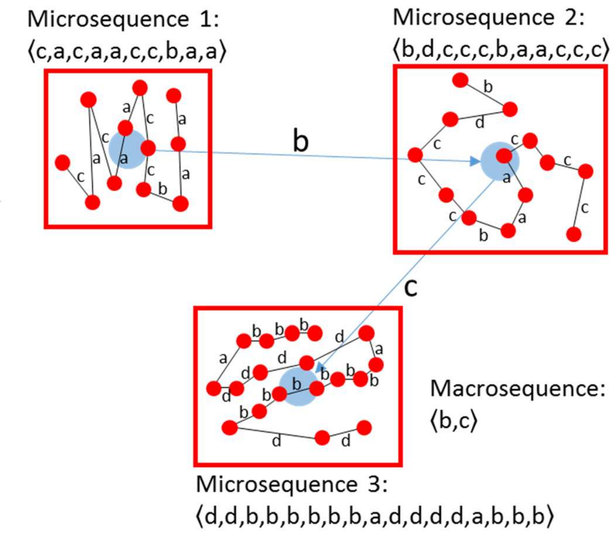


Fig. 3. Illustration of a Macrosequence and Associated Microsequences

The algorithm for creating the multi-level directional sequence encoding is shown in Algorithm 1. The input to the algorithm is a set of gaze points $P = \{p_1, p_2, ..., p_n\}$ and the $minpts$ threshold for the DBSCAN algorithmd. The output is a

Algorithm 1 Multi-Level Directional Sequence Encoding

```
Input: An ordered set of gaze points $P = \{p_1, p_2, ..., p_n\}$, $minpts$
Output: macrosequence $\mathcal{MA}$ and microsequences $\mathcal{MI}$ for the set of ordered gaze points $P$
$\mathcal{MA} \leftarrow \emptyset$;
$\mathcal{MI} \leftarrow \emptyset$;
//Calculate $epsilon$ using KNN Search
$P_{norm} \leftarrow$ min-max normalization of $P$
Build KD-Tree on $P_{norm}$
KNN Search $P_{norm}$
$D \leftarrow$ Average KNN Distance
$h \leftarrow$ histogram($D$)
$\epsilon$ = center of maximum histogram
//Create micro gaze points $P_{micro}$ and a set of macro gaze points $P_{macro}$ using density-based clustering
$C \leftarrow$ DBSCAN($P_{norm}$,$\epsilon$,$minpts$)
$P^C_{micro} \leftarrow P \in C$
$P_{macro} \leftarrow C_{centers}$
//Create macrosequences
for ($\forall p_i \in P_{macro}$) do
    Calculate $sa$
    Assign $dse$
end for
//Create microsequences
for ($\forall P_j \in P^C_{micro}$) do
    for ($\forall p_k \in P_j$) do
        Calculate $sa$
        Assign $dse$
    end for
end for
Return $\mathcal{MA}$
Return $\mathcal{MP}$
```

single macrosequence $\mathcal{MA}$ and a set of microsequences $\mathcal{MP}$ Because the algorithm only requires one scan of the dataset, the computational complexity of the algorithm $O(n)$.

3) Mining Frequent Macrosequences and Microsequences: Given a macrosequence $\mathcal{MA}$ and a set of associated microsequences $\mathcal{MI}$ the objective is to find frequent patterns in these sequences. The aim is to use the resulting frequent sequences to classify both users and interfaces based on eye tracking patterns. For example, Figure 4 depicts example frequent sequences that indicate different types of visual processing. In Figure 4 a) the sequence ⟨a,c,a⟩ indicates that the user is scanning the interface vertically. The sequence ⟨b,d,b⟩ in Figure 4 b) indicates that the user is scanning the interface horizontally. The sequence ⟨b,c,b⟩ shown in Figure 4 c) indicates that the user is scanning the interface from left to right and down. This pattern would be expected to be observed when a user is reading text. Finally, in Figure 4 d) the pattern 4 shows that the user is scanning the interface in a circular pattern.

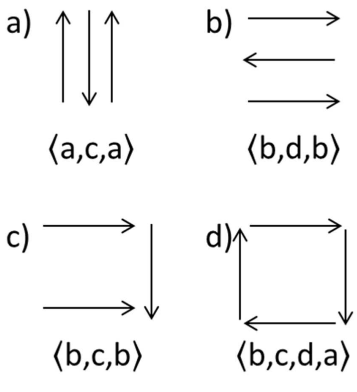


Fig. 4. Example directional sequence pattern templates

In the following approach, a top-k algorithm is used to find frequent macrosequences in a set of gaze points. Then, an algorithm based on the generalized sequential pattern (GSP) algorithm [22] is employed to find frequent microsequences where each microsequence is modeled as a transaction and frequent sequences are generated in a level-wise fashion.

C. Mining Frequent Macrosequences

Given a macrosequence $\mathcal{MA}$, frequent macrosequences are mined using a top-k approach where each possible subset $\mathcal{MA}_{sub} \in \mathcal{MA}$ is counted and the cardinality $|\mathcal{MA}_{sub} \in \mathcal{MA}|$ is calculated. Then, given a value of k the Top-k $\mathcal{MA}_{sub} \in \mathcal{MA}$ are the subsequences $MA_{sub} \in \mathcal{MA}$ with the k largest cardinality values such that the top-k frequent macrosequences $\mathcal{FMA}$ is the k-largest values of $|\mathcal{MA}_{sub} \in \mathcal{MA}|$. A sliding window-based approach is used to generate candidate subsequences where candidates are generated by the window progressively moving over $\mathcal{MA}$. The window progressively increases in size by a factor of one and a threshold α is used to set the maximum window size such that the window expands from 1 to α.

Algorithm 2 Top-k Frequent Macrosequence Mining

```
Input: A macrosequence $\mathcal{MA}$, $k$ value, maximum candidate subsequence length $\alpha$
Output: Top-$k$ frequent macrosequences $\mathcal{FMA}$
$\mathcal{MA}_{sub} \leftarrow \emptyset$;
$sequencelist \leftarrow \emptyset$;
$\mathcal{FMA} \leftarrow \emptyset$;
$cnt \leftarrow 1$;
//Sliding window to calculate frequency for each $\mathcal{MA}_{sub} \in \mathcal{MA}$; loop until $\alpha$ threshold is met
for ($i$ from 1 to $\alpha$) do
    for ($j$ from 1 to $|\mathcal{MA}| - \alpha$) do
        $\mathcal{MA}_{sub} \leftarrow \mathcal{MA}(j : j + i)$
        if ($\mathcal{MA}_{sub} \notin sequencelist$) then
            $sequencelist(cnt) \leftarrow \mathcal{MA}_{sub}$
            $\mathcal{MA}^{freq}_{sub} \leftarrow |\mathcal{MA}_{sub} \in \mathcal{MA}|$
            $cnt \leftarrow cnt + 1$;
        end if
    end for
end for
Top-$k$ $\mathcal{FMA} \in \mathcal{MA} \leftarrow$ SORT($\mathcal{MA}_{sub}$)($1 : k$)
Return Top-$k$ frequent $\mathcal{FMA} \in \mathcal{MA}$
```

The algorithm for finding Top-k frequent macrosequences is presented in 2. The algorithm takes as input a macrosequence $\mathcal{MA}$, a k value, and a maximum candidate subsequence length α. The output of the algorithm are the Top-k frequent subsequences $\mathcal{MA}_{sub} \in \mathcal{MA}$. The complexity for the sliding window algorithm is $O(\alpha n)$. Then sorting the sequence frequency using quick sort is $O(n \log n)$. Therefore the overall complexity of the algorithm is $O(\alpha n \log n)$.

1) Mining Frequent microsequences: The approach for generating frequent microsequences is based on the GSP algorithm for frequent sequence mining [22]. The GSP algorithm is an apriori-like algorithm that finds frequent sequences at multiple lengths based on a minimum support value. The minimum support value is the number of times that an individual subsequence occurs over a set transactions. With this in mind each $\mathcal{MI} \in \mathcal{MP}$ is treated as an individual transaction where each sequence label is an item such that a finite number of items exist consisting of the set $\{a, b, c, d\}$. The algorithm works in a level-wise fashion where frequent sequences are first found for level 1 sequences consisting of a single item then, level 1 sequences, level 2 sequences consisting of 2 items are formed. Level 3 sequences consisting of 3 items are then formed based on the frequent level 2 sequences and the algorithm keeps generating candidates at successive levels until no frequent sequences of that length exist. One area that this approach is different from the GSP algorithm is the candidate generation step. In this approach, the sequence is grown by one item at each level. To do this, the frequent level 1 sequences are appended as both a prefix and suffix to each frequent sequence to generate the next level.

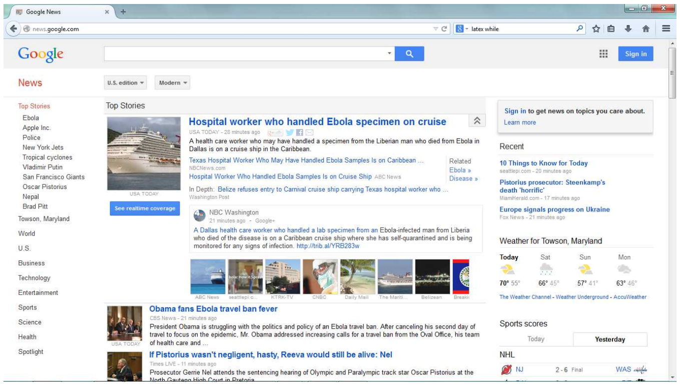
Algorithm 3 Frequent Microsequence Mining

```
Input: A set of microsequences $\mathcal{MP} = \{MI_1, MI_2, ...MI_t\}$, minimum support value $minsup$
Output: Frequent microsequences $\mathcal{FMI} \in \mathcal{MP}$
//Initialize level 1 microsequence candidates
$\mathcal{MI}_{cand} \leftarrow \{a, b, c, d\}$ ;
$seqcount \leftarrow 0$;
$L \leftarrow= 1$;
//Loop until there are no frequent microsequences $\mathcal{FMI}$
while ($\mathcal{FMI} \neq \emptyset$); do
//Calculate frequency of each $\mathcal{MI}^{cand} \in \mathcal{MI}$ for each $\mathcal{MI} \in \mathcal{MP}$
    for ($i$ from 1 to $|\mathcal{MI} \in \mathcal{MP}|$) do
        for ($j$ from 1 to $|mi^{cand} \in \mathcal{MI}^{cand}$) do
            $seqcount \leftarrow seqcount + |mi_j^{cand} \in \mathcal{MI}_i|$;
            $mi_{freq}^{cand} \leftarrow seqcount$;
        end for
    end for
 //Generate candidates for next level
    $\mathcal{FMI}_L \leftarrow MI_{freq}^{cand} > minsup$;
    $cnt \leftarrow 1$;
    for ($i$ from 1 to $|fmi \in \mathcal{FMI}_L|$) do
        for ($j$ from 1 to $|fmi \in \mathcal{FMI}_1$) do
            $\mathcal{MI}_{cnt}^{cand} \leftarrow fmi_i + fmi_j$;
            $cnt \leftarrow cnt + 1$;
            $\mathcal{MI}_{cnt}^{cand} \leftarrow fmi_j + fmi_i$;
            $cnt \leftarrow cnt + 1$;
        end for
    end for
    $L/leftarrowL + 1$;
end while
Return $\mathcal{FMI}$;
```

The algorithm for mining frequent microsequences is shown in Algorithm 3. The algorithm takes as input a set of microsequences $\mathcal{MP} = \{MI_1, MI_2, ...MI_t\}$ and a minimum support threshold value $minsup$. The algorithm outputs the frequent microsequences $\mathcal{FMI} \in \mathcal{MP}$. The complexity of the algorithm is $O(n \log m)$ where n is the number of microsequences and m is the alphabet size of the sequence.

IV. Experimental Design and Results

Eye tracking data was collected as part of a study to test differences in information foraging behavior. The participants in the study consisted of ten students with ages between 18 and 20. Data in this experiment was collected using the Tobii X2 eye tracking system. The participants were first asked to complete a calibration program to calibrate the eye tracking system to their individual physical characteristics. Then, each participant was asked to open an Internet browser and navigate to Google News (http://news.google.com) shown in Figure 5 or NewsMap (http://www.Newsmap.jp) shown in Figure 6. Five participants were asked to navigate to Google News first and the other five navigated to NewsMap first. The participants were then asked to search through the site and identify the top three stories in the categories of World News, Business News and Sports and share their answer. The answer was then recorded by the investigator.



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Obama fans Ebola travel ban fever
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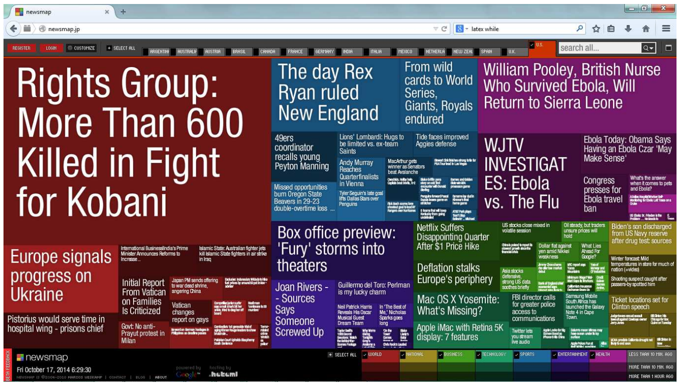
Fig. 5. Google News User Interface (http://news.google.com)

Upon completion, the user was asked to browse to the other news website and similarly search through the website to identify the top three stories in the categories of World News, Business News and Sports, in the user's opinion. As with the first website, the answers were said out loud and were recorded by the investigator who checked for their correctness using the color coded news categorization used by the website.



Rights Group: More Than 600 Killed in Fight for Kobani
Europe signals progress on Ukraine
Pistorius would serve time in hospital wing - prisons chief
International BusinessIndia's Prime Minister Announces Reforms to Increase...
Islamic State: Australian fighter jets kill Islamic State fighters in air strike in Iraq
Initial Report From Vatican on Families Is Criticized
Japan PM sends offering to war dead shrine, angering China
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Govt: No anti-Prayut protest in Milan
The day Rex Ryan ruled New England
From wild cards to World Series, Giants, Royals endured
49ers coordinator recalls young Peyton Manning
Lions' Lombardi: Hugs to be limited vs. ex-team Saints
Tide faces improved Aggies defense
Andy Murray Reaches Quarterfinalists in Vienna
MacArthur gets winner as Senators beat Avalanche
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Joan Rivers - - Sources Says Someone Screwed Up
Guillermo del Toro: Perlman is my lucky charm
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In 'The Best of Me,' Nicholas Sparks goes long
William Pooley, British Nurse Who Survived Ebola, Will Return to Sierra Leone
WJTV INVESTIGATES: Ebola vs. The Flu
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Netflix Suffers Disappointing Quarter After $1 Price Hike
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What Lies Ahead For Google?
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Winter forecast: Mild temperatures in store for much of nation (+video)
Shooting suspect caught after passers-by spotted him
Ticket locations set for Clinton speech

Fig. 6. Newsmap User Interface (http://Newsmap.jp)

All ten participants successfully navigated through both websites and provided answers to the investigator. The correct answers were not shared with the participants. Five of the participants were asked to search through Google News first and the other five were asked to search through Newsmap first in order to avoid bias.

The data was then extracted to include the recording time stamp, gaze point X, and gaze point Y attributes. The gaze point X and gaze point Y attributes were recorded in the ADCSpx coordinate reference system. The prototype algorithms were developed in the Matlab programming language. The algorithms were then run on the data for each participant and the directional sequence encoding, frequent macrosequences, and frequent microsequences were recorded.

The rest of this section is organized as follows: In Section IV-A a sample result of the directional sequence encoding is presented. In Section IV-B the Top=k frequent macrosequences are presented. In Section IV-C the frequent microsequences are presented. Finally, in section IV-D the percent saccade direction is discussed to give additional insight into scan path pattern summaries.

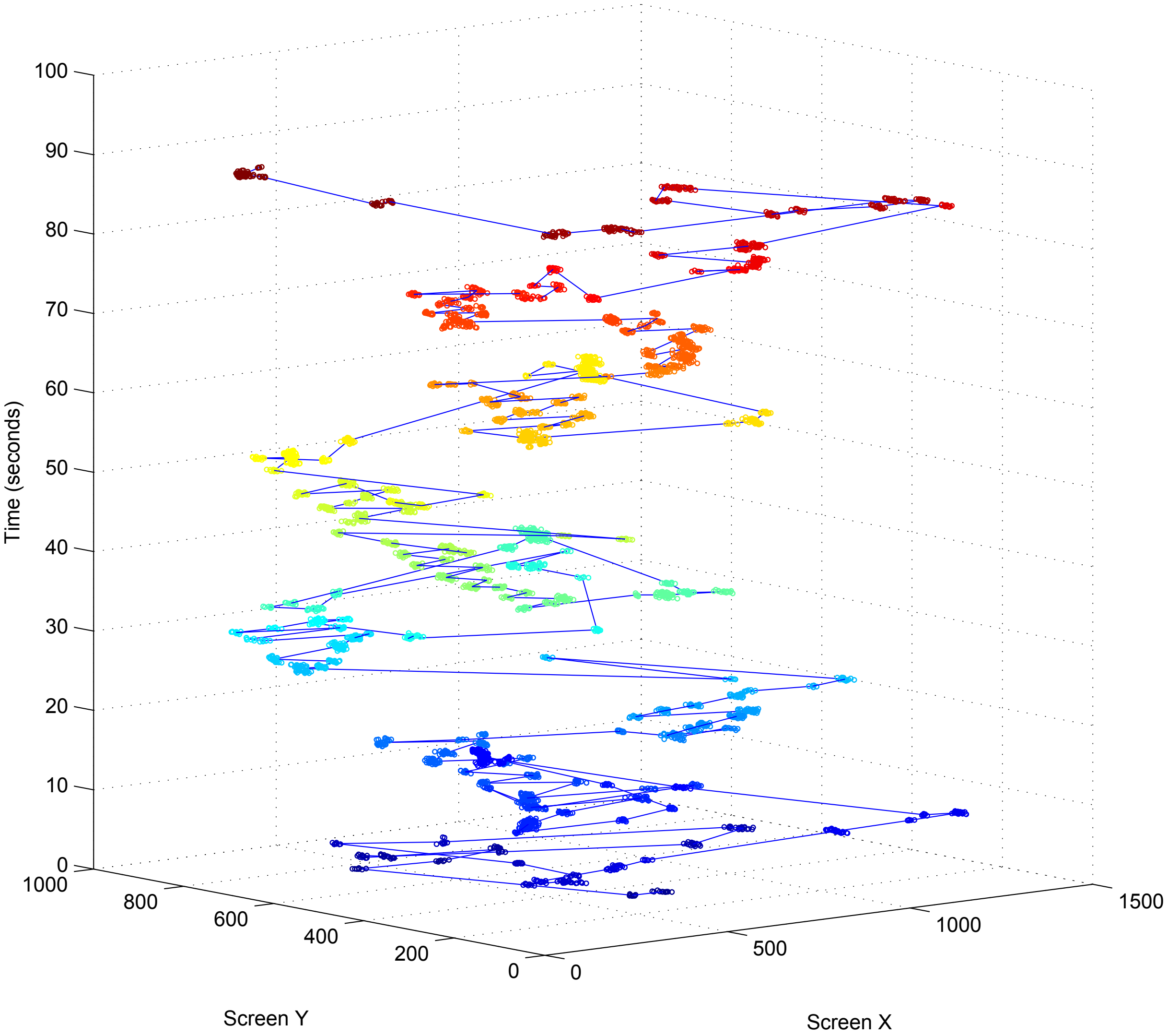

Fig. 7. Space Time Cube showing a macrosequence (blue line) combined with micro gaze points colored by cluster

A. Directional Sequence Encoding

The directional sequence encoding algorithm resulted in macrosequences and microsequences for the gaze points for each participant. An example of macro and micro gaze points for participant 6 are shown in Figure 7. This figure uses a space-time cube to visualize the macro gaze points, colored by cluster, and the micro gaze points, colored red. The screen x and screen y dimensions are represented on the axes at the base of the space-time cube and time is represented on the vertical axis of the cube.

The figure shows dense areas of micro gaze points and the resulting macrosequence moving through the dense areas. Also, it is evident that there is a salient region in the lower left portion of the screen because this area has the highest concentration of gaze points. This figure also illustrates the complexity of the eye tracking data as well as challenge in determining patterns from visualizations alone.

B. Exploring Top-k Frequent Macrosequences

The directional sequence encoding was run for all ten participant's eye tracking results and the Top-k frequent macrosequences were found for each set of results. In this analysis, k was set to 5 so that the 5 most frequent macrosequences were found.

The top-k macrosequences for each participant for both Google News and NewsMap are shown in Table I. The table shows the top-k frequent macrosequences as arrows that represent each letter where a=↑, b=→, c=↓, and d=←. The results show that the participants generally follow a horizontal saccade pattern at the macroscale for both interfaces.

TABLE I. TOP-k FREQUENT MACROSEQUENCES (k=5)

Google News					
P1	→→	→←	←→	←←	↓↑
P2	→→	↓→	→←	↓↓	←←
P3	←→	→→	→←	↑→	→↓
P4	←←	←←←	→←	→→→→	↓→
P5	→←	←→	→↑	↓↑	↑→
P6	→→	→→→	←←←	←→	←←←←
P7	→→	←→	→←	←←←	→←→
P8	→→	→→→	→←	→→←	←↑
P9	→→	→←	→→→	←→	→→←
P10	→→	→←	←→	→↓	→→→
NewsMap					
P1	→←	←→	←←	→→	←↑
P2	→→	←→	→←	←↓	→→→
P3	→←	←→	↓→	→→	↑↓
P4	→→	←→	→←	←←	←→→
P5	←→	→←	←↑	↑←	↓←
P6	→→	←→	→←	←→←	←←
P7	→←	←→	→→	←←	→←→
P8	←→	→←	←←	←↑	←←
P9	→←	←←	←→	↓←	→→←
P10	→←	→←	→→	↓→	→↑
Legend:	↑: a	→: b	↓: c	←: d	

TABLE II. LONGEST FREQUENT MICROSEQUENCES ($minsup$ = .5)

	Longest Frequent microsequence (Google News)	Support	Longest Frequent microsequence (NewsMap)	Support
P1	↓↑↑	1	↑→↑	0.8
P2	↓↑↑↑	0.67	↑→↑	0.61
P3	↑↓↑↑	0.51	↑→↑	0.64
P4	↑→↑	0.73	→↑	1
P5	↑↓↑↑	1	↓↑↑	1
P6	↑↑↑	1	→↑↑	0.69
P7	↑↑↑	0.88	↑→↑	0.56
P8	↑↓↑↑	0.5	↑↓↑↑	0.56
P9	↑↑↑	0.98	↑→↑	0.56
P10	↑↑↑	1	↑→↑	0.79
Legend:	↑: a	→: b	↓: c	←: d

This is consistent with the layout of both Google News and NewsMap where Google News has a menu on the left side that provides links to different categories of news. The news stories in the treemap on the NewsMap site are positioned in a more horizontal layout where the top news stories appear as larger cells in the treemap at the top of the screen. Of particular interest here is the relationship between scan path direction and cognitive load when performing a visualization task. According to Hunter et al. [2010], eye tracking combined with EEG analysis indicated that scan paths that move from left to right indicate increased cognitive load. Considering this result, the Top-k scan paths for Google News are generally more left to right than that of NewsMap. This could indicate that the layout of Google News increases cognitive load and that the treemap visualization in News Map could potentially reduce cognitive load in information foraging tasks.

C. *Exploring Frequent Microsequences*

Frequent microsequences were also found for all participants in the study. The results of this analysis are shown in Table II. This table shows the longest frequent microsequence for each participant for both Google News and NewsMap.

In contrast to the frequent macrosequences shown above, all of the longest frequent microsequences exhibit a vertical pattern. Google News exhibited a more pronounced vertical pattern and generally had higher support values. NewsMap has a mix of vertical and horizontal scan path patterns at the micro scale where horizontal saccades generally moved from left to right indicating that users could have a higher cognitive load within fixations on NewsMap.

D. *Percent Saccade Direction*

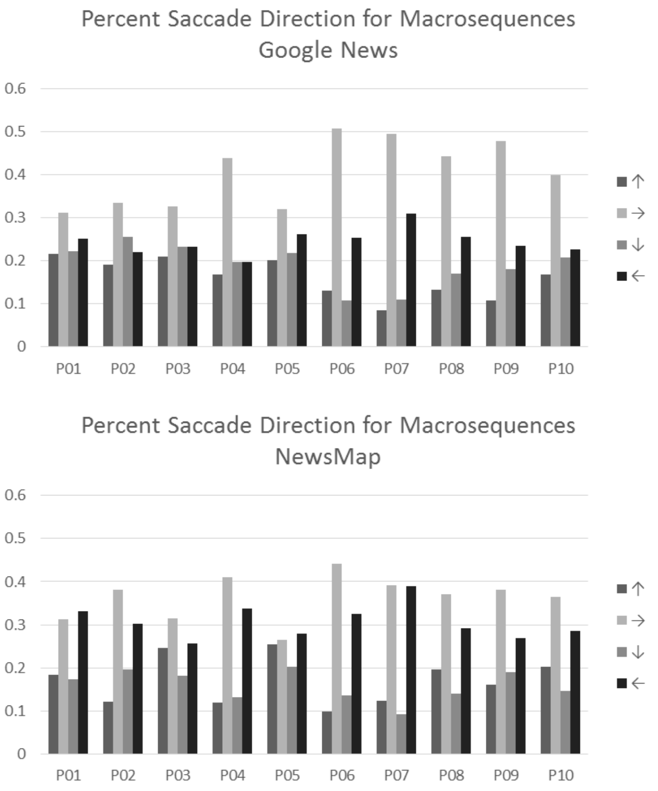

Fig. 8. Percent Saccade Direction for macrosequences

To further examine differences the scan path direction between individual users, the percentage of each saccade direction for each macrosequence and microsequence was calculated. The results for macrosequences are shown in Figure 8.

This figure suggests some subtle differences between Google Maps and NewsMap where all users viewing Google News have a higher right to left saccade direction. For the NewsMap interface, differences in the percentage saccade direction between left to right and right to left are less pronounced. This indicates that the NewsMap interface requires users to scan horizontally in both directions more than Google News. We can also see individual differences for users in this figure where participants 4, 6, 7, 8, and 9 have higher right to left scan paths when using Google News when compared to

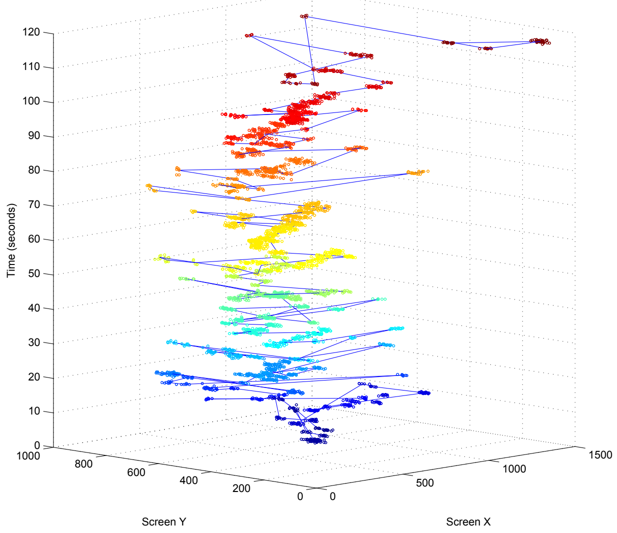

Fig. 9. Space Time Cube showing macrosequences and microsequences for participant 1

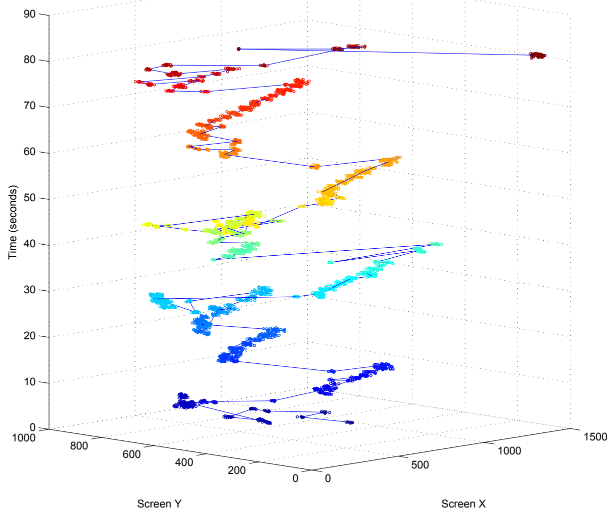

Fig. 10. Space Time Cube showing macrosequences and microsequences for participant 6

other users.

To illustrate this further the directional sequence encoding for Google News for participant 1 and participant 6 are shown in in Figures 9 and 10 respectively. It is evident in Figure 9 that participant 1 has a more erratic scan path that suggests an increased cognitive load to complete the task. Conversely, in Figure 10, participant 6 exhibits a much more deliberate scan path between fixation locations which suggests that participant 6 uses more targeted and therefore more efficient approach in visual information seeking. Efficiency is indicated further by the amount of time that it takes each participant to complete the task where participant 1 takes 115 seconds and participant 6 takes 80 seconds.

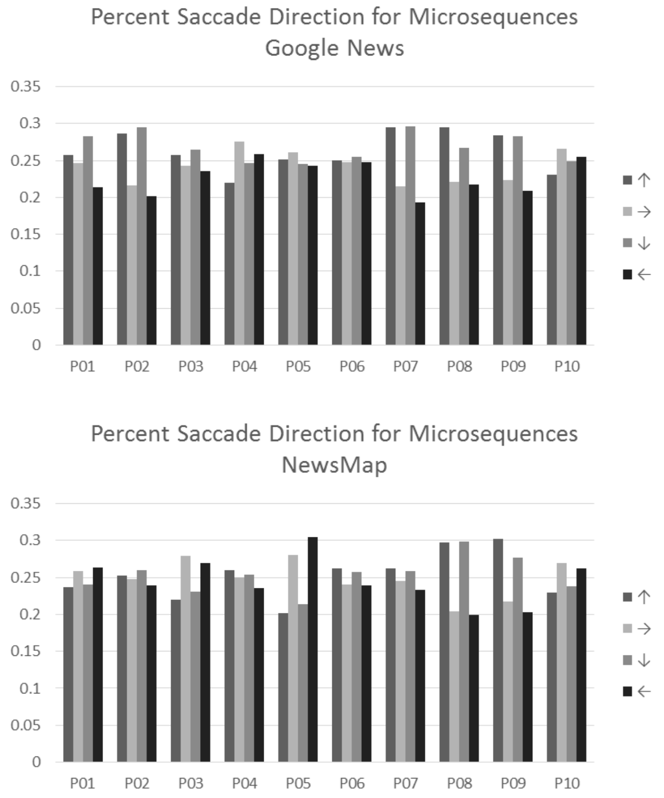

Fig. 11. Percent Saccade Direction for microsequences

The percent saccade direction results for microsequences are shown in Figure 11. Here we see that micro scan paths are more uniform across all directions and the up and down direction is prevalent in a number of users. This pattern suggests that within fixation locations at the microscale, eye movements are more variable and that there is no dominant scan path direction.

V. Discussion and Conclusion

This paper presented a multi-scale method to summarize and analyze scan paths. The method is based on a directional sequence encoding which converts saccade angles into a set of characters that represent the eight cardinal and intercardinal directions. The saccades are divided into two levels based on a distance threshold. The macroscale represents saccade patterns that are expressed at the interface scale where these patterns move between salient regions of the interface. The microscale represents patterns within the salient regions of the interface. An algorithm was then presented for finding top-k frequent macrosequences and an apriori-like algorithm was presented for finding frequent microsequences.

The results show interesting patterns and suggest a dual influence of the interface and the individual user to control patterns at the macroscale while very similar patterns exist a the microscale suggesting cognitive influences related to how the human eye scans text. The resulting macrosequences and microsequences suggest that both individual differences between users and differences between the two interfaces. In particular, the frequent macro sequences appear to be dependent on both the characteristics of the interface where the layout of salient features contribute to saccade patterns. For example, the left navigation menu of Google News causes the user to move in a horizontal fashion between the menu and the links to news stories and NewsMap, because of it's treemap structure, lends itself to a horizontal browsing pattern. This is consistent with the literature that suggests that eye tracking results directly reflect the visual scene [3]. Furthermore, the macrosequences of Google News exhibited a more pronunced right to left frequent scan path pattern suggesting an increased cognitive load when using Google News for information foraging.

There are some limitations to the approach. First, we deal with the temporal dimension by including the time stamp in density-based clustering. While this works for the experiments described in this paper, it might be more appropriate in some cases to treat the temporal dimension separately. Also, our experimental design included a simple information foraging task. A more complex information visualization task might introduce more interesting results related to relationships between cognitive load and scan path direction. Finally, we have suggested the relationship between scan path direction and cognitive load. This hypothesis could be tested in more detail by applying this method on eye tracking data combined with EEG data.

This approach shows promise in a number of areas associated with human computer interaction. First, the approach could be very useful to researchers studying how users process information using different types of visualization interfaces. Furthermore, this approach could be very useful in contributing to studies concerned with making interfaces more adaptable and thereby more accessible to users with cognitive disabilities. Finally, this research is a first step in designing algorithms for adaptive interfaces based on eye tracking patterns. Future research directions include additional experiments to introduce stimuli to elicit cognitive responses and develop a catalog of patterns that can be used to adapt an interface in real time.

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