

Package ‘hicVennDiagram’

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Title Venn Diagram for genomic interaction data

Version 1.5.1

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

biocViews DNA3DStructure, HiC, Visualization

Depends R (>= 4.3.0)

Imports GenomeInfoDb, GenomicRanges, IRanges, InteractionSet, rtracklayer, ggplot2, ComplexUpset, reshape2, eulerr, S4Vectors, methods, utils, htmlwidgets, svglite

Suggests BiocStyle, knitr, rmarkdown, testthat, CHIPpeakAnno, grid, TxDb.Hsapiens.UCSC.hg38.knownGene

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Author Jianhong Ou [aut, cre] (ORCID: <<https://orcid.org/0000-0002-8652-2488>>)

Maintainer Jianhong Ou <jou@morgridge.org>

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| | |
|------------|-----------------------------|
| browseVenn | <i>Browse the venn plot</i> |
|------------|-----------------------------|

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 *Shiny bindings for browseVenn*

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. |

createGIbackground *Create background by input GInteractions*

Description

Create background based on the distance distribution of input GInteractions.

Usage

```
createGIbackground(gi, size = 2 * lengths(gi))
```

Arguments

| | |
|------|---|
| gi | A vector of bedpe files or a list of genomic interaction data (Pairs or GInteractions). |
| size | The maximal size of the background |

Examples

```
pd <- system.file("extdata", package = "hicVennDiagram", mustWork = TRUE)
fs <- dir(pd, pattern = ".bedpe", full.names = TRUE)[1]
set.seed(123)
# createGIbackground(fs)
```

| | |
|-----------|---------------------------|
| gleamTest | <i>Perform GLEAM test</i> |
|-----------|---------------------------|

Description

Run Genomic Loops Enrichment Analysis Method test

Usage

```
gleamTest(query, subject, background, method = c("binom", "hyper"), ...)
```

Arguments

| | |
|----------------|---|
| query, subject | A vector of bedpe files or a list of genomic interaction data (Pairs or GInteractions) or a list of GRanges object. 'subject' is optional if length of query > 1. |
| background | The test will restricted within the region. The background is the background of subject if subject is available. Otherwise, the background is the the background of second element of comparison group. |
| method | Distribution type for p-value. |
| ... | parameters used by findOverlaps . |

Examples

```
# example code
pd <- system.file("extdata", package = "hicVennDiagram", mustWork = TRUE)
fs <- dir(pd, pattern = ".bedpe", full.names = TRUE)
library(TxDb.Hsapiens.UCSC.hg38.knownGene)
## set.seed(123)
## background <- createGIbackground(fs)
## gleamTest(fs, background = background)
## gleamTest(fs, background = background, method = 'hyper')
gr1 <- GRangesList(exons=reduce(exons(TxDb.Hsapiens.UCSC.hg38.knownGene)),
  genes=reduce(genes(TxDb.Hsapiens.UCSC.hg38.knownGene)))
gleamTest(fs[seq_along(gr1)], gr1, background = gr1[['exons']])
gleamTest(gr1[c(2, 1)], gr1, background = gr1[['exons']])
gleamTest(gr1, background = gr1[['genes']])
```

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

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 vennCount . |
| label_all | A list of parameters used by geom_label 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 upset 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)
upset_themes_fix <- lapply(ComplexUpset::upset_themes, function(.ele){
  .ele[names(.ele) %in% names(formals(ggplot2::theme))]
})
upsetPlot(vc, theme = upset_themes_fix)
## change the font size of lables and numbers
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)))
)
themes <- lapply(themes, function(.ele){
  .ele[names(.ele) %in% names(formals(ggplot2::theme))]
})
upsetPlot(vc, label_all=list(
  na.rm = TRUE,
  color = 'gray30',
  alpha = .7,
  label.padding = grid::unit(0.1, "lines"),
  size = 5
), themes = themes)
```

vennCount

Construct intersections of sets

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 vector of bedpe files or a list of genomic interaction data ([Pairs](#) or [GInteractions](#))

`FUN` Function to summarize the overlapping 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

| | |
|---------------------|--|
| <code>...</code> | Each argument in <code>...</code> becomes a slot in the new <code>vennTable</code> . |
| <code>x</code> | an object of <code>vennTable</code> |
| <code>name</code> | slot name of <code>vennTable</code> |
| <code>value</code> | values to assign |
| <code>i</code> | slot name of <code>vennTable</code> |
| <code>object</code> | an object of <code>vennTable</code> . |

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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