Category

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 data sets. This requires availability of intuitive and interactive visualization tools which 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 which 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 data sets. A widely used type of visualization to report biological results are matrix heatmaps, that represent a data set

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 TCGA glioblastoma samples (columns) depend 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 which 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 CNA status and Expression. The contextual menu revealed at the top-right in the figure offers interactions over the heatmap.
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 in order to explore complex data sets. 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 which can be included in any web-platform to interactively explore heatmaps over a web browser without any further software barriers. This could be compared to the creation of Cytoscape-Web (Lopes et al., 2010) which maintains basic features for network visualization of Cytoscape desktop application. The data is visualized in a heatmap matrix that can contain multiple values per cell and thus allows loading multidimensional data sets such as alteration data from oncogenic study cohorts. Each cell is associated to 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 properties associated to rows and columns can be color coded or printed as text.

2 USAGE & IMPLEMENTATION

jHeatmap is a JavaScript plugin for jQuery and only has to be referenced 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 what 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 \( \uparrow \) will sort the matrix by the selected rows or columns. Rows and columns used for sorting will be labeled with triangles (\( \uparrow, \downarrow \)) indicating the ordering 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 website.

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 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 data sets. jHeatmap is already in use within the IntOGen platform (Gundem et al., 2010; Gonzalez-Perez et al., 2013), 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 in order to visualize multidimensional data sets 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 Gitools (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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