Package 'EnrichedHeatmap'

April 23, 2016

Type Package

Title Making Enriched Heatmaps

Version 1.0.0

Date 2015-10-12

Author Zuguang Gu

Maintainer Zuguang Gu <z.gu@dkfz.de>

Depends R (>= 3.1.2), grid, ComplexHeatmap (>= 1.4.0), GenomicRanges, IRanges, locfit

Imports methods, matrixStats, stats

Suggests testthat (>= 0.3), knitr, markdown, circlize (>= 0.3.1)

VignetteBuilder knitr

Description Enriched heatmap is a special type of heatmap which visualizes the enrichment of genomic signals on specific target regions. Here we implement Enriched heatmap by ComplexHeatmap package. Since this type of heatmap is just a normal heatmap but with some special settings, with the functionality of ComplexHeatmap, it would be much easier to customize the heatmap as well as concatenating to a list of heatmaps to show correspondance between different data sources.

biocViews Software, Visualization, Sequencing, GenomeAnnotation, Coverage

URL https://github.com/jokergoo/EnrichedHeatmap

License GPL (>= 2)

Repository Bioconductor

Date/Publication 2015-10-12 00:00:00

NeedsCompilation no

R topics documented:

`+.AdditiveUnit` *Add heatmaps or row annotations to a heatmap list*

Description

Add heatmaps or row annotations to a heatmap list

Usage

```
## S3 method for class 'AdditiveUnit'
x + y
```

Arguments

x	an `EnrichedHeatmap-class` object, a `Heatmap-class` object, a `HeatmapAnnotation-class` object or a `HeatmapList-class` object.
y	an `EnrichedHeatmap-class` object, a `Heatmap-class` object, a `HeatmapAnnotation-class` object or a `HeatmapList-class` object.

Details

It overwrites `+.AdditiveUnit` in the ComplexHeatmap package.

Value

A `HeatmapList-class` object or an `EnrichedHeatmapList-class` object

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# users should not use it directly
NULL
```

---

anno_enriched *Annotation function to show the enrichment*

Description

Annotation function to show the enrichment

Usage

```
anno_enriched(gp = gpar(col = "red"), pos_line = TRUE, pos_line_gp = gpar(lty = 2),
    yaxis = TRUE, ylim = NULL, value = c("mean", "sum"), yaxis_side = "right",
    yaxis_gp = gpar(fontsize = 8), show_error = FALSE)
```

Arguments

gp	graphical parameters for the line
pos_line	whether draw vertical lines which represent the position of target
pos_line_gp	graphical parameters for lines
yaxis	whether show yaxis
ylim	ranges on y-axis
value	what type of value corresponds to the y-axis
yaxis_side	side of y-axis
yaxis_gp	graphical parameters for yaxis
show_error	whether show error regions which are +-1 sd to the mean value

Details

This annotation functions shows mean values of columns in the normalized matrix which represents the enrichment of the signals to the targets.

If rows are splitted, there will also be multiple lines for this annotation.

It should only be placed as column annotation of the Enriched Heatmap.

Value

A column annotation function which can be set to top_annotation argument

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
load(paste0(system.file("extdata", "chr21_test_data.RData", package = "EnrichedHeatmap")))
tss = promoters(genes, upstream = 0, downstream = 1)
mat1 = normalizeToMatrix(H3K4me3, tss, value_column = "coverage",
    extend = 5000, mean_mode = "w0", w = 50)
EnrichedHeatmap(mat1, col = c("white", "red"), name = "H3K4me3",
    top_annotation = HeatmapAnnotation(lines = anno_enriched(gp = gpar(col = 2:4))),
    top_annotation_height = unit(2, "cm"),
    km = 3, row_title_rot = 0)
```

---

draw-dispatch *Method dispatch page for draw*

Description

Method dispatch page for `draw`.

Dispatch

`draw` can be dispatched on following classes:

- `draw,EnrichedHeatmapList-method`, `EnrichedHeatmapList-class` class method
- `draw,EnrichedHeatmap-method`, `EnrichedHeatmap-class` class method

Examples

```
# no example
NULL
```

---

draw-EnrichedHeatmap-method *Draw a single heatmap*

Description

Draw a single heatmap

Usage

```
## S4 method for signature 'EnrichedHeatmap'
draw(object, internal = FALSE, ...)
```

Arguments

object	an EnrichedHeatmap-class object.
internal	only used internally.
...	pass to draw,HeatmapList-method.

Details

The function creates an EnrichedHeatmapList-class object which only contains a single heatmap and call draw,EnrichedHeatmapList-method to make the final heatmap.

Value

An EnrichedHeatmapList-class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# see documentation of EnrichedHeatmap
NULL
```

---

draw-EnrichedHeatmapList-method

Draw a list of heatmaps

Description

Draw a list of heatmaps

Usage

```
## S4 method for signature 'EnrichedHeatmapList'
draw(object, padding = unit(c(2, 2, 2, 2), "mm"), ..., newpage= TRUE)
```

Arguments

object	an EnrichedHeatmapList-class object
padding	padding of the plot. Elements correspond to bottom, left, top, right paddings.
...	pass to make_layout,HeatmapList-method
newpage	whether to create a new page

Details

It calls draw,HeatmapList-method to make the plot but with some adjustment specificly for enriched heatmaps.

Value

An EnrichedHeatmapList object

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# see documentation of EnrichedHeatmap
NULL
```

EnrichedHeatmap *Constructor method for EnrichedHeatmap class*

Description

Constructor method for EnrichedHeatmap class

Usage

```
EnrichedHeatmap(mat, score_fun = enriched_score, pos_line = TRUE,
    pos_line_gp = gpar(lty = 2), axis_name = NULL, axis_name_rot = NULL,
    axis_name_gp = gpar(fontsize = 10), border = TRUE, cluster_rows = FALSE,
    show_row_dend = FALSE, ...)
```

Arguments

mat	a matrix which is returned by normalizeToMatrix
score_fun	a function which calculates enriched scores for rows in mat
pos_line	whether draw vertical lines which represent the position of target
pos_line_gp	graphic parameters for lines
axis_name	names for axis which is below the heatmap. If the targets are single points, axis_name is a vectorof length three which corresponds to upstream, target itself and downstream. If thetargets are regions with width larger than 1, axis_name should be a vector of length four which corresponds to upstream, start of targets, end of targets and downstream.
axis_name_rot	rotation for axis names
axis_name_gp	graphic parameters for axis names
border	whether show border of the heatmap
cluster_rows	clustering on rows are turned off by default
show_row_dend	whether show dendrograms on rows
...	pass to Heatmap

Details

EnrichedHeatmap-class is inherited from Heatmap-class. Following parameters are set with pre-defined values:

row_order the rows are sorted by the enriched score which is calcualted by score_fun.The sorting is applied decreasingly.

cluster_columns enforced to be FALSE

show_row_names enforced to be FALSE

show_column_names enforced to be FALSE

bottom_annotation enforced to be NULL

column_title_side enforced to be top

With above pre-defined values, no graphics will be drawn below the heatmap, then the space below the heatmap can be used to add a new graph which contains the axis. A (or two) line which corresponds to the position of target will be added to the heatmap body as well.

Same as the Heatmap-class, users can make more controls on the heatmap such as apply clustering on rows, or split rows by data frame or k-means clustering. Users can also add more than one heatmaps by + operator.

For a detailed demonstration, please go to the vignette.

Value

An EnrichedHeatmap-class object which is inherited from Heatmap-class.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
load(paste0(system.file("extdata", "chr21_test_data.RData",
    package = "EnrichedHeatmap")))
mat3 = normalizeToMatrix(meth, cgi, value_column = "meth", mean_mode = "absolute",
    extend = 5000, w = 50, empty_value = 0.5)
EnrichedHeatmap(mat3, name = "methylation", column_title = "methylation near CGI")
EnrichedHeatmap(mat3, name = "meth1") + EnrichedHeatmap(mat3, name = "meth2")
# for more examples, please go to the vignette
```

EnrichedHeatmap-class *Class for a single heatmap*

Description

Class for a single heatmap

Details

The structure of EnrichedHeatmap-class is the same as HeatmapList-class and the class is inherited from Heatmap-class.

The EnrichedHeatmap-class pre-defines some parameters for Heatmap-class such as the order of rows and supressing column clustering. Also there are several new parameters that are attached in the object.

Methods

The EnrichedHeatmap-class provides following methods:

- EnrichedHeatmap: constructor method.
- draw,EnrichedHeatmap-method: draw a single heatmap.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# There is no example
NULL
```

EnrichedHeatmapList *Constructor method for EnrichedHeatmapList class*

Description

Constructor method for EnrichedHeatmapList class

Usage

```
EnrichedHeatmapList(...)
```

Arguments

...	arguments

Details

There is no public constructor method for the EnrichedHeatmapList-class.

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# no example
NULL
```

EnrichedHeatmapList-class

Class for a list of heatmaps

Description

Class for a list of heatmaps

Details

The structure of EnrichedHeatmapList-class is the same as HeatmapList-class and the class is inherited from HeatmapList-class.

Methods

The EnrichedHeatmapList-class provides following methods:

- draw,EnrichedHeatmapList-method: draw a list of heatmaps.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# There is no example
NULL
```

enriched_score *Enriched scores*

Description

Enriched scores

Usage

```
enriched_score(x1, x2, x3)
```

Arguments

x1	a vector corresponding to values in upstream windows
x2	a vector corresponding to values in target windows
x3	a vector corresponding to values in downstream windows

Details

The function calculates how the signal is enriched in the targets. The score is the sum of values weighted by the reciprocal of the distance to the targets.

Value

A numeric value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
enriched_score(c(1, 2, 3), c(1, 2, 1), c(3, 2, 1))
enriched_score(c(3, 2, 1), c(2, 1, 2), c(1, 2, 3))
```

makeWindows *Split regions into windows*

Description

Split regions into windows

Usage

```
makeWindows(gr, w = NULL, k = NULL, direction = c("normal", "reverse"),
    short.keep = FALSE)
```

Arguments

gr	a GRanges object.
w	window size, a value larger than 1 means the number of base pairs and a value between 0 and 1is the percent to the current region.
k	number of partitions for each region. If it is set, all other arguments are ignored.
direction	where to start the splitting. See 'Details' section.
short.keep	if the the region can not be splitted equally under the window size, whether to keep the windows that are smaller than the window size. See 'Details' section.

Details

Following illustrates the meaning of `direction` and `short.keep`:

```
->--->--->  one region, split by 3bp window
aaabbbccc   direction = "normal",  short.keep = FALSE
aaabbbcccd  direction = "normal",  short.keep = TRUE
 aaabbbccc  direction = "reverse", short.keep = FALSE
abbbcccddd  direction = "reverse", short.keep = TRUE
```

There is one additional column `.row` attached which contains the correspondance between small windows and original regions in `gr` and one additional column `.column` which contains the index of the small window on the current region.

Value

A GRanges object.

Author(s)

Zuguang gu <z.gu@dkfz.de>

Examples

```
gr = GRanges(seqnames = "chr1", ranges = IRanges(start = c(1, 11, 21), end = c(10, 20, 30)))
makeWindows(gr, w = 2)
makeWindows(gr, w = 0.2)
makeWindows(gr, w = 3)
makeWindows(gr, w = 3, direction = "reverse")
makeWindows(gr, w = 3, short.keep = TRUE)
makeWindows(gr, w = 3, direction = "reverse", short.keep = TRUE)
makeWindows(gr, w = 12)
makeWindows(gr, w = 12, short.keep = TRUE)
makeWindows(gr, k = 2)
makeWindows(gr, k = 3)
gr = GRanges(seqnames = "chr1", ranges = IRanges(start = c(1, 11, 31), end = c(10, 30, 70)))
makeWindows(gr, w = 2)
makeWindows(gr, w = 0.2)
```

normalizeToMatrix *Normalize associations between genomic signals and target regions into a matrix*

Description

Normalize associations between genomic signals and target regions into a matrix

Usage

```
normalizeToMatrix(signal, target, extend = 5000, w = extend/50, value_column = NULL,
    mapping_column = NULL, empty_value = 0, mean_mode = c("absolute", "weighted", "w0"),
    include_target = any(width(target) > 1), target_ratio = 0.1, smooth = FALSE,
    s = 1, trim = 0.01)
```

Arguments

signal	a GRanges object which is the genomic signals.
target	a GRanges object.
extend	extended base pairs to the upstream and downstream of target. It can be a vector of length one or two.If it is length one, it means extension to the upstream and downstream are the same.
w	window size for splitting upstream and downstream, and probably target itself.
value_column	column index in signal that will be mapped to colors. If it is NULL, an internal columnwhich all contains 1 will be attached.
mapping_column	mapping column to restrict overlapping between signal and target. By default it tries to look forall regions in signal that overlap with every target.
empty_value	values for small windows that don't overlap with signal.
mean_mode	when a window is not perfectly overlapped to signal, how to correspond the values to this window. See 'Details' section for a detailed explanation.
include_target	whether include target in the heatmap. If the width of all regions in target is 1, include_targetis enforced to FALSE.
target_ratio	the ratio of width of target part compared to the full heatmap
smooth	whether apply smoothing on rows in the matrix. The smoothing is applied by locfit. Pleasenote the data range will change, you need to adjust values in the new matrix afterward.
s	findOverlaps sometimes uses a lot of memory. target is splitted into s parts and eachpart is processed serialized (note it will be slow!).
trim	percent of extreme values to remove, currently it is disabled.

Details

In order to visualize associations between `signal` and `target`, the data is transformed into a matrix and visualized as a heatmap afterward.

Upstream and downstream also with the target body are splitted into a list of small windows and overlap to `signal`. Since regions in `signal` and small windows do not always 100 percent overlap, averaging should be applied.

Following illustrates different settings for `mean_mode`:

```
   4      5      2     values in signal
++++++   +++   +++++   signal
  ================     window (16bp)
    4     3     3      overlap

absolute: (4 + 5 + 2)/3
weighted: (4*4 + 5*3 + 2*3)/(4 + 3 + 3)
w0:       (4*4 + 5*3 + 2*3)/16
```

Value

A matrix with following additional attributes:

upstream_index column index corresponding to upstream of `target`

target_index column index corresponding to `target`

downstream_index column index corresponding to downstream of `target`

extend extension on upstream and downstream

smooth whether smoothing was applied on the matrix

The matrix is wrapped into a simple `normalizeToMatrix` class.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
signal = GRanges(seqnames = "chr1",
  ranges = IRanges(start = c(1, 4, 7, 11, 14, 17, 21, 24, 27),
                   end = c(2, 5, 8, 12, 15, 18, 22, 25, 28)),
    score = c(1, 2, 3, 1, 2, 3, 1, 2, 3))
target = GRanges(seqnames = "chr1", ranges = IRanges(start = 10, end = 20))
normalizeToMatrix(signal, target, extend = 10, w = 2)
normalizeToMatrix(signal, target, extend = 10, w = 2, include_target = TRUE)
normalizeToMatrix(signal, target, extend = 10, w = 2, value_column = "score")
```

print.normalizeToMatrix *Print normalized matrix*

Description

Print normalized matrix

Usage

```
## S3 method for class 'normalizeToMatrix'
print(x, ...)
```

Arguments

x	the normalized matrix returned by normalizeToMatrix
...	other arguments

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# There is no example
NULL
```

show-dispatch *Method dispatch page for show*

Description

Method dispatch page for show.

Dispatch

show can be dispatched on following classes:

- show,EnrichedHeatmapList-method, EnrichedHeatmapList-class class method
- show,EnrichedHeatmap-method, EnrichedHeatmap-class class method

Examples

```
# no example
NULL
```

---

show-EnrichedHeatmap-method
Draw the single heatmap with default parameters

Description

Draw the single heatmap with default parameters

Usage

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

Arguments

object	an EnrichedHeatmap-class object.

Details

Actually it calls draw,EnrichedHeatmap-method, but only with default parameters. If users want to customize the heatmap, they can pass parameters directly to draw,EnrichedHeatmap-method.

Value

An EnrichedHeatmapList-class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# see documentation of EnrichedHeatmap
NULL
```

show-EnrichedHeatmapList-method *Draw a list of heatmaps with default parameters*

Description

Draw a list of heatmaps with default parameters

Usage

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

Arguments

object	an EnrichedHeatmapList-class object.

Details

Actually it calls draw,EnrichedHeatmapList-method, but only with default parameters. If users want to customize the heatmap, they can pass parameters directly to draw,EnrichedHeatmapList-method.

Value

An EnrichedHeatmapList-class object.

Examples

```
# see documentation of EnrichedHeatmap
NULL
```

[.normalizeToMatrix *Subset normalized matrix by rows*

Description

Subset normalized matrix by rows

Usage

```
## S3 method for class 'normalizeToMatrix'
x[i, j, drop = FALSE]
```

Arguments

x	the normalized matrix returned by normalizeToMatrix
i	row index
j	column index
drop	whether drop the dimension

Value

A normalizeToMatrix class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# There is no example
NULL
```

Index