

Package ‘hicVennDiagram’

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Title Venn Diagram for genomic interaction data

Version 1.0.0

Description A package to generate high-resolution Venn and Upset plots for genomic interaction data from HiC, ChIA-PET, HiChIP, PLAC-Seq, Hi-TrAC, HiCAR and etc. The package generates plots specifically crafted to eliminate the deceptive visual representation caused by the counts method.

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Encoding UTF-8

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VignetteBuilder knitr

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Suggests BiocStyle, knitr, rmarkdown, testthat, GenomicRanges, ChIPpeakAnno, grid

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BugReports <https://github.com/jianhong/hicVennDiagram/issues>

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browseVenn	<i>Browse the venn plot</i>
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Description

Brow the venn plot in a web browser to adjust the plot and export the result.

Usage

```
browseVenn(plot, width = NULL, height = NULL)
```

Arguments

plot	plots of vennPlot or upsetPlot
width	width of the figure
height	height of the figure

Value

An object of class `htmlwidget` that will intelligently print itself into HTML in a variety of contexts including the R console, within R Markdown documents, and within Shiny output bindings.

Examples

```
pd <- system.file("extdata", package = "hicVennDiagram", mustWork = TRUE)
fs <- dir(pd, pattern = ".bedpe", full.names = TRUE)
vc <- vennCount(fs)
p <- vennPlot(vc)
browseVenn(p)
```

browseVenn-shiny	<i>Shiny bindings for browseVenn</i>
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Description

Output and render functions for using browseVenn within Shiny applications and interactive Rmd documents.

Usage

```
browseVennOutput(outputId, width = "100%", height = "400px")
```

```
renderbrowseVenn(expr, env = parent.frame(), quoted = FALSE)
```

Arguments

outputId	output variable to read from
width, height	Must be a valid CSS unit (like '100%', '400px', 'auto') or a number, which will be coerced to a string and have 'px' appended.
expr	An expression that generates a browseVenn
env	The environment in which to evaluate expr.
quoted	Is expr a quoted expression (with quote())? This is useful if you want to save an expression in a variable.

upsetPlot	<i>UpSet plot for the Venn count table</i>
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Description

Plot the overlaps counts by ComplexUpset.

Usage

```
upsetPlot(
  vennTable,
  label_all = list(na.rm = TRUE, color = "gray30", alpha = 0.7, label.padding = unit(0.1,
    "lines")),
  coln_prefix = NULL,
  ...
)
```

Arguments

vennTable	An vennTable object, the first element in the output of <code>vennCount</code> .
label_all	A list of parameters used by <code>geom_label</code> for text labels of counts for each group. If it set to FALSE or length of the list is zero, the labels will be ignored.
coln_prefix	The prefix to be removed for colnumn names of vennTable.
...	Parameters could be passed to <code>upset</code> except data and intersect.

Value

A ggplot object.

Examples

```
pd <- system.file("extdata", package = "hicVennDiagram", mustWork = TRUE)
fs <- dir(pd, pattern = ".bedpe", full.names = TRUE)
vc <- vennCount(fs)
upsetPlot(vc)
## change the font size of lables and numbers
upsetPlot(vc, label_all=list(
  na.rm = TRUE,
  color = 'gray30',
  alpha = .7,
  label.padding = grid::unit(0.1, "lines"),
  size = 5
), themes = ComplexUpset::upset_modify_themes(
  ## get help by vignette('Examples_R', package = 'ComplexUpset')
  list('intersections_matrix'=
    ggplot2::theme(axis.text.y=ggplot2::element_text(size=24)))
))
```

vennCount	<i>Construct intersections of sets</i>
-----------	--

Description

Given a collection of bedpe files or a list of genomic interaction data, `vennCount` will compute all possible combinations of interactions and return an object of class `vennTable`, storing the combinations as well as the number of elements in each intersection.

Usage

```
vennCount(gi, FUN = min, ...)
```

Arguments

gi	A list of bedpe files or a list of genomic interaction data (Pairs or GInteractions)
FUN	Function to summarize the oberlapping number.
...	parameters used by findOverlaps

Value

An object of [vennTable](#)

Examples

```
pd <- system.file("extdata", package = "hicVennDiagram", mustWork = TRUE)
fs <- dir(pd, pattern = ".bedpe", full.names = TRUE)
vc <- vennCount(fs)
```

 vennPlot

Venn diagram for the Venn count table

Description

Plot the overlaps counts by euler.

Usage

```
vennPlot(vennTable, shape = "circle", ...)
```

Arguments

vennTable	An vennTable object, the first element in the output of vennCount .
shape	Geometric shape used in the diagram used by euler .
...	parameters to update fills and edges with and thereby a shortcut to set these parameters plot.euler .

Value

A grid object.

Examples

```
pd <- system.file("extdata", package = "hicVennDiagram", mustWork = TRUE)
fs <- dir(pd, pattern = ".bedpe", full.names = TRUE)
vc <- vennCount(fs)
vennPlot(vc)
## change the font size of venn plot lables and numbers,
## both cex or fontsize should work
vennPlot(vc, quantities=list(fontsize=24), labels=list(cex=1.5))
```

vennTable-class *Class "vennTable"*

Description

An object of class "vennTable" represents Venn counts.

Usage

```
vennTable(...)

## S4 method for signature 'vennTable'
x$name

## S4 replacement method for signature 'vennTable'
x$name <- value

## S4 method for signature 'vennTable,ANY,ANY'
x[[i]]

## S4 replacement method for signature 'vennTable,ANY,ANY'
x[[i]] <- value

## S4 method for signature 'vennTable'
show(object)
```

Arguments

...	Each argument in ... becomes an slot in the new vennTable.
x	an object of vennTable
name	slot name of vennTable
value	values to assign
i	slot name of vennTable
object	an object of vennTable.

Value

An object of vennTable.

Slots

combinations A logical "matrix", specify the combinations.
 counts A "numeric" vector, the overall counts number for each combination.
 vennCounts A "matrix" object, specify the counts number for each sample in the combination.
 overlapList "list", overlapping list of the genomic interactions.

Examples

```
vt <- vennTable()
```

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