# Path Maps:

## Visualization of Trajectories in Large-Scale Temporal Data

David Borland<sup>1</sup>

Eugenia McPeek Hinz<sup>2</sup>

Leigh Ann Herhold<sup>3</sup>

Vivian L. West<sup>3</sup>

W. Ed Hammond<sup>3</sup>

<sup>1</sup>RENCI, University of North Carolina at Chapel Hill

<sup>2</sup>Duke Health Technology Solutions

<sup>3</sup>Duke Center for Health Informatics

## Background

Diabetes mellitus (DM)

- Complex disease
- Different disease trajectories can lead to different outcomes

#### Data

Hemoglobin A1c (HbA1c) levels

- 546 and 3638 patient cohorts
- Sampled every six months
- Aligned by death at right
- Categorized as



Controlled

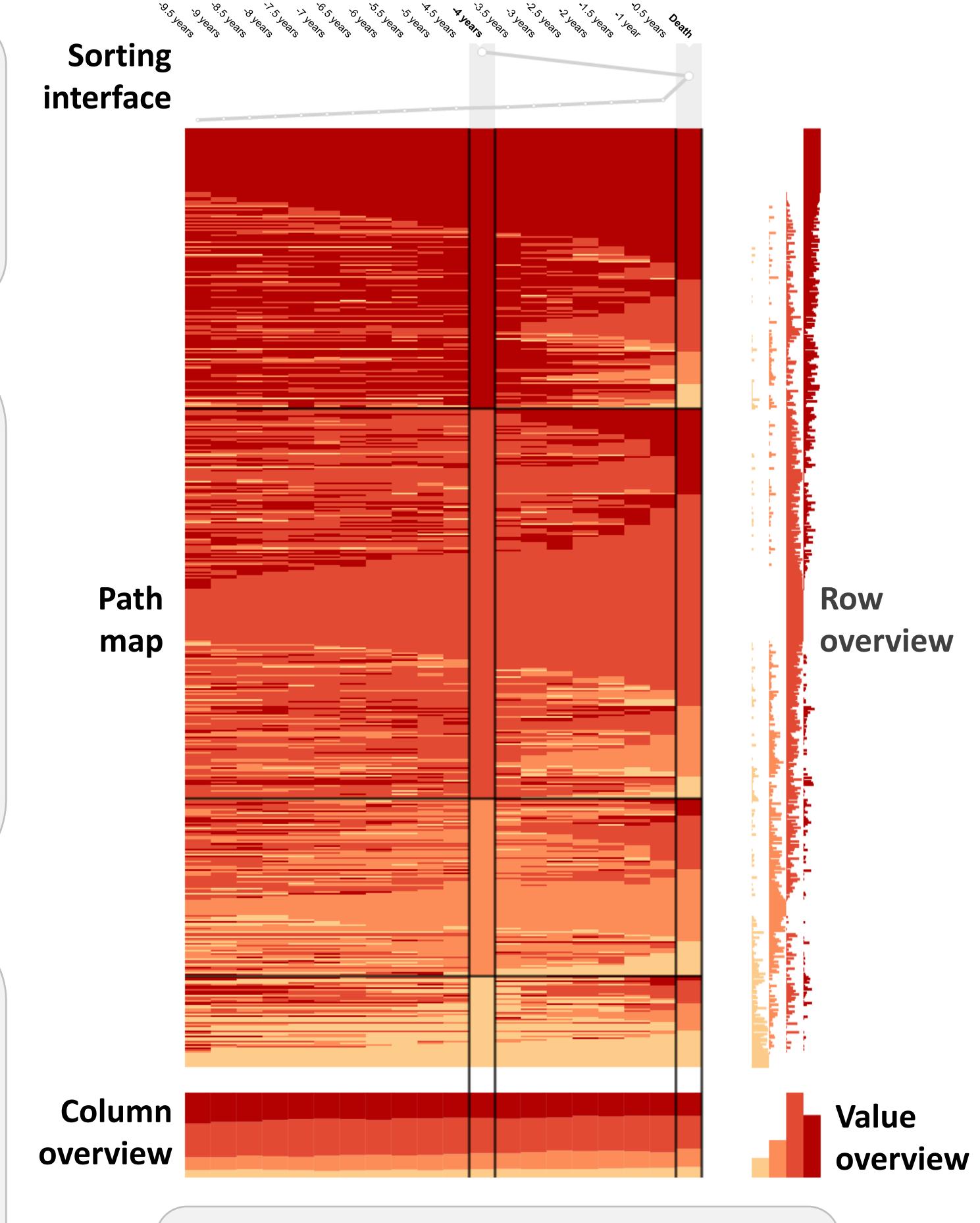
Borderline

Normal

## Problem

Understand temporal patterns of HbA1c levels representing different disease trajectories

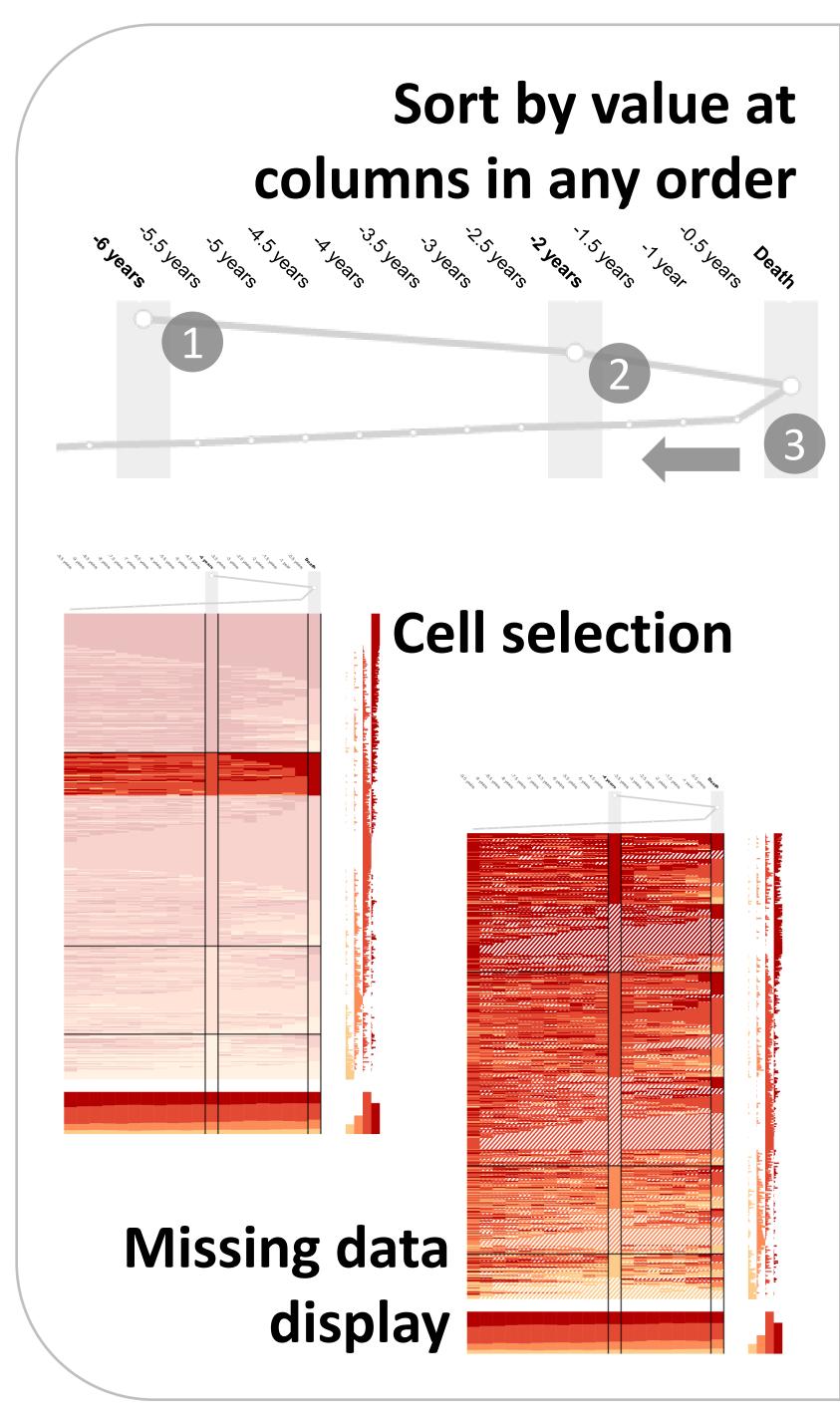
- Many patients
- Multiple temporal samples
- Missing data
- Standard line plots too confusing



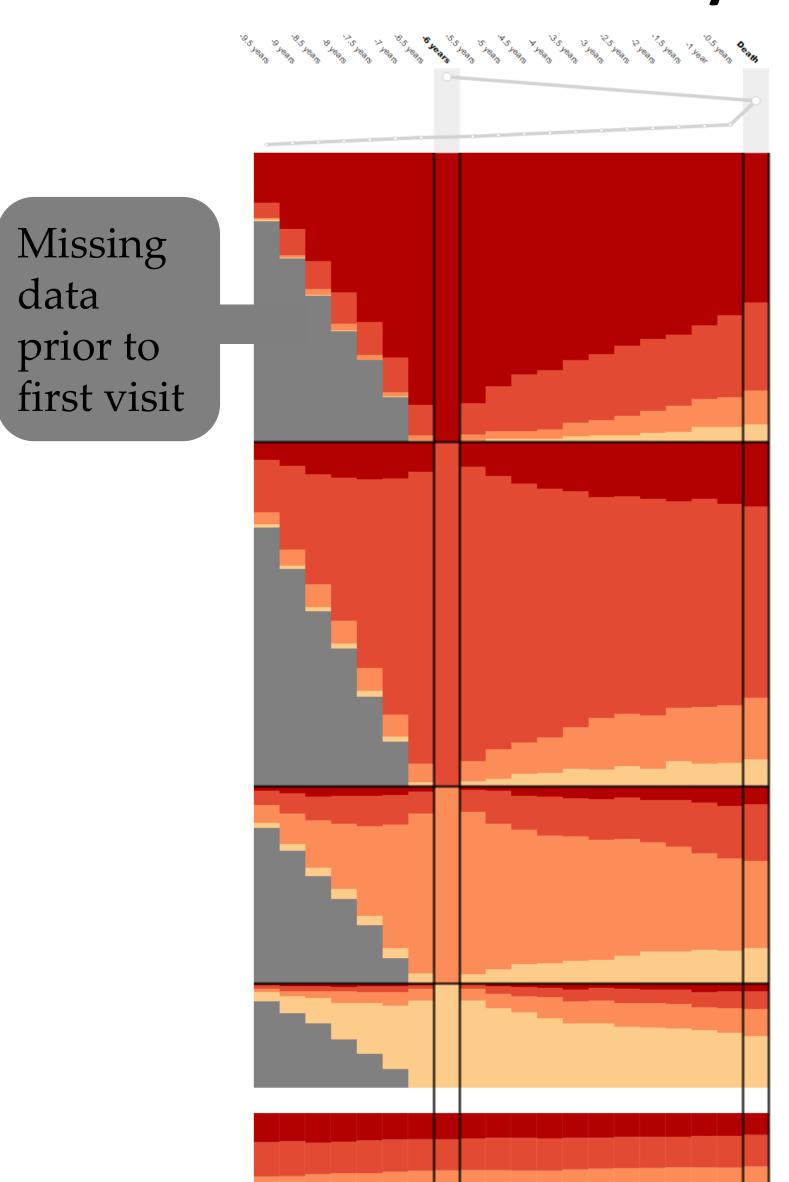
Sorting at -4 years from death, then at death, shows the breakdown of patients that moved from one value to another in that time period, while also showing the intervening variability.

## Basic path map

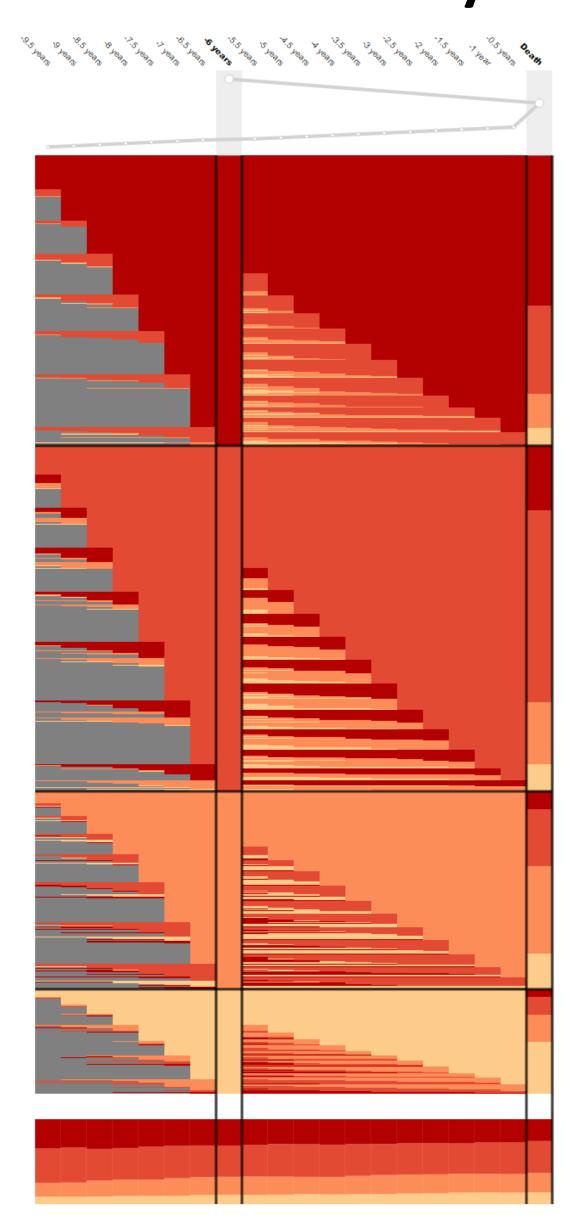
- 546 patients
- Each row a patient
- Sort rows by value at userselected columns
- Generate cells from contiguous regions per column
- Information-dense display



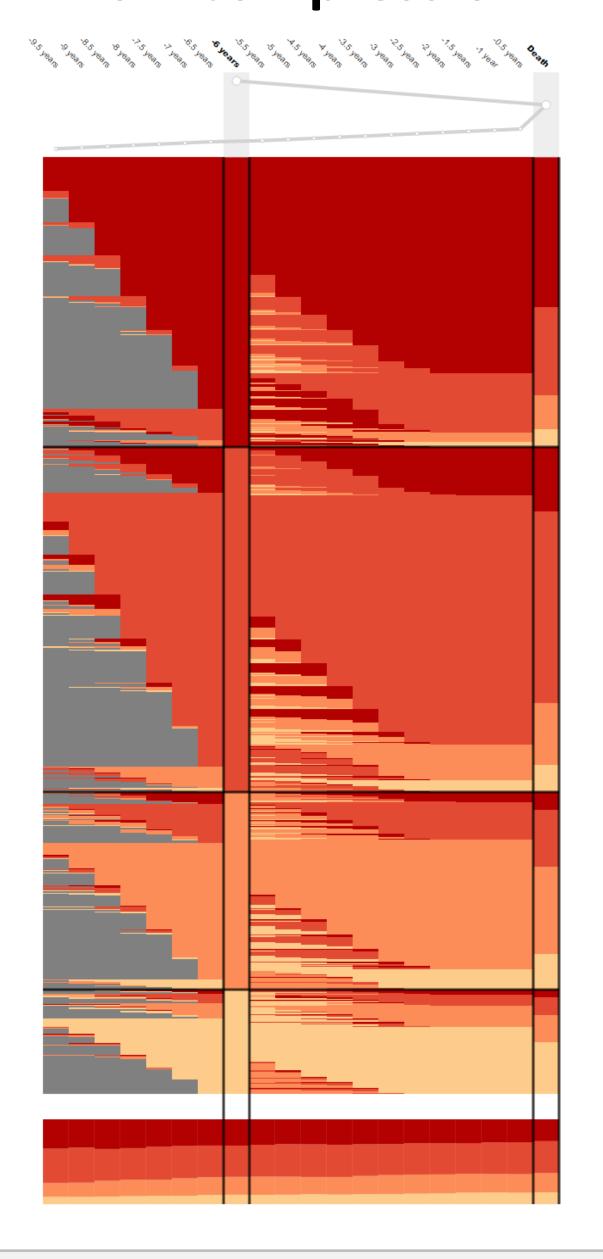
## Column summary



## Row hierarchy



### **Row compression**



### Data aggregation

- 3638 patients
  - Results in over-plotting with one patient per row
- Aggregation map methods
  - Column summary
    - Show general trends over time
  - Row hierarchy
  - Row compression
    - Select groups of rows with certain characteristics



