Investigations of disease outbreaks are being better supported by advances in technology that help public health agencies collect and analyze increasing amounts of complex data, including genomic data. Alongside the growth of data, there has also been greater demand for visualization tools that help to explore data and communicate findings. Although there exist tools for data visualization, our research found that currently, none support the full needs of public health data analysts and that these tools generally had limited expressivity — that is, these tools supported a very narrow range of possible data visualizations. To better support public health data analysts, we implemented a software architecture called gevitR, which supports the expressive creation of data visualizations by reducing the amount of code that analysts must write to generate a visualization. The architectural design of gevitR is informed by GEViT, a genomic epidemiology visualization typology that was developed from a detailed systematic analysis of public health data visualizations. The design of gevitR allows analysts to quickly generate complex visualizations for exploration or communication of public health data. gevitR is implemented in the R programming language and is freely available for anyone to use, and we are also in the process of testing how well gevitR supports data visualization expressivity. As climate change and human activity impact the frequency and nature of disease outbreaks, the availability and usefulness of data visualization tools will become important for understanding and controlling outbreaks.

Themes:

Check (highlight) the most applicable theme according to the abstract.

| Innovation and Technology | Health and Wellness | Culture and Society | Sustainability and Conservation |

Comments: Interesting study. Can you further explain how gevitR and GEViT worked together? What were your findings? Do you have a hypothesis?