Introduction

We introduced Clustered Heat Maps (CHMs) in the early 1990s for visualizing pharmacogenomic data (Weinstein, Stem Cells, 1994) and later for integrated visualization of genomic, transcriptomic, proteomic, and functional data (Weinstein, Science, 1997). As the ubiquitous first-order way of visualizing omic data, CHMs have appeared in thousands of publications and have been used extensively to represent TCGA data. Their limitations have been summarized, along with cautions about improper use (Weinstein, Science, 2008).

One such limitation is that currently popular approaches to the generation of CHMs don’t scale well. They produce fundamentally static images. It’s difficult to use a single representation for both the entirety of a large data set and details of individual data points. What we really wanted was a visualization tool suited to dynamic exploration of large omic data sets as a whole and also in detail. We therefore initiated the Next-Generation CHM project, focusing it on TCGA data. The new web-based visualization tool brings new levels of scalability and interactivity to this popular visualization paradigm.

http://bioinformatics.mdanderson.org/main/NG-CHM:Overview

Goals

- Interactive
- Customizable
- Production-quality graphics to meet journal publication requirements
- Scalable

Other Features

- Maintains and reports detailed metadata to aid reproducibility
- Fluidly navigates from summary views of large data sets down to a detailed level
- Allows toggling between different data layers
- Decoupled from specific clustering algorithms and implementations

Context-specific menus

- Configurable menus let map makers link the data in the map with external resources and provide other operations
- Based on an easily extensible, type-based database:
  - Map builder specifies types of axes
  - Appropriate link-outs automatically added to resulting NG-CHM

Approach

- Web-based map viewer implemented using HTML, JavaScript, and CSS. No browser plugins are required.
- Four NG-CHM builder levels for different levels of expertise
  - Simple GUI-based web-generator
  - Full-featured GUI-based generator
  - R package for better integration with statistical processing
  - Command line tool

Conclusions

Our CHM tool offers new levels of scalability and interactivity necessary for exploring large data sets. The JavaScript-based approach works well to balance the competing requirements of high-level and detailed views of very large heat maps, and users can fluidly navigate between the two. There are suitable interfaces to incorporate a wide range of interactions and annotations. CHM is customizable to support many different data types.

Availability

You can freely download the NG-CHM system for use either on your own server or in the cloud. We provide it as Docker container images: http://bioinformatics.mdanderson.org/main/NG-CHM:Docker

References

Weinstein, JN. Science 319; 1772, 2008.
Bradley M. Broom, Michael C. Ryan, Chris Wakefield, Robert Brown, Futa Ikeda, Mark Stocky, David W. Kane, Rehan Akbani, James Melotli, and John N. Weinstein 1,2
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See http://bioinformatics.mdanderson.org/TCGA/NGCHMPortal/

http://bioinformatics.mdanderson.org/main/NG-CHM:Docker

Try It

We provide a test server running the simple GUI-based web-generator. You can use example data or upload your own data at http://bioinformatics.mdanderson.org/TCGA/NGCHMPortal/

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