

jHeatmap: an interactive heatmap viewer for the web

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ABSTRACT

Summary: The generation of large volumes of omics data to conduct exploratory studies has become feasible and is now extensively used to gain new insights in life sciences. The effective exploration of the generated data by experts is a crucial step for the successful extraction of knowledge from these datasets. This requires availability of intuitive and interactive visualization tools that can display complex data. Matrix heatmaps are graphical representations frequently used for the description of complex omics data. Here, we present jHeatmap, a web-based tool that allows interactive matrix heatmap visualization and exploration. It is an adaptable javascript library designed to be embedded by means of basic coding skills into web portals to visualize data matrices as interactive and customizable heatmaps.

Availability: jHeatmap is freely available at the GitHub code repository at <https://github.com/jheatmap/jheatmap>. Working examples and the documentation may be found at <http://jheatmap.github.io/jheatmap>.

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1 INTRODUCTION

The need for effective tools for data visualization is rising with the increasing data volumes generated by scientific studies. Effective data visualization lets the researcher understand his/her data at both broad and detailed levels and enables barrier-free exploration of the datasets. A widely used type of visualization to report biological results are matrix heatmaps, which represent a dataset with two dimensions, commonly genes and samples. The values in the matrix may represent any widely measurable property such as expression values. The static nature of such plots is a limiting factor to explore complex datasets. Therefore, we introduced the use of interactive heatmaps and developed Gitools, a desktop application for this purpose (Perez-Llamas and Lopez-Bigas, 2011). With jHeatmap, we provide a javascript library that can be included in any web platform to interactively explore heatmaps over a web browser without any further software barriers. This could be compared with the creation of Cytoscape-Web (Lopes *et al.*, 2010), which maintains basic features for network visualization of Cytoscape desktop application. The data are visualized in a heatmap matrix that can contain multiple values per cell and

thus allows loading multidimensional datasets such as alteration data from oncogenomic study cohorts. Each cell is associated with two features, e.g. genes and samples, with additional information, e.g. clinical information for samples, and a set of values. Columns and rows can be moved freely, and can be filtered and sorted based on values in the cells or based on annotations. All of the properties associated with rows and columns can be color coded or printed as text.

2 USAGE AND IMPLEMENTATION

jHeatmap is a JavaScript plug-in for jQuery and has to be referenced only from within an HTML file with the necessary configuration linking the data matrix file and the visualization options. The browser will load the data and draw the heatmap in the web browser as desired.

As depicted in Figure 1, the heatmap has four components: the matrix heatmap, labels and color annotations for columns on top and for rows to the left and right and finally a control area on the top left. In the control area, the user may select whatever value is displayed in case the cells, rows or columns are associated with multiple values. For each of the three areas, a drop-down menu reveals to the user the different values that are available for cells, rows or columns, respectively. Columns and rows can be selected, moved, sorted and hidden, which gives the user great flexibility to focus on the data points of interest. Columns and rows can be selected by click and drag actions. Clicking on ♦ will sort the matrix by the selected rows or columns. Rows and columns used for sorting will be labeled with triangles (▲ ▼) indicating the order applied, and clicking them will toggle the direction. The row and column annotations offer the same possibility. Further interactions can be accessed through a contextual menu revealed by a long click on the row or column labels.

jHeatmap is designed for incorporation into web portals and applications. Documentation about several extension points can be found at the jHeatmap Web site.

3 RESULTS AND DISCUSSION

Given the possibility to generate large amount of biological data with high-throughput technologies, the need for data visualization and analysis in biology is increasing. The shift from hypothesis-driven to data-driven analyses requires field experts to directly access the data. The visual and interactive access to complex data enables experts to reason and decide over further analytical procedures. For example, in cancer genomics, researchers

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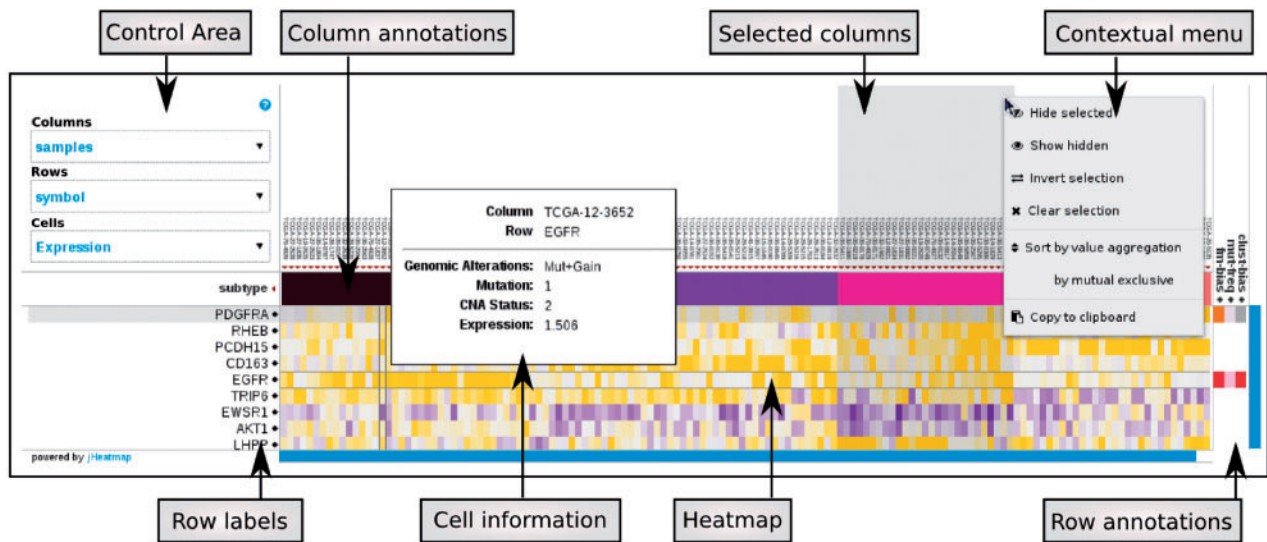


Fig. 1. A jHeatmap screenshot with available pop-ups and annotation. The heatmap shows that the expression status of some genes (rows, low expression in violet, high in yellow) in the The Cancer Genome Atlas glioblastoma samples (columns) depends on the tumor subtype as, for example, seen for the genes EGFR and TRIP6. The three drop-down menus in the control area allow changing the value that is displayed in the cells, rows and columns. The cell information pop-up reveals all values of the clicked cell, in this case *Genomic Alteration*, *Mutation* and *Copy Number Status* and *Expression*. The contextual menu revealed at the top-right in the figure offers interactions over the heatmap

need to visualize and analyze complex multidimensional genomic data often of large number of patients (Schroeder *et al.*, 2013).

For the above stated reasons, we present the *jHeatmap* software library for easy representation of big datasets. *jHeatmap* is already in use within the IntOGen platform (Gonzalez-Perez *et al.*, 2013; Gundem *et al.*, 2010), the Achilles Project (Cheung *et al.*, 2011) and GenomeSpace (Liefeld, 2013) web platforms. *jHeatmap* is open source, reusable and extendable. The web creator may easily include the library to existing projects to visualize multidimensional datasets of any size. Basic coding skills are required. For more advanced users, it is possible to adapt and extend the code as needed.

With *jHeatmap*, we complement already existing stand-alone desktop solutions for interactive heatmaps such as Gitoools (Perez-Llamas and Lopez-Bigas, 2011) or Java TreeView (Saldanha, 2004) with an open source matrix heatmap visualizer prepared for integration into webs. *jHeatmap* offers a set of actions to provide an interactivity that allows the user to visually mine the data. According to the defined software interactions (Yi *et al.*, 2007), *jHeatmap* lets the user *select*, *explore*, *reconfigure*, *encode* and *filter* rows, columns and cells of the heatmap.

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