

Package: CanvasXpressBio (via r-universe)

October 7, 2026

Title CanvasXpress Visualizations for Bioconductor Data Structures

Version 0.99.4

Description Bridges the CanvasXpress interactive visualization library to core Bioconductor data structures. Provides a generic to render a SummarizedExperiment, and any class that extends it such as SingleCellExperiment or DESeqDataSet, as an interactive CanvasXpress heatmap that carries its row and column annotations, together with a volcano helper for differential-expression result tables. Charts are reproducible CanvasXpress widgets usable in R, R Markdown and Shiny.

License GPL-3

Encoding UTF-8

biocViews Software, Visualization, GeneExpression, DifferentialExpression, RNASeq, SingleCell, Transcriptomics

Depends R (>= 4.5.0)

Imports methods, stats, canvasXpress (>= 1.70.3), SummarizedExperiment

Suggests SingleCellExperiment, S4Vectors, airway, BiocStyle, knitr, rmarkdown, testthat (>= 3.0.0)

URL <https://github.com/neuhausi/canvasXpress>

BugReports <https://github.com/neuhausi/canvasXpress/issues>

VignetteBuilder knitr

Config/testthat/edition 3

RoxygenNote 7.3.3

Config/pak/sysreqs cmake make libuv1-dev libssl-dev zlib1g-dev

Repository <https://biocstaging.r-universe.dev>

Date/Publication 2026-10-06 21:27:44 UTC

RemoteUrl <https://github.com/BiocStaging/CanvasXpressBio>

RemoteRef HEAD

RemoteSha aad7c522b9a496c8a0d02ae39aaca69f275c4b2b

Contents

cxboxplot	2
cxplot	3
cxsurvival	4
cxvolcano	5
Index	7

cxboxplot	<i>Paired boxplot with per-subject connections using CanvasXpress</i>
-----------	---

Description

Draws a grouped boxplot of one measurement across conditions, overlaying the individual points and drawing a line between the repeated measurements of each subject. The measurement is one feature (row) of a [SummarizedExperiment::SummarizedExperiment] assay, and the grouping, faceting, connecting and colouring are taken from its ‘colData’.

Usage

```
cxboxplot(  
  object,  
  feature,  
  group,  
  segregate = NULL,  
  connect = NULL,  
  color = NULL,  
  assay = 1L,  
  ...  
)
```

Arguments

object	A ‘SummarizedExperiment’.
feature	The assay feature (row name) whose values are plotted.
group	‘colData’ column that defines the box groups along the x-axis (for example a time point).
segregate	Optional ‘colData’ column that splits the plot into panels (for example a cohort).
connect	Optional ‘colData’ column identifying the subject, so repeated measurements are joined by a line.
color	Optional ‘colData’ column used to colour the points and connecting lines.
assay	Assay to read, given as a name or index. Defaults to the first.
...	Additional CanvasXpress configuration passed to [canvasXpress::canvasXpress()].

Value

A ‘canvasXpress’ htmlwidget.

Examples

```
se <- SummarizedExperiment::SummarizedExperiment(
  assays = list(expr = matrix(rnorm(8), nrow = 1,
    dimnames = list("IL6", paste0("s", 1:8)))),
  colData = data.frame(
    Subject = rep(paste0("P", 1:4), each = 2),
    Condition = rep(c("Baseline", "Week 12"), 4),
    row.names = paste0("s", 1:8))
  )
cxboxplot(se, feature = "IL6", group = "Condition", connect = "Subject")
```

cxplot

*Visualize a Bioconductor object with CanvasXpress***Description**

Renders a Bioconductor data object as an interactive CanvasXpress chart. The assay matrix becomes the chart data, with ‘colData’ supplied as sample (column) annotations and ‘rowData’ as variable (row) annotations, so the annotations are available for interactive grouping, coloring and sorting.

Usage

```
cxplot(object, ...)

## S4 method for signature 'SummarizedExperiment'
cxplot(
  object,
  assay = 1L,
  graphType = "Heatmap",
  n = NULL,
  overlays = NULL,
  var_overlays = NULL,
  cluster = FALSE,
  ...
)
```

Arguments

object	A Bioconductor data object. Currently a [SummarizedExperiment::SummarizedExperiment] or any class extending it (e.g. ‘SingleCellExperiment’, ‘DESeqDataSet’).
...	Additional CanvasXpress configuration passed through to [canvasXpress::canvasXpress()] (for example ‘title’ or ‘colorScheme’).

assay	Assay to plot, given as a name or an index. Defaults to the first assay.
graphType	CanvasXpress graph type. Defaults to "Heatmap".
n	Optional integer. When supplied, only the 'n' most variable features (rows) are kept before plotting — a common convenience for large genomics matrices. Defaults to 'NULL', which keeps all features.
overlays	Sample ('colData') annotations to draw as overlay tracks beside the heatmap. 'TRUE' shows every 'colData' column; a character vector names specific ones; 'NULL' (the default) shows none.
var_overlays	Feature ('rowData') annotations to draw as overlay tracks, accepting the same values as 'overlays'.
cluster	Logical; when 'TRUE' both samples and features are hierarchically clustered (adding dendrograms). Defaults to 'FALSE'.

Value

A 'canvasXpress' htmlwidget.

Examples

```
se <- SummarizedExperiment::SummarizedExperiment(
  assays = list(counts = matrix(rnorm(20), nrow = 5,
    dimnames = list(paste0("g", 1:5), paste0("s", 1:4)))),
  colData = data.frame(group = rep(c("A", "B"), 2),
    row.names = paste0("s", 1:4)))
cxplot(se, title = "Example heatmap")
```

cxsurvival

Kaplan-Meier survival plot with CanvasXpress

Description

Draws an interactive Kaplan-Meier survival curve from per-subject survival data, optionally stratified into groups. Survival columns are read from the 'colData' of a [SummarizedExperiment::SummarizedExperiment] (so the same object that feeds [cxplot()]) can produce the survival plot) or from a plain data frame.

Usage

```
cxsurvival(object, time = "time", status = "status", group = NULL, ...)
```

Arguments

object	A 'SummarizedExperiment' (its 'colData' is used) or a data-frame-like table with one row per subject.
time, status	Column names holding the follow-up time and the event status ('1'/'TRUE' = event, '0'/'FALSE' = censored).

group	Optional column name used to stratify and colour the curves (for example a treatment arm or cohort). 'NULL' draws a single curve.
...	Additional CanvasXpress configuration passed to [canvasXpress::canvasXpress()].

Value

A 'canvasXpress' htmlwidget.

Examples

```
cd <- data.frame(
  time = c(5, 12, 18, 24, 7, 15, 22, 30),
  status = c(1, 1, 0, 1, 1, 0, 1, 0),
  arm = rep(c("A", "B"), each = 4))
cxsurvival(cd, time = "time", status = "status", group = "arm")
```

cxvolcano

*Volcano plot of differential-expression results with CanvasXpress***Description**

Draws an interactive volcano plot (log fold change against $-\log_{10}$ p-value) from a table of differential-expression results. The input is coerced with [as.data.frame()], so a 'DESeqResults' object, a 'limma::topTable()' data frame, or any comparable table works.

Usage

```
cxvolcano(
  x,
  logfc = "log2FoldChange",
  pval = "padj",
  label = TRUE,
  label_genes = NULL,
  label_fc = 1,
  label_p = 2,
  ...
)
```

Arguments

x	A data-frame-like table of results.
logfc, pval	Column names holding the log fold change and the (adjusted) p-value. The defaults suit 'DESeq2' output.
label	Logical; when 'TRUE' (the default) genes are labelled with their row names. Set to 'FALSE' to draw an unlabelled volcano.

`label_genes` Optional character vector of gene (row) names to label. When supplied, only these genes are labelled — useful for calling out a named set on a dense plot. When 'NULL' (the default) every significant gene is labelled instead.

`label_fc, label_p` Thresholds that decide which genes are labelled: a gene is labelled when its absolute log fold change exceeds 'label_fc' and its $-\log_{10}$ p-value exceeds 'label_p'. Defaults of '1' and '2' label points outside a two-fold change and below $p \approx 0.01$.

... Additional CanvasXpress configuration passed to `[canvasXpress::canvasXpress()]`.

Value

A 'canvasXpress' htmlwidget.

Examples

```
res <- data.frame(
  log2FoldChange = rnorm(100),
  padj           = runif(100),
  row.names      = paste0("gene", 1:100))
cxvolcano(res, title = "Volcano")
```

Index

cxboxplot, [2](#)
cxplot, [3](#)
cxplot, SummarizedExperiment-method
 (cxplot), [3](#)
cxsurvival, [4](#)
cxvolcano, [5](#)