Package ‘EnrichedHeatmap’

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**Type** Package

**Title** Making Enriched Heatmaps

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**Depends** R (>= 3.1.2), grid, ComplexHeatmap (>= 1.11.1), GenomicRanges, IRanges, locfit

**Imports** methods, matrixStats, stats, GetoptLong

**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 correspondence between different data sources.

**biocViews** Software, Visualization, Sequencing, GenomeAnnotation, Coverage

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

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**R topics documented:**

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Add heatmaps or row annotations to a heatmap list

### Description

Add heatmaps or row annotations to a heatmap list

### Usage

```r
## 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

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

---

**anno_enriched**

Annotation function to show the enrichment

**Description**

Annotation function to show the enrichment

**Usage**

```r
anno_enriched(gp = gpar(col = "red"), pos_line = TRUE, pos_line_gp = gpar(1ty = 2),
yaxis = TRUE, ylim = NULL, value = c("mean", "sum", "abs_mean", "abs_sum"), yaxis_side = "right",
yaxis_gp = gpar(fontsize = 8), show_error = FALSE)
```

**Arguments**

- **gp** graphic parameters
- **pos_line** whether draw vertical lines which represent the position of target
- **pos_line_gp** graphic parameters
- **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** graphic parameters for yaxis
- **show_error** whether show error regions which are ±1 se to the mean value. Color of error area is same as the corresponding lines with 75 percent transparency.

**Details**

This annotation function 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 in 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 in EnrichedHeatmap.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
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, trim = c(0, 0.01))
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)
```
copyAttr

Description
Copy attributes to another object

Usage
copyAttr(x, y)

Arguments
x  object 1
y  object 2

Details
The `normalizeToMatrix` object actually is a matrix but with more additional attributes attached. This function is used to copy these new attributes when dealing with the matrix.

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
NULL

default_smooth_fun

Description
Default smooth function

Usage
default_smooth_fun(x)

Arguments
x  input numeric vector

Details
The smooth function is applied to every row in the normalized matrix. For this default smooth function, `locfit` is first tried on the vector. If there is error, `loess` smoothing is tried afterwards. If both smoothing are failed, there will be an error.
draw-dispatch

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
# There is no example
NULL

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>an EnrichedHeatmap-class object.</td>
</tr>
<tr>
<td>internal</td>
<td>only used internally.</td>
</tr>
<tr>
<td>...</td>
<td>pass to draw,HeatmapList-method.</td>
</tr>
</tbody>
</table>
draw-EnrichedHeatmapList-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
```r
# see documentation of EnrichedHeatmap
NULL
```

draw-EnrichedHeatmapList-method

Draw a list of heatmaps

Description
Draw a list of heatmaps

Usage
```r
## 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.
- `newpage` whether to create a new page
- `...` pass to `make_layout,HeatmapList-method` or `draw,HeatmapList-method`

Details
It calls `draw,HeatmapList-method` to make the plot but with some adjustment specifically 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, row_order = NULL, 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. This function can be self-defined, take a look at enriched_score to find out how to design it. Note if row clustering is turned on, this argument is ignored.
row_order row order. If it is specified, score_fun is ignored.
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 vector of length three which corresponds to upstream, target itself and downstream. If the targets 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 calculated 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 EnrichedHeatmap-class is inherited from Heatmap-class.

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>
EnrichedHeatmapList

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 EnrichedHeatmapList-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

```r
# There is no example
NULL
```
getSignalsFromList

Get signals from a list

Description
Get signals from a list

Usage
getSignalsFromList(lt, fun = function(x) mean(x, na.rm = TRUE))

Arguments

- `lt`: a list of objects which are returned by `normalizeToMatrix`. Objects in the list should come from same settings.
- `fun`: a self-defined function which gives mean signals across samples. If we assume the objects in the list correspond to different samples, then different regions in the targets are the first dimension, different positions upstream or downstream of the targets are the second dimension, and different samples are the third dimension. This self-defined function can have one argument which is the vector containing values in different samples in a specific position to a specific target region. Or it can have a second argument which is the index for the current target.

Details
Let's assume you have a list of histone modification signals for different samples and you want to visualize the mean pattern across samples. You can first normalize histone mark signals for each sample and then calculate means values across all samples. In following example code, `hm_gr_list` is a list of GRanges objects which contain positions of histone modifications, `tss` is a GRanges object containing positions of gene TSS.

```r
mat_list = NULL
for(i in seq_along(hm_gr_list)) {
    mat_list[[i]] = normalizeToMatrix(hm_gr_list[[i]], tss, value_column = "density")
}
```

Applying `getSignalsFromList()` to `mat_list`, it gives a new normalized matrix which contains mean signals and can be directly used in `EnrichedHeatmap()`.

```r
mat = getSignalsFromList(mat_list)
EnrichedHeatmap(mat)
```

Next let's consider a second scenario: we want to see the correlation between histone modification and gene expression. In this case, `fun` can have a second argument so that users can correspond histone signals to the expression of the associated gene. In following code, `expr` is a matrix of expression, columns in `expr` correspond to elements in `hm_gr_list`, rows in `expr` are same as `tss`.

```r
mat = getSignalsFromList(mat_list,
    fun = function(x, i) cor(x, expr[i, ], method = "spearman"))
```
Then mat here can be used to visualize how gene expression is correlated to histone modification around TSS.

```
EnrichedHeatmap(mat)
```

**Value**

A `normalizeToMatrix` object which can be directly used for `EnrichedHeatmap`.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

NULL

---

**makeWindows**

*Split regions into windows*

**Description**

Split regions into windows

**Usage**

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

**Arguments**

- `query` a `GRanges` object.
- `w` window size, a value larger than 1 means the number of base pairs and a value between 0 and 1 is 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 (">") means the direction of the sequence
aaabbccc direction = "normal", short.keep = FALSE
aaabbcccd direction = "normal", short.keep = TRUE
aaabbbccc direction = "reverse", short.keep = FALSE
abbbccccdd direction = "reverse", short.keep = TRUE
```
**normalizeToMatrix**

**Value**

A GRanges object with two additional columns attached:

- `.i_query` which contains the correspondence between small windows and original regions in query
- `.i_window` which contains the index of the small window on the current region.

**Author(s)**

Zuguang gu <z.gu@dkfz.de>

**Examples**

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

**Description**

Normalize associations between genomic signals and target regions into a matrix

**Usage**

```r
normalizeToMatrix(signal, target, extend = 5000, w = max(extend)/50,
value_column = NULL, mapping_column = NULL, empty_value = ifelse(smooth, NA, 0),
mean_mode = c("absolute", "weighted", "w0", "coverage"), include_target = any(width(target) > 1),
target_ratio = ifelse(all(extend == 0), 1, 0.1), k = min(c(20, min(width(target)))),
smooth = FALSE, smooth_fun = default_smooth_fun, trim = 0)
```

**Arguments**

- `signal` a GRanges object.
- `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.
normalizeToMatrix

w
value_column
mapping_column
empty_value
mean_mode
include_target
target_ratio
k
smooth
smooth_fun
trim

Details

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

Upstream and downstream also with the target body are split into a list of small windows and overlap to signal. Since regions in signal and small windows do not always 100 percent overlap, there are four different average modes:

Following illustrates different settings for mean_mode (note there is one signal region overlapping with other signals):

<table>
<thead>
<tr>
<th>signal region overlap</th>
<th>values in signal</th>
<th>absolute: ((40 + 30 + 50 + 20)/4)</th>
<th>weighted: ((40<em>4 + 30</em>6 + 50<em>3 + 20</em>3)/(4 + 6 + 3 + 3))</th>
<th>w0: ((40<em>4 + 30</em>6 + 50<em>3 + 20</em>3)/(4 + 6 + 3 + 3 + 3))</th>
<th>coverage: ((40<em>4 + 30</em>6 + 50<em>3 + 20</em>3)/17)</th>
</tr>
</thead>
<tbody>
<tr>
<td>++++++ +++ +++++</td>
<td>++++++ ++++++</td>
<td>++++++ ++++++</td>
<td>++++++ ++++++</td>
<td>++++++ ++++++</td>
<td>++++++ ++++++</td>
</tr>
<tr>
<td>40 50 20</td>
<td>signal</td>
<td>values in signal</td>
<td>values in signal</td>
<td>values in signal</td>
<td>window (17bp), there are 4bp not overlapping to any signal region.</td>
</tr>
<tr>
<td>30</td>
<td>values in signal</td>
<td></td>
<td></td>
<td></td>
<td>overlap</td>
</tr>
<tr>
<td></td>
<td>signal</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

To explain it more clearly, let’s consider three scenarios:
First, we want to calculate mean methylation from 3 CpG sites in a 20bp window. Since methylation is only measured at CpG site level, the mean value should only be calculated from the 3 CpG sites while not the non-CpG sites. In this case, absolute mode should be used here.

Second, we want to calculate mean coverage in a 20bp window. Let's assume coverage is 5 in 1bp ~ 5bp, 10 in 11bp ~ 15bp and 20 in 16bp ~ 20bp. Since coverage is kind of attribute for all bases, all 20 bp should be taken into account. Thus, here w0 mode should be used which also takes account of the 0 coverage in 6bp ~ 10bp. The mean coverage will be calculated as \((5*5 + 10*5 + 20*5)/(5+5+5+5)\).

Third, genes have multiple transcripts and we want to calculate how many transcripts exist in a certain position in the gene body. In this case, values associated to each transcript are binary (either 1 or 0) and coverage mean mode should be used.

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
- **failed_rows** index of rows which are failed for smoothing

The matrix is wrapped into a simple normalizeToMatrix class.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
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.normalizedMatrix**

Print normalized matrix

---

**Description**

Print normalized matrix

**Usage**

```r
## S3 method for class 'normalizedMatrix'
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

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

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

```r
# no example
NULL
```
**show-EnrichedHeatmap-method**

*Draw the single heatmap with default parameters*

---

**Description**

Draw the single heatmap with default parameters

**Usage**

```r
## 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**

```r
# 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**

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

`.normalizedMatrix
Subset normalized matrix by rows

Description
Subset normalized matrix by rows

Usage
```r
## S3 method for class 'normalizedMatrix'
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 `normalizedMatrix` class object.

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
```r
# There is no example
NULL
```
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