MARCARviz: Interactive visualization of microarray data with HTML and JavaScript

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HTML, JavaScript, and CSS provide the tools to port traditional visualization software into web-based platforms. Wet-lab researchers can use these platforms with their usual web browser to visualize their biological data.

With MARCARviz (https://tea.cs.uni-tuebingen.de [1]), we provide a proof-of-concept for the interactive visualization of microarray data without requiring the installation of complex software or a particular operating system.

We developed a framework that provides the most commonly used visualizations (Figure 1) for preprocessed microarray data and populated our prototype with data from the MARCAR project, which investigates nongenotoxic carcinogens, i.e., substances that cause cancer without inducing DNA mutations.

**Key Features**

- **Interactive:** Zoom in on details, select genes of interest, or get additional information on the fly.
- **Platform-independent:** Only a current browser needed, no additional software.
- **Easy sharing:** Share results by sending a link to colleagues or export images for talks or publications.
- **Job history:** Remember and revisit your results later.
- **State-of-the-art:** MARCARviz uses modern, scalable web-technology and popular JavaScript visualization libraries.

![Fig. 1: Examples of visualizations with MARCARviz.](image)

(a) Expression table. (b) Volcano plot. (c) Heatmap [2]. (d) PCA scatter plot.

**References:**

2. Škuta C, Bartuňek P, Svozil D. InCHlib – interactive cluster heatmap for web applications. Journal of Cheminformatics 2014, 6 (44)