

# Package ‘RJSplot’

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**Description** Creates interactive graphs with 'R'. It joins the data analysis power of R and the visualization libraries of JavaScript in one package.

**URL** <http://rjsplot.net>

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**Depends** R (>= 3.0.0)

**Suggests** IRdisplay

**NeedsCompilation** no

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---

barplot_rjs	<i>Produce interactive bar plot(s).</i>
-------------	---

---

## Description

barplot\_rjs produce interactive bar plot(s) of the given values.

## Usage

```
barplot_rjs(height, xlab = "", ylab = "", ylim = NA, cex = 1,
            plot = TRUE, jupyter = FALSE, dir = "Barplot")
```

## Arguments

height	either a vector or matrix of values describing the bars which make up the plot.
xlab	a title for the x axis.
ylab	a title for the y axis.
ylim	a vector with two values which specifies the Y minimum and maximum values in the representation.
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive barplot in the folder "Barplot" of your local machine
## Live examples on http://rjsplot.net
barplot_rjs(USArrests, "states", "arrests")
```

---

boxplot\_rjs

---

*Produce interactive box-and-whisker plot(s).*


---

**Description**

boxplot\_rjs produce interactive box-and-whisker plot(s) of the given values.

**Usage**

```
boxplot_rjs(data, xlab = "", ylab = "", ylim = NA, cex = 1,
            plot = TRUE, jupyter = FALSE, dir = "Boxplot")
```

**Arguments**

data	a Data Frame or Matrix from which the data for each box will be taken.
xlab	a title for the x axis.
ylab	a title for the y axis.
ylim	a vector with two values which specifies the Y minimum and maximum values in the representation.
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive boxplot in the folder "Boxplot" of your local machine
## Live examples on http://rjsplot.net
boxplot_rjs(attitude, "attitude", "favourable responses")
```

---

bubbles\_rjs

---

*Produce interactive bubble plots.*


---

**Description**

bubbles\_rjs produce interactive bubble plot(s) of the given values.

**Usage**

```
bubbles_rjs(data, size = NULL, plot = TRUE, jupyter = FALSE, dir = "BubblePlot")
```

**Arguments**

data	a numeric Data Frame or Matrix with two columns and one row per bubble which contains represented values for each bubble. Row names will be used as bubble names.
size	a vector giving each bubble size.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>

[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#), [scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#), [piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive barplot in the folder "BubblePlot" of your local machine
## Live examples on http://rjsplot.net
bubbles_rjs(scale(mtcars[,c("mpg", "hp")], FALSE), mtcars$wt)
```

---

circularfv\_rjs

*Produce a circular sequence viewer.*

---

**Description**

circularfv\_rjs creates a circular sequence viewer.

**Usage**

```
circularfv_rjs(sequence, features = FALSE,
               plot = TRUE, jupyter = FALSE, dir = "CircularFV")
```

**Arguments**

sequence	a "character" string giving the DNA sequence.
features	Data Frame with the segments that will be seen in the viewer. It contains 5 columns which describe the identifier, start coordinate, stop coordinate, segment type and segment color.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Creates a circular sequence viewer in the folder "CircularFV" of your local machine
## Generate test input data
sequence <- paste(sample(c("c","a","t","g"), 10000, replace = TRUE), collapse = "")
data <- matrix(round(runif(12,0,10000)),6,2)
features <- data.frame(id = 0:5, start = data[,1], stop = data[,2],
  type = c("voluptate","non","voluptate","sit","et","proident"),
  color = c("SandyBrown","Tan","Wheat","SteelBlue","LightSkyBlue","LightBlue"))

## Create the circular sequence viewer
circularfv_rjs(sequence, features)
```

---

createAssembly	<i>Creates a genome assembly for genomemap_rjs or manhattan_rjs.</i>
----------------	--

---

**Description**

createAssembly create assemblies for their use as parameter of genomemap\_rjs or manhattan\_rjs.

**Usage**

```
createAssembly(name, size)
```

**Arguments**

name	a vector with the chromosome or scaffold names.
size	a vector with the chromosome or scaffold sizes.

**Value**

a data frame in BED format to be used as an assembly in genomemap\_rjs or manhattan\_rjs.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[genomemap\\_rjs](#).  
[manhattan\\_rjs](#).

**Examples**

```
## Creates a fake genome assembly for its posterior use as parameter of genomemap or manhattan plot
## Live examples and full tutorial on http://rjsplot.net

## Generate a test assembly with three scaffolds
assembly <- createAssembly(c("scaffold1","scaffold2","scaffold3"), c(1000000,800000,650000))
```

---

dendrogram_rjs	<i>Draw a Dendrogram.</i>
----------------	---------------------------

---

**Description**

dendrogram\_rjs creates a dendrogram.

**Usage**

```
dendrogram_rjs(data, metadata = NULL, method = "complete", cex = 1,
               plot = TRUE, jupyter = FALSE, dir = "Dendrogram")
```

**Arguments**

data	a dissimilarity object of class dist (p.e. produced by function dist).
metadata	a data frame with metadata information for leaf features (p.e. sample phenotypes). Corresponding Leaf/Sample should be provided as row name.
method	Name of the agglomeration method to be used. It should be (an unambiguous abbreviation of) one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	A "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create a dendrogram in the folder "Dendrogram" of your local machine
## Live examples on http://rjsplot.net
densityplot_rjs(dist(USArrests), USArrests)
```

---

densityplot_rjs	<i>Draw an interactive density plot.</i>
-----------------	--

---

**Description**

densityplot\_rjs creates density plots.

**Usage**

```
densityplot_rjs(data, xlab = "", ylab = "", cex = 1,
                plot = TRUE, jupyter = FALSE, dir = "DensityPlot")
```

**Arguments**

data	a data frame from which distribution will be represented for each column.
xlab	a title for the x axis.
ylab	a title for the y axis.
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>

[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#), [scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#), [piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Creates a density plot in the folder "DensityPlot" of your local machine
## Live examples on http://rjsplot.net

## Generate test input data
data <- data.frame(Uni05 = (1:100)/21, Norm = rnorm(100), `5T` = rt(100, df = 5),
Gam2 = rgamma(100, shape = 2))

# Create the density plot
densityplot_rjs(data, "x", "y")
```

---

genomemap_rjs	<i>Create an interactive genome map.</i>
---------------	--

---

**Description**

genomemap\_rjs creates an interactive genome map.

**Usage**

```
genomemap_rjs(assembly, track = NA, plot = TRUE, jupyter = FALSE, dir = "GenomeMap")
```

**Arguments**

assembly	a genome assembly data frame. RJSplot provides human assemblies (NCBI36, GRCh37, GRCh38), human assemblies with cytobands (GRCh37.bands or GRCh38.bands), or methods for creating your own assembly from a FASTA file <a href="#">getAssemblyFromFasta</a> .
track	a data frame with values to represent on the genome map (chromosome, position, value).
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with Firefox. If you want to open this file stored in your local machine with other Web browser, please visit the help section on the RJSplot Web site (<http://rjsplot.net>).

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive Genome map in the folder "GenomeMap" of your local machine
## Live examples on http://rjsplot.net

# Create test data
chr <- character()
pos <- numeric()

for(i in 1:nrow(GRCh38)){
  chr <- c(chr,as.character(rep(GRCh38[i,"chr"],100)))
  pos <- c(pos,sample(GRCh38[i,"start"]:GRCh38[i,"end"],100))
}

value <- round(rexp(length(pos)),2)

# Create a genome map
track <- data.frame(chr,pos,pos+1,NA,value)
genomemap_rjs(GRCh38.bands, track)
```

---

getAssemblyFromFasta    *Create an assembly from a FASTA file for its use as parameter of genomemap\_rjs or manhattan\_rjs.*

---

**Description**

getAssemblyFromFasta create assemblies from a FASTA file for their use as parameter of genomemap\_rjs or manhattan\_rjs.

**Usage**

```
getAssemblyFromFasta(fasta)
```

**Arguments**

`fasta` a "character" string representing the input Fasta file to be added in the genome browser.

**Value**

a data frame in BED format ready to use as an assembly in `genomemap_rjs` or `manhattan_rjs`.

**Note**

FASTA format is a text-based format for representing either nucleotide sequences or peptide sequences, in which nucleotides or amino acids are represented using single-letter codes.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[genomemap\\_rjs](#).  
[manhattan\\_rjs](#).

**Examples**

```
## Live examples and full tutorial on http://rjsplot.net
```

---

GRCh37

*Length of human chromosomes based on GRCh37 assembly*

---

**Description**

Length of human chromosomes based on GRCh37 assembly.

**Source**

See [http://www.ncbi.nlm.nih.gov/assembly/GCF\\_000001405.13/#/st](http://www.ncbi.nlm.nih.gov/assembly/GCF_000001405.13/#/st).

---

GRCh37.bands	<i>Cytoband information based on GRCh37</i>
--------------	---

---

**Description**

A Data Frame containing cytobands of GRCh37 assembly.

**Source**

See [http://grch37.ensembl.org/Homo\\_sapiens/Location/Genome](http://grch37.ensembl.org/Homo_sapiens/Location/Genome).

---

GRCh38	<i>Length of human chromosomes based on GRCh38 assembly</i>
--------	---

---

**Description**

Length of human chromosomes based on GRCh38 assembly.

**Source**

See <http://www.ncbi.nlm.nih.gov/assembly/883148/#/st>.

---

GRCh38.bands	<i>Cytoband information based on GRCh38</i>
--------------	---

---

**Description**

A Data Frame containing cytobands of GRCh38 assembly.

**Source**

See [http://www.ensembl.org/Homo\\_sapiens/Location/Genome](http://www.ensembl.org/Homo_sapiens/Location/Genome).

---

heatmap_rjs	<i>Produce an interactive heatmap.</i>
-------------	--

---

### Description

heatmap\_rjs creates interactive heatmaps.

### Usage

```
heatmap_rjs(data, metadata = NULL, scale = c("row", "column", "none"), cluster = TRUE,
            color = c("Reds", "Greens", "Blues", "RdBkGr", "RdWhBu"),
            na.color = "transparent", cex = 1, plot = TRUE, jupyter = FALSE,
            dir = "Heatmap", distfun = dist, hclustfun = hclust)
```

### Arguments

data	numeric matrix of the values to be plotted.
metadata	a data frame with metadata information for column features (p.e. sample phenotypes). Samples are given in rows and features in columns.
scale	character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. The default value is "none".
cluster	logical value to enable (TRUE) or disable (FALSE) data clustering.
color	character indicating the color scale to paint values. The default value is "Blues".
na.color	character indicating the color to use for missing values. Transparent by default.
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.
distfun	function used to compute the distance between rows and columns.
hclustfun	function used to compute the hierarchical clustering.

### Value

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

### Author(s)

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive heatmap in the folder "Heatmap" of your local machine
## Live examples on http://rjsplot.net
metadata <- data.frame(phenotype1 = sample(c("yes","no"),ncol(mtcars),TRUE),
                      phenotype2 = sample(1:5,ncol(mtcars),TRUE))

heatmap_rjs(data.matrix(mtcars), metadata, scale="column")
```

---

hiveplot_rjs	<i>Produce interactive hive plot</i>
--------------	--------------------------------------

---

**Description**

hiveplot\_rjs creates an interactive hive plot.

**Usage**

```
hiveplot_rjs(links, nodes = NA, group = NULL, size = NULL, color = NULL,
             cex = 1, plot = TRUE, jupyter = FALSE, dir = "HivePlot")
```

**Arguments**

links	an edge list table stored in a data frame with three possible columns (source node id, target node id and link value).
nodes	node attributes stored in a data frame with rownames as node id.
group	column name of nodes data frame which describes visualized axes.
size	column name of nodes data frame which describes each node size.
color	column name of nodes data frame which describes each node color.
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive hive plot in the folder "HivePlot" of your local machine
## Live examples on http://rjsplot.net
# Prepare data
x <- 1-cor(t(mtcars))

source <- rep(rownames(x),nrow(x))
target <- rep(rownames(x),rep(ncol(x),nrow(x)))
links <- data.frame(source=source,target=target,value=as.vector(x))

# Generate the hive plot
hiveplot_rjs(links, mtcars, group = "cyl", size = "wt", color = "carb")
```

---

manhattan\_rjs

---

*Create an interactive manhattan plot*


---

**Description**

manhattan\_rjs creates an interactive Manhattan plot.

**Usage**

```
manhattan_rjs(data, assembly, axisv, distv, cell = 1e+06, outliers = TRUE, ylab = "score",
yscale = NA, cex = 1, plot = TRUE, jupyter = FALSE, dir = "ManhattanPlot")
```

**Arguments**

data	a data frame with four columns (identifier, chromosome/scaffold, position, score).
assembly	a data frame with an assembly to be used. It should be one of the following human assemblies data frames provided by RJSplot: NCBI36, GRCh37, GRCh38.
axisv	value for the coordinate of the main horizontal axis.
distv	distance between the main horizontal axis and the secondary axes (which establishes the limit for the outlier representation).
cell	segment size which is represented.

outliers	logical value to enable (TRUE) or disable (FALSE) outliers.
ylab	a title for the y axis.
yscale	a vector with two values which specifies the minimum and maximum limits in the representation. By default maximum and minimum scores are taken as the limits.
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

### Value

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

### Author(s)

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

### See Also

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

### Examples

```
## Create an interactive Manhattan plot in the folder "ManhattanPlot" of your local machine
## Live examples on http://rjsplot.net

# Create test data
chr <- character()
pos <- numeric()

for(i in 1:nrow(GRCh38)){
  chr <- c(chr,as.character(rep(GRCh38[i,"chr"],100)))
  pos <- c(pos,sample(GRCh38[i,"start"]:GRCh38[i,"end"],100))
}

value <- round(rexp(length(pos)),2)

# Create a manhattan plot
data <- data.frame(paste0("ProbeSet_",seq_along(pos)),chr,pos,value)
manhattan_rjs(data, GRCh38, 0, 1, 0, TRUE, "log2Ratio")
```

NCBI36

*Length of human chromosomes based on NCBI36 assembly***Description**

Length of human chromosomes based on NCBI36 assembly.

**Source**

See [http://www.ncbi.nlm.nih.gov/assembly/GCF\\_000001405.12/#/st](http://www.ncbi.nlm.nih.gov/assembly/GCF_000001405.12/#/st).

network\_rjs

*Produce interactive network graph***Description**

network\_rjs creates an interactive network graph.

**Usage**

```
network_rjs(links, nodes = NA,
            weight = NULL, linkLabel = NULL, linkColor = NULL,
            group = NULL, size = NULL, color = NULL, label = NULL,
            nodeColorScale = c("RdBk", "RdBkGr"), cex = 1,
            plot = TRUE, jupyter = FALSE, dir = "Network")
```

**Arguments**

links	an edge list table stored in a data frame with at least two columns (source node id and target node id).
nodes	a node list stored in a data frame object with rownames as node id.
weight	a vector giving the column of links to show as weight. If NULL but third links column is numeric, this one will be used as weight.
linkLabel	a vector giving the column of links to show as link text.
linkColor	a vector giving the column of links to compute link color or directly a vector of colors.
group	a vector giving the column of nodes to show as group.
size	a vector giving the column of nodes to show as size.
color	a vector giving the column of nodes to compute node color or directly a vector of colors.
label	a vector giving the column of nodes to show as label.
nodeColorScale	a "character" string representing the color scale applied to nodes by default.

cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive network graph in the folder "Network" of your local machine
## Live examples on http://rjsplot.net
# Prepare data
x <- 1-cor(t(mtcars))

source <- rep(rownames(x),nrow(x))
target <- rep(rownames(x),rep(ncol(x),nrow(x)))
links <- data.frame(source=source,target=target,value=as.vector(x))

# Generate the network graph
network_rjs(links[links[,3]>0.1,], mtcars, group = "cyl", size = "hp", color = "mpg")
```

---

newInput	<i>Produce a newInput object for R4web.</i>
----------	---

---

**Description**

newInput produce newInput object for R4web.

**Usage**

```
newInput(name, type = c("character", "numeric", "matrix", "data.frame", "factor"),
         default = "", levels = NULL, multi = FALSE)
```

**Arguments**

name	character string with the variable name.
type	character string which describes the variable type. Possible values are "character", "numeric", "matrix", "data.frame" or "factor".
default	default value for this input.
levels	a vector with the possible input values. It is described only for factor data type.
multi	boolean value which indicates if multiple selection are enabled for this input. It is described only for factor data type.

**Value**

Return a newInput object.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

---

piechart\_rjs                      *Produce interactive pie charts.*

---

**Description**

piechart\_rjs produce interactive pie charts.

**Usage**

```
piechart_rjs(data, cex = 1, plot = TRUE, jupyter = FALSE, dir = "Piechart")
```

**Arguments**

data	a Data Frame or Matrix from which the data for each pie will be taken.
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive pie chart in the folder "Piechart" of your local machine
## Live examples on http://rjsplot.net
piechart_rjs(VADeaths)
```

---

R4web

*Generate a PHP website which runs an R function.*

---

**Description**

R4web generate a PHP website which runs an R function.

**Usage**

```
R4web(...,fnfile,dir)
```

**Arguments**

...	one or more newInput objects which will be included as form fields. Form values will be used as parameters for the R script.
fnfile	a character string representing the R script file to be executed with the website.
dir	a "character" string representing the directory where the PHP code will be saved.

**Value**

The function creates a folder in the working directory of your computer with some PHP files. Resulting folder should be added to the Apache applications directory and enable writing permissions.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>

[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#), [scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#), [piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

---

report_rjs	<i>Create a report web page.</i>
------------	----------------------------------

---

**Description**

report\_rjs creates a report web page.

**Usage**

```
report_rjs(dir = "RJSreport")
addCSS2report(report, css)
addHTML2report(report, HTML)
addParagraph2report(report, p)
addPlot2report(report, plot, height=600)
addImage2report(report, img)
```

**Arguments**

dir	a "character" string representing the directory where the report will be saved.
report	a RJSreport object produced by the function report_rjs.
css	a character string representing the CSS path to be added.
HTML	a character string giving the HTML code to be added.
p	a character string giving the new paragraph to be added.
plot	a character string representing the plot directory to be added.
height	an integer vector giving a default height of the plot.
img	a character string representing the image path to be added.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the report. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>

[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#), [scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#), [piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

---

RJSplot

*Interactive graphs with R*

---

**Description**

Create interactive graphs with 'R'.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>

[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#), [scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#), [piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

---

scatter3d\_rjs

*Produce and interactive 3D Scatter plot (XYZ plot).*

---

**Description**

scatter3d\_rjs generates an interactive 3D Scatter Plot.

**Usage**

```
scatter3d_rjs(x, y, z, color="#000", xlab = "x", ylab = "y", zlab = "z",
              plot = TRUE, jupyter = FALSE, dir = "Scatter3d")
```

**Arguments**

x	a vector with the x data of each point.
y	a vector with the y data of each point.
z	a vector with the z data of each point.
xlab	a title for the x axis.
ylab	a title for the y axis.
zlab	a title for the z axis.
color	a vector with the colour of each represented point.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>

[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#), [scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#), [piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive 3D Scatter plot in the folder "ScatterPlot" of your local machine
## Live examples on http://rjsplot.net

# 3D Scatter plot creation
scatter3d_rjs(iris$Sepal.Width, iris$Sepal.Length, iris$Petal.Width, color = iris$Species,
             xlab = "Sepal Width (cm)", ylab = "Sepal Length (cm)", zlab = "Petal Width (cm)")
```

---

scatterplot\_rjs      *Produce and interactive Scatter plot (XY plot).*

---

### Description

scatterplot\_rjs generates an interactive Scatter Plot.

### Usage

```
scatterplot_rjs(x, y, id = NA, xlab = "", ylab = "", xlim = NA, ylim = NA, col = NA,
               pch = NA, abline.x = NA, abline.y = NA, cex = 1,
               plot = TRUE, jupyter = FALSE, dir = "ScatterPlot")
```

### Arguments

x	a vector with the x data of each point.
y	a vector with the y data of each point.
id	a vector giving the id of each point.
xlab	a title for the x axis.
ylab	a title for the y axis.
xlim	a vector with two values which specifies the X minimum and maximum values in the representation.
ylim	a vector with two values which specifies the Y minimum and maximum values in the representation.
col	a vector with the colour of each represented point.
pch	a character vector with the shape of each point. It should be one of: 1-"circle", 2-"triangle-up", 3-"cross", 4-"square", 5-"diamond", 6-"triangle-down".
abline.x	a numeric vector with x coordinates where a vertical line will be placed.
abline.y	a numeric vector with y coordinates where a horizontal line will be placed.
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

### Value

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

### Author(s)

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>

[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#), [scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#), [piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive Scatter plot in the folder "ScatterPlot" of your local machine
## Live examples on http://rjsplot.net
```

```
# Scatter plot creation
scatterplot_rjs(iris$Sepal.Width, iris$Sepal.Length,
               abline.x = c(3.4,3.8), abline.y = c(5.8,7),
               col = iris$Species, pch = as.numeric(iris$Species), id = iris$Species,
               xlab = "Sepal Width (cm)", ylab = "Sepal Length (cm)")
```

---

surface3d_rjs	<i>Produce and interactive 3D surface.</i>
---------------	--

---

**Description**

surface3d\_rjs generates an interactive 3D surface.

**Usage**

```
surface3d_rjs(x, color = "#fff", xlab = "x", ylab = "y", zlab = "z",
             plot = TRUE, jupyter = FALSE, dir = "Surface3d")
```

**Arguments**

x	numeric matrix of the values to be plotted.
color	a vector with colors to construct the color scale.
xlab	a title for the x axis.
ylab	a title for the y axis.
zlab	a title for the z axis.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive 3D Surface in the folder "Surface3d" of your local machine
## Live examples on http://rjsplot.net

# 3D surface creation
surface3d_rjs(volcano,color=c("red","green"))
```

---

symheatmap_rjs	<i>Creates a Symetric Heatmap representation.</i>
----------------	---

---

**Description**

symheatmap\_rjs creates an interactive symetric heatmap.

**Usage**

```
symheatmap_rjs(links, nodes = NA, group = NULL, label = NULL, cex = 1,
               plot = TRUE, jupyter = FALSE, dir = "SymHeatmap")
```

**Arguments**

links	an edge list table stored in a data frame with three possible columns (source node id, target node id and a link value).
nodes	a node list stored in a data frame object with rownames as node id.
group	a vector giving the column of nodes to show as group.
label	a vector giving the column of nodes to show as label.
cex	number indicating the amount by which plotting text and symbols should be scaled relative to the default.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive symetric heatmap in the folder "SymHeatmap" of your local machine
## Live examples on http://rjsplot.net
# prepare data
x <- 1-cor(t(mtcars))

source <- rep(rownames(x),nrow(x))
target <- rep(rownames(x),rep(ncol(x),nrow(x)))
links <- data.frame(source=source,target=target,value=as.vector(x))

# Create symetric heatmap
symheatmap_rjs(links, mtcars, group = "cyl")
```

---

tables_rjs	<i>Produce interactive html tables.</i>
------------	---

---

**Description**

tables\_rjs produce interactive html tables of the given values.

**Usage**

```
tables_rjs(data, plot = TRUE, jupyter = FALSE, dir = "DataTable")
```

**Arguments**

data	a Data Frame or Matrix to display.
plot	open resulting table in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the table. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive html table in the folder "DataTable" of your local machine
## Live examples on http://rjsplot.net
tables_rjs(swiss)
```

---

wordcloud_rjs	<i>Draw a wordcloud.</i>
---------------	--------------------------

---

**Description**

wordcloud\_rjs creates a wordcloud.

**Usage**

```
wordcloud_rjs(data, plot = TRUE, jupyter = FALSE, dir = "WordCloud")
```

**Arguments**

data	a two column data Frame with the words to display and their frequency.
plot	open resulting graph in your browser.
jupyter	embed the graph as an iframe into a Jupyter Notebook.
dir	a "character" string representing the directory where the graph will be saved.

**Value**

The function creates a folder in your computer with an HTML document named index.html which contains the graph. This file can be directly opened with your browser.

**Author(s)**

David Barrios and Carlos Prieto. Bioinformatics Service of Nucleus, University of Salamanca. See <http://bioinfo.usal.es/>

**See Also**

The 'RJSplot' Website: <http://rjsplot.net>  
[dendrogram\\_rjs](#), [densityplot\\_rjs](#), [genomemap\\_rjs](#), [heatmap\\_rjs](#), [manhattan\\_rjs](#), [network\\_rjs](#),  
[scatterplot\\_rjs](#), [symheatmap\\_rjs](#), [wordcloud\\_rjs](#), [boxplot\\_rjs](#), [bubbles\\_rjs](#), [hiveplot\\_rjs](#),  
[piechart\\_rjs](#), [barplot\\_rjs](#), [tables\\_rjs](#), [surface3d\\_rjs](#), [scatter3d\\_rjs](#).

**Examples**

```
## Create an interactive heatmap in the folder "WordCloud" of your local machine
## Live examples on http://rjsplot.net

## Format test data
words <- data.frame(word = rownames(USArrests), freq = USArrests[,4])

# Create WordCloud
wordcloud_rjs(words)
```

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