## Lineage: Visualizing Multivariate Clinical Data in Genealogy Graphs

## **Supplementary Material**

Carolina Nobre

cnobre@sci.utah.edu University of Utah

Nils Gehlenborg

nils@hms.harvard.edu Harvard Medical School

Hilary Coon

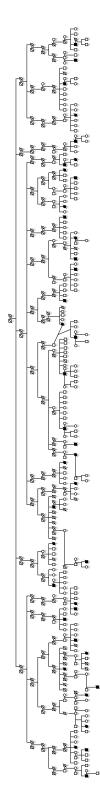
hilary.coon@utah.edu University of Utah

Alexander Lex

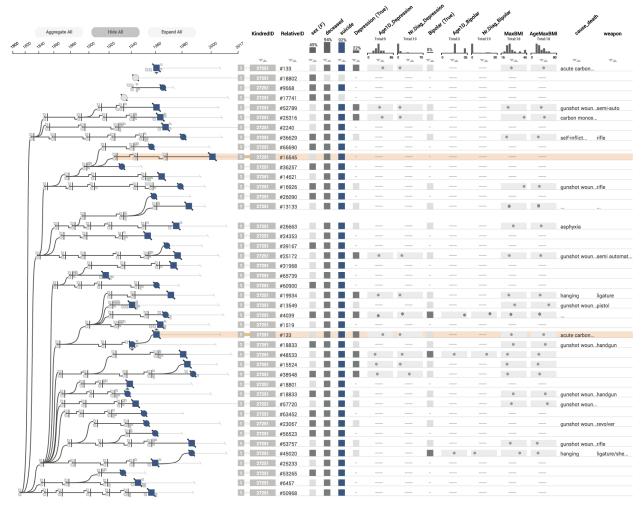
alex@sci.utah.edu University of Utah

## **Scalability Demonstrations**

Here we compare Lineage to Progeny, the tool currently used by our collaborators. Progeny is a commercial genealogy drawing tool that closely follows the standard for visualizing genealogies. For details, visit http://www.progenygenetics.com/. Figures S1 and S2 show the same dataset visualized with Progeny (Figure S1) and Lineage (Figure S2). Progeny shows three attributes, while Lineage shows 15.



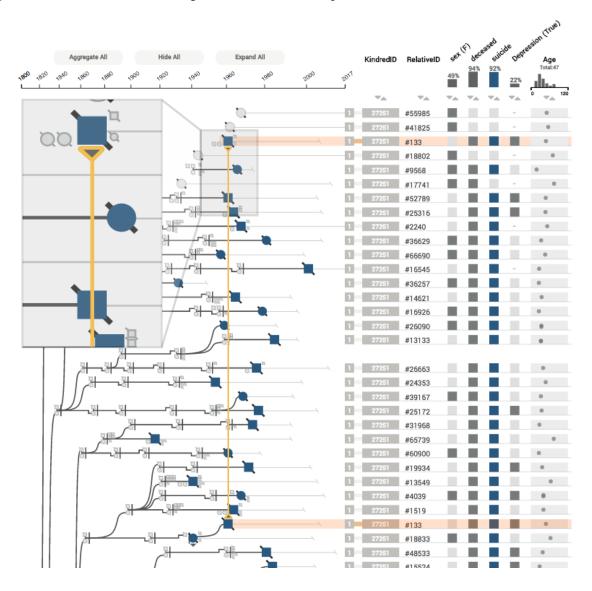
**Figure S1:** Screenshot of Progeny, the tool previously used by our collaborators. This figure shows a family with 404 members and three attributes.



**Figure S2:** The same family as shown in S1 in Lineage. The 404 family members conveniently fit on a single screen on a 2560x1600 pixel display while 15 different attributes are shown in the table.

## **Duplicated Nodes**

Figure S3 shows the visual encoding for nodes that were duplicated.



**Figure S3:** Screenshot of Lineage highlighting nodes that were duplicated in the process of removing cycles from the graph. The arrow glyph indicates both the presence of a duplicate as well as its direction in the graph. The arrow is shown at all times. Hovering over the arrow glyph draws a line connecting it to its duplicate and highlights the corresponding rows in the table.