

canvasXpress: A versatile interactive high-resolution scientific multi-panel visualization toolkit

Baohong Zhang¹, Shanrong Zhao¹, Isaac Neuhaus^{2*}

¹Early Clinical Development, Pfizer Inc., Cambridge, Massachusetts, USA

²Computational Genomics, Bristol-Myers Squibb Company, New Jersey, USA

*Correspondence should be addressed to I.N. (isaac.neuhaus@bms.com)

EMAIL ADDRESSES

B.Z: baohong.zhang@pfizer.com

S.Z: shanrong.zhao@pfizer.com

I.N: isaac.neuhaus@bms.com

To the Editor: CanvasXpress (<http://canvasxpress.org>) was developed as the core visualization component for bioinformatics and systems biology analysis at Bristol-Myers Squibb and further enhanced by scientists around the world and served as a key visualization engine for many popular bioinformatics tools^{1,2,3,4,5,6}. It offers a rich set of interactive plots to display scientific and genomics data, such as oncoprint of cancer mutations, heatmap, 3D scatter, violin, radar, and profile plots (Figure 1, canvasXpress plots arranged by canvasDesigner <https://baohongz.github.io/canvasDesigner>). Recently, the reproducibility and usability of the package in real world bioinformatics and clinical use cases have been improved significantly witnessed by continuous add-on features and wide adoption of the toolkit in the scientific communities. Furthermore, It is the first noteworthy package harmonizing real time interactive exploring and analyzing of big data, full-fledged customizing of look-n-feel, and producing multi-panel publication-ready figures in PDF format simultaneously.

Emphasizing reproducible research, canvasXpress captures all programmatic and user interactions including modifications done through the menus, on plot controls and the comprehensive configurator as illustrated at <http://canvasxpress.org/html/user-interface.html>. The customization is recorded in real time as the user modifying a graph and is embedded in the saved SVG file as metadata. The file can then be opened in a webpage containing a canvasXpress panel to reproduce the exact plot. Please see a step-by-step example at <http://canvasxpress.org/html/reproducible-research.html>.

CanvasXpress also includes a standalone unobtrusive data table and a filtering widget to allow data exploration and filtering similar to those only seen in high-end commercial tools. Data can be easily sorted, grouped by multiple levels, segregated, transposed, transformed or clustered dynamically. The fully customizable mouse events as well as the zooming, panning and drag-n-drop capabilities are features that make this library capable of further expansion of functionalities.

CanvasXpress is a standalone JavaScript library that works in all modern browsers on mobile, tablets and desktop devices. The following example shows the basic usage which consists of four elements: the JavaScript and the CSS framework in the <head> section; the data also in the <head>; a <canvas> element in the <body>; and lastly including a mechanism to instantiate the canvasXpress object which in this example is a call to a function triggered after loading the web page.

```
<html>
<head>
<link rel="stylesheet" href="https://canvasxpress.org/css/canvasXpress.css" type="text/css"/>
<script type="text/javascript" src="https://canvasxpress.org/js/canvasXpress.min.js"></script>
<script>
var initPage = function () {
  var data = {"y": {"vars": ["Gene1"],
    "smps": ["Smp1", "Smp2", "Smp3"],
    "data": [[10, 35, 88]]
  };
  var conf = {"graphType": "Bar"};
  var cX = new CanvasXpress("canvasId", data, conf);
}
</script>
</head>
<body onload="initPage();">
<canvas id="canvasId" width="540" height="540"></canvas>
</body>
</html>
```

CanvasXpress can be now simply used within R at the console to generate conventional plots, in R-Studio or seamlessly embedded in Shiny web applications. A list of examples of the canvasXpress R library including the mouse events, zooming, and broadcasting capabilities are included under the shiny directory in the github package (<https://github.com/neuhausi/canvasXpress>). This R library was created with the htmlwidgets package.

Facilitated by canvasDesigner, the bundled graphics layout tool written in JavaScript, the end user can easily arrange any number of different types of plots in SVG format outputted by canvasXpress or other sources on a HTML page. Each individual plot could be adjusted in size and positioned freely. At last, printing as PDF can generate a high-resolution multi-panel plot as shown in Figure 1, which is a standard option on all modern Internet browsers. This design tool relieves scientists from days if not weeks of

struggle of using multiple tools, sometime even programming in R or some scripting languages in order to get job done.

CanvasXpress is the first open source package with unprecedented functionalities that are not even seen in expensive commercial tools. It empowers biologists who don't possess advanced computer skills to perform analysis and generate complex publication-ready figures required by the prestigious journals at ease in the big data era.

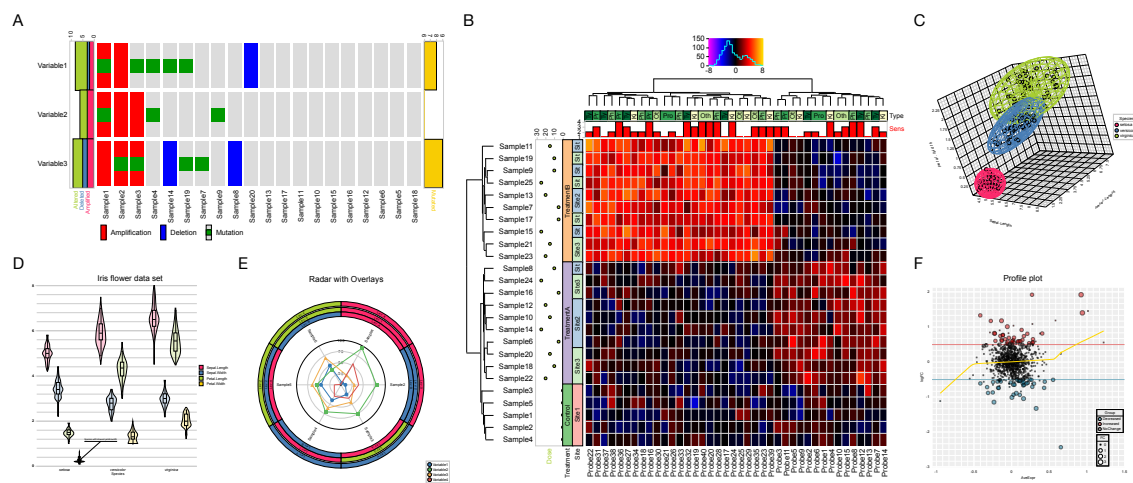


Figure 1. Versatile plots generated by canvasXpress. A) Oncoprint of cancer mutations; B) Gene expression heatmap with comprehensive annotations; C) 3D scatter plot; D) Violin plot; E) Radar plot with annotations; F) Profile plot of gene expression.

AUTHOR CONTRIBUTIONS

I.N. conceived the project. I.N. wrote the canvasXpress software. B.Z. wrote canvasDesigner tool. B.Z, S.Z. and I.N. wrote the manuscript.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

1. Ankenbrand, M.J. *et al. Database* **0**, baw146 (2016).
2. TrinotateWeb: <https://trinotate.github.io/TrinotateWeb.html>
3. Zhao, S. *et al. BMC Genomics* **17**, 39-43 (2016).
4. Zhao, S. *et al. BMC Bioinformatics* **18**, 180-193 (2017).

5. Davenport, E.E. *et al.* *bioRxiv* **118703** (2017).
6. Dower, K. *et al.* PLOS ONE **12(7)**: e0181861 (2017).

Supplementary of canvasXpress

Contents

Web URLs to tools and online user guide	2
SVG (Scalable Vector Graphics) files generated by canvasXpress	3
Layout multiple SVG files by canvasDesigner	4
Inkscape to annotate and convert images to SVG if needed	5
Optimize SVG files by SVGOMG	6

Web URLs to tools and online user guide

Google Chrome (<https://www.google.com/chrome>) is recommended for optimal use of the web based tools.

canvasXpress: <https://canvasxpress.org>

canvasXpress source code: <https://github.com/neuhausi/canvasXpress>

canvasXpress download: <https://canvasxpress.org/html/download.html>

canvasXpress user interface: <https://canvasxpress.org/html/user-interface.html>

canvasXpress examples: <https://canvasxpress.org/html/bar-1.html>

canvasDesigner: <https://baohongz.github.io/canvasDesigner>

canvasDesigner source code: <https://github.com/baohongz/canvasDesigner>

canvasDesigner example #1: all SVG files are generated by canvasXpress.

<https://baohongz.github.io/canvasDesigner/example1.html>

canvasDesigner example #2: mixed SVG files from canvasXpress and other sources.

<https://baohongz.github.io/canvasDesigner/example2.html>

Example SVG files: <https://github.com/baohongz/canvasDesigner/tree/gh-pages/SVG>

Inkscape: Edit SVG files, convert image files in other formats to SVG format.

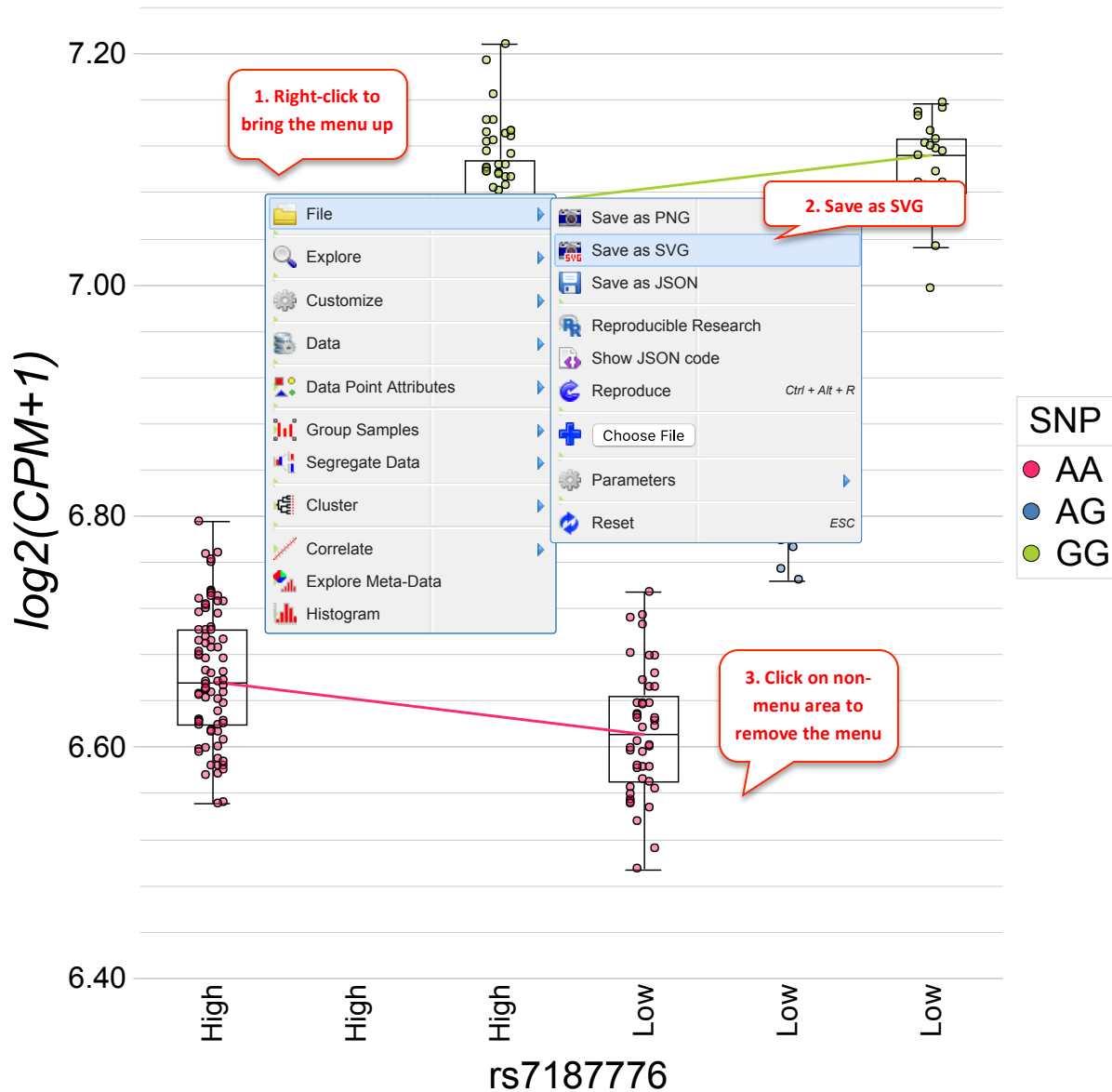
<https://inkscape.org>

SVGOMG: Optimize SVG files. <https://jakearchibald.github.io/svgomg>

SVG (Scalable Vector Graphics) files generated by canvasXpress

All plots generated by canvasXpress can be saved as SVG file by following the menu.

Gene expression of TUFM



Layout multiple SVG files by canvasDesigner

The HTML based tool can easily arrange multiple plots in SVG format outputted by canvasXpress or other sources. Each individual plot could be adjusted in size and positioned freely.

The image shows a screenshot of the canvasDesigner web application interface. It features a central workspace with several plots: a radar chart, violin plots, a 3D scatter plot, a profile plot, and a heatmap. The interface includes an 'Add Plot' button, an 'Add Control' button, and a trash bin icon. A dashed box on the left contains instructions for uploading SVG files. Red callout boxes with numbers 1 through 7 provide detailed instructions for using the tool's features.

1. Drag-n-drop a SVG file
Drop a SVG file here or click to upload. Then click "Add Plot" to add to the designing canvas. Note: use Inkscape to convert PNG, JPG, GIF, TIFF to SVG format.

2. Add the plot to the canvas below

3. Add zoom and pan control

4. Change the size of the container

5. Change the size of the plot

6. Change the label of a figure

7. Print to PDF by Chrome

Additional callouts include: "Drag a plot over the trash bin to remove", "After 'Add Control', click '+' to increase/decrease plot size. Drag the plot to move in the blue container. Print to PDF to get the final figure in the end.", "drag to change the container size", "Drag to move", and "figure number drag to move".

canvasDesigner example #1: all SVG files are generated by canvasXpress.

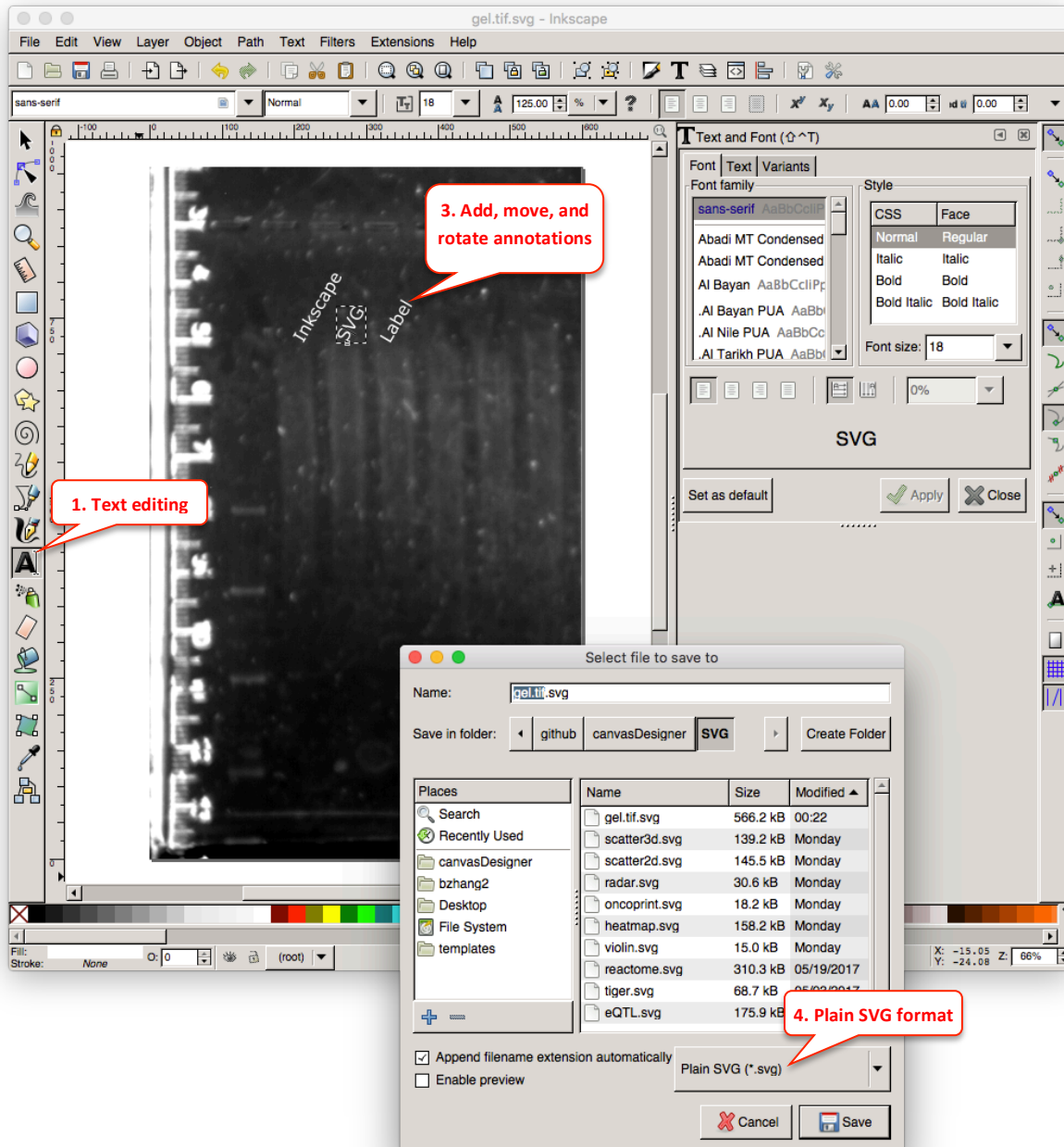
<https://baohongz.github.io/canvasDesigner/example1.html>

canvasDesigner example #2: mixed SVG files from canvasXpress and other sources.

<https://baohongz.github.io/canvasDesigner/example2.html>

Inkscape to annotate and convert images to SVG if needed

Inkscape (<https://inkscape.org>) is powerful open-source vector graphics editor. You can add text annotations to jpeg, png, gif, and tiff image and save it as “Plain SVG” file. The example is to show how to add annotations to a TIFF image.



Optimize SVG files by SVGOMG

SVG files, especially exported from various tools, usually contain a lot of redundant and useless information such as editor metadata, comments, hidden elements, default or non-optimal values and other stuff that can be safely removed or converted by the online tool SVGOMG (<https://jakearchibald.github.io/svgomg>) without affecting SVG rendering result.

The screenshot displays the SVGOMG web application interface. At the top, there are navigation tabs for 'IMAGE' and 'CODE'. The main workspace shows a box plot titled 'Gene expression of TUFM' for the SNP rs7187776. The y-axis is labeled $\log_2(\text{CPM}+1)$ and ranges from 6.40 to 7.20. The x-axis shows 'High' and 'Low' expression levels for three SNP categories: AA (red), AG (blue), and GG (green). A red callout bubble points to the workspace with the text '1. Drag-n-drop a SVG file'. A green callout bubble points to the 'Precision' slider with the text '2. (Optional) Change optimization parameters'. On the right side, there is a 'Global settings' panel with toggle switches for 'Show original', 'Compare gzipped', 'Prettify code', and 'Multipass'. Below this is a 'Precision' slider. A 'Features' panel on the right lists various optimization options, all of which are currently enabled. At the bottom right, there is a '3. Save' callout bubble pointing to a download icon, and a status bar indicating '3.24k - 72.62% saving'.

1. Drag-n-drop a SVG file

2. (Optional) Change optimization parameters

3. Save

3.24k - 72.62% saving