

Demonstration of Temporal Visualization of Diabetes Mellitus via Hemoglobin A1c Levels

Hina Shah¹, David Borland², Eugenia McPeek Hinz³, Vivian L. West¹, W. Ed Hammond¹

¹Duke Center for Health Informatics, Duke University, Durham, NC;

²RENCI, The University of North Carolina at Chapel Hill, Chapel Hill, NC;

³DHTS Duke Medicine, Durham, NC

Introduction

In this demonstration we present a visualization tool for a cohort of patients with diabetes (via ICD9 codes) from Duke University's data warehouse, visualizing their Hemoglobin A1c (HbA1c) levels over time, aligned by death, to explore trajectories of glycemic control. To the best of our knowledge, temporal visualization of glycemic control for a diabetic population standardized on death has not previously been presented. Our visualization groups HbA1c values into ordered categories of glycemic control, utilizing a method based on parallel sets and Sankey diagrams to view temporal patterns in HbA1c values. We incorporate a number of features for interactive data exploration like: viewing the progression of values either forwards or backwards in time, highlighting multiple subpopulations, coloring based on the category along each path in the data or at the beginning/end of each path, and the incorporation of demographic data, such as gender.

Methods

Data from Duke University's data warehouse were extracted using DEDUCE, an electronic health record (EHR) query tool developed at Duke University. The final cohort includes data from 121 patients with diabetes mellitus (with and without complications), a death indicator, prescribed antihyperglycemics, and at least 10 years of HbA1c laboratory values. We average HbA1c values over 6 month time intervals. In the case of missing HbA1c values within a 6 month period, we first attempt to impute a HbA1c value from average glucose (AG) values over that period of time if available, otherwise the previous HbA1c value (measured or imputed) is carried forward. HbA1c values are then categorized based on the severity of diabetes: Normal < 5.7, Borderline [5.7, 6.5), Controlled [6.5, 8), and Uncontrolled ≥ 8 . The sampled data is time-aligned by the death event for each patient. The visual representation of diabetes progression propagates backwards in time initially. Time is represented as number of years before death in six month increments.

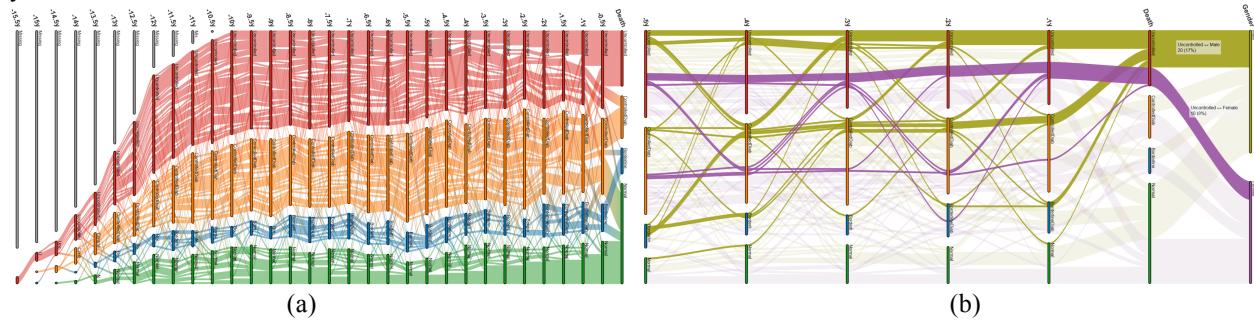


Figure 1. Diabetes progression visualizations without and with a gender axis: (a) Overview visualization with paths colored by the current HbA1c at each time step, useful for emphasizing overall temporal trends. (b) Adding a gender axis and selecting two groups, we can compare the variability of males who were Uncontrolled at death (olive) to women who were Uncontrolled at death (purple). Men appear to have more variability over the 5-year period being visualized, as shown by the large number of transitions between different categories.

Our visualization tool was developed using the D3 JavaScript library. The aim of this visualization is to investigate temporal trajectories of HbA1c levels for a large cohort of diabetes patients over a number of years prior to death. Parallel sets is chosen for showing HbA1c summary trajectories. Each vertical axis is a time step. The user can choose the frequency of these time steps, with a minimum sampling frequency of six months, and also the maximum number of years before death. The death event axis is placed at the right with all other time steps moving backwards in time to the left (Figure 1). Each vertical axis is split into the four HbA1c categories (Normal in green, Borderline in blue, Controlled in orange, and Uncontrolled in red), and a Missing category in grey (for patients with more than 10 years of data). The height of each axis category represents the proportion of the patients in that category at that point in time. Paths moving between axes recursively split, moving backwards from death to show the trajectories of similar groups of patients. The visualization can show trends either starting at the death event, i.e. going backwards

in time, or starting at the last year in the visualization, i.e. going forward in time. The user can highlight one or more groups of patients by clicking on categories or trajectories to highlight the behavior of that group of patients going backward and forward in time, reducing visual clutter (Figure 2). We also include the ability to incorporate demographic data, such as gender, as additional axes (Figure 1). This feature enables the comparison of trajectories for different subpopulations based on data other than just HbA1c levels.

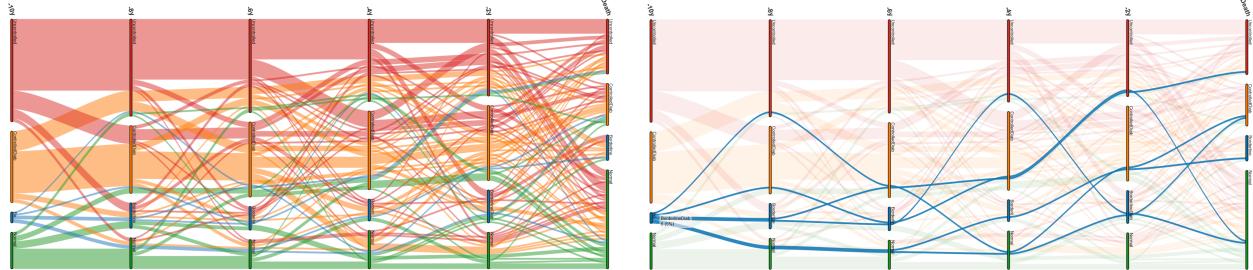


Figure 2. A 10-year range of data, sampled every two years, with forward propagation to show how the trajectories of patients change moving forward in time (left). Highlighting enables a focused view of a single category, reducing visual clutter (right).

The user can also chose between different types of coloring schemes for the paths: 1) color by the category at the first or last year (depending on the propagation direction), which shows the level of variation for a category over the length of the visualization; 2) color by transition, where the transition has a gradient from the source to target category color, useful for showing overall trends; and 3) color by reverse transition, where the transition path has a gradient from the target category to the source category, useful for category-level analysis of the distribution of source and target categories at a particular time step's category (Figure 3). To reduce visual clutter, there is also an option to look at only static transitions (i.e. no change in category between time steps), and to look at only variations (i.e. only changes in the categories).

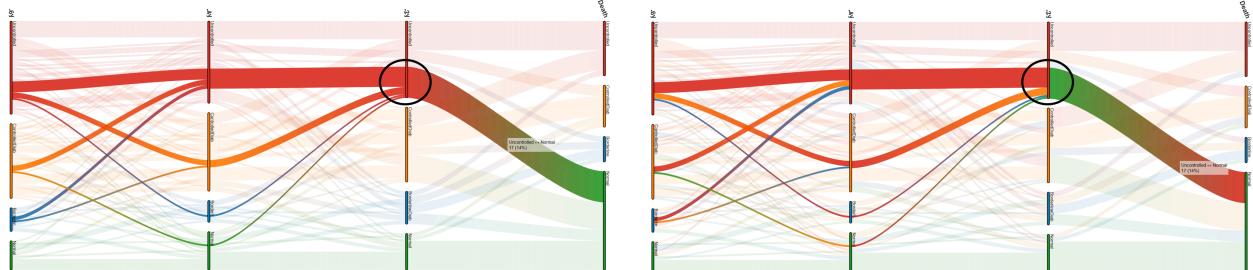


Figure 3. In addition to coloring by the starting category, paths can be colored by a gradient from source to target category (left), which redundantly encodes the category at each axis to emphasize overall trends, or by target to source category (right), which enables a rapid analysis of where paths are moving to/from at each category. The circled regions highlight this difference. On the right, it is immediately obvious what category this trajectory came from at death (Normal in green) and how this group is distributed at the previous time step.

Acknowledgments

This work is supported by the US Army Medical Research and Materiel Command (USAMRMC) under Grant No. W81XWH-13-1-0061. The views, opinions and/or findings in this report are those of the authors and should not be construed as an official Department of the Army position, policy or decision unless so designated by other documentation. We acknowledge the assistance from Meghana Ganapathiraju in helping to refine the visualization. Our implementation was adapted from the d3.parsets reusable chart by Jason Davies.

References:

1. Gebregziabher M, Egede LE, Lynch CP, Echols C, Zhao Y. Effect of trajectories of glycemic control on mortality in type 2 diabetes: a semiparametric joint modeling approach. *Am J Epidemiol.* 2010;171(10):1090-1098.
2. Bendix F, Kosara R, Hauser H. Parallel sets: visual analysis of categorical data. *IEEE Symp on Info Vis.* 2006;12(4):133-140.
3. Wongsuphasawat K, Gotz D. Exploring flow, factors, and outcomes of temporal event sequences with the outflow visualization. *IEEE TransVis Comput Graph.* 2012;18(12):2659-2668.