

# RBioinfoUtils

March 6, 2014

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heatmap.3

*heatmap.3*

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## Description

heatmap.3

## Usage

```
heatmap.3(x, Rowv = TRUE, Colv = if (symm) "Rowv" else TRUE,
  distfun = dist, hclustfun = hclust, dendrogram = c("both", "row",
    "column", "none"), symm = FALSE, scale = c("none", "row", "column"),
  na.rm = TRUE, revC = identical(Colv, "Rowv"), add.expr, breaks,
  symbreaks = max(x < 0, na.rm = TRUE) || scale != "none",
  col = "heat.colors", colsep, rowsep, sepcolor = "white",
  sepwidth = c(0.05, 0.05), cellnote, notecex = 1, notecol = "cyan",
  na.color = par("bg"), trace = c("none", "column", "row", "both"),
  tracecol = "cyan", hline = median(breaks), vline = median(breaks),
  linecol = tracecol, margins = c(5, 5), ColSideColors, RowSideColors,
  side.height.fraction = 0.3, cexRow = 0.2 + 1/log10(nr), cexCol = 0.2 +
  1/log10(nc), labRow = NULL, labCol = NULL, key = TRUE, keysize = 1.5,
  density.info = c("none", "histogram", "density"), denscol = tracecol,
  symkey = max(x < 0, na.rm = TRUE) || symbreaks, densadj = 0.25,
  main = NULL, xlab = NULL, ylab = NULL, lmat = NULL, lhei = NULL,
  lwid = NULL, NumColSideColors = 1, NumRowSideColors = 1,
  KeyValueName = "Value", ...)
```

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`loadRData`*loadRData - Load all objects saved in the most recent archive*

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**Description**

`loadRData` - Load all objects saved in the most recent archive

**Usage**

```
loadRData(dir, prefix = "R")
```

**Arguments**

`dir`                      Directory in which the objects will be loaded

**Value**

Type NULL

none

**Author(s)**

matheus

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`multiplot`*Do multiple plots in one image <http://www.cookbook-r.com/>*

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**Description**

Do multiple plots in one image <http://www.cookbook-r.com/>

**Usage**

```
multiplot(..., plotlist = NULL, file, cols = 1, layout = NULL)
```

**Arguments**

`...`                      plots objects from ggplot2 (gg object)  
`plotlist`                  a list of plots objects from ggplot2 (gg object)  
`cols`                      Number of columns in layout  
`layout`                    A matrix specifying the layout. If present, 'cols' is ignored.

**References**

[http://www.cookbook-r.com/Graphs/Multiple\\_graphs\\_on\\_one\\_page\\_\(ggplot2\)/](http://www.cookbook-r.com/Graphs/Multiple_graphs_on_one_page_(ggplot2)/)

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plotBox	<i>Boxplot</i>
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**Description**

Boxplot

**Usage**

```
plotBox(x, alpha = 0.5, binwidth = 0.5)
```

**Arguments**

x                      a matrix or data frame

**Value**

a ggplot2 object

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plotDensities	<i>Plor densities</i>
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**Description**

Plor densities

**Usage**

```
plotDensities(x, alpha = 0.5)
```

**Arguments**

x                      a matrix or data frame

**Value**

a ggplot2 object

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plotHist	<i>Plot histogram</i>
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**Description**

Plot histogram

**Usage**

```
plotHist(x, alpha = 0.5, binwidth = 0.5)
```

**Arguments**

x                      a matrix or data frame

**Value**

a ggplot2 object

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plotViolin	<i>Violin plot</i>
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**Description**

Violin plot

**Usage**

```
plotViolin(x, alpha = 0.5, binwidth = 0.5)
```

**Arguments**

x                      a matrix or data frame

**Value**

a ggplot2 object

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saveRData	<i>saveRData - Save all objects in a archive, named with pattern name.</i>
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**Description**

saveRData - Save all objects in a archive, named with pattern name.

**Usage**

```
saveRData(dir, prefix = "R")
```

**Arguments**

dir	Directory in which the objects will be saved
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**Value**

Type NULL  
none

**Author(s)**

matheus, daniel

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unfactor	<i>Unfactor</i>
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**Description**

Unfactor

**Usage**

```
unfactor(x)
```

**Arguments**

x	a factor
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**Value**

a vector

# Index

heatmap, [3](#), [1](#)

loadRData, [2](#)

multiplot, [2](#)

plotBox, [3](#)

plotDensities, [3](#)

plotHist, [4](#)

plotViolin, [4](#)

saveRData, [5](#)

unfactor, [5](#)