Package ‘heatmaps’

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**Title**  Flexible Heatmaps for Functional Genomics and Sequence Features

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**License**  Artistic-2.0

**Description**  This package provides functions for plotting heatmaps of genome-wide data across genomic intervals, such as ChIP-seq signals at peaks or across promoters. Many functions are also provided for investigating sequence features.

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R topics documented:

coords ................................................................. 2
CoverageHeatmap .................................................... 3
default_color .......................................................... 4
getScale ................................................................. 5
Heatmap ................................................................. 5
Heatmap-class .......................................................... 6
HeatmapExamples ....................................................... 7
heatmapOptions ........................................................ 8
image ................................................................. 10
label ................................................................. 10
length,Heatmap-method ............................................. 11
metadata ............................................................. 12
nseq ................................................................. 12
PatternHeatmap ........................................................ 13
plot_clusters .......................................................... 14
plot_legend ............................................................ 15
plotHeatmap ........................................................... 16
plotHeatmapList ....................................................... 17
plotHeatmapMeta ...................................................... 18
plotPatternDensityMap ............................................... 19
PWMScanHeatmap ..................................................... 20
rev,Heatmap-method ................................................ 21
scale ................................................................. 21
smoothHeatmap ........................................................ 22
width,Heatmap-method .............................................. 23
xm ................................................................. 23
ym ................................................................. 24

Index ............................................................................ 25

coords  

Return or set the coords in a Heatmap

Description

Return or set the coords in a Heatmap

Usage

coords(x)

## S4 method for signature 'Heatmap'
coords(x)

coords(x) <- value
CoverageHeatmap

## S4 replacement method for signature 'Heatmap'
\texttt{coords(x) <- value}

**Arguments**

- **x**  
  A heatmap
- **value**  
  Replacement value

**Value**

integer, length 2, value of \texttt{x@coords}

**Examples**

\begin{verbatim}
data(HeatmapExamples)  
coords(hm) = c(-100, 100)
\end{verbatim}

---

**CoverageHeatmap**  
*Generate a Heatmap of coverage*

**Description**

Generate a Heatmap of coverage

**Usage**

\begin{verbatim}
CoverageHeatmap(windows, track, ...)  
\end{verbatim}

**Arguments**

- **windows**  
  A set of GRanges of equal length
- **track**  
  A GRanges or RleList object specifying coverage
- **...**  
  additional arguments used by methods

This function generates a Heatmap object from a set of windows and an object containing genome-wide information about coverage. Either a GRanges or an RleList can be used. In the former case, the "weight" parameter is passed directly to the 'coverage' function. If nbin is set, binned coverage is calculated which will save memory and time when plotting and average out variable data.
If the coverage track contains negative values, then the scale will be centered on zero, i.e. \(c(-\max(\text{abs}(\text{image}(hm))), \max(\text{abs}(\text{image}(hm))))\). This makes more sense for most color schemes which are centered on zero, and avoids misleading plots where either positive or negative values are over-emphasised. See `?getScale` for details. The scale can be manually reset if desired using the "scale" method.

- **coords**: Co-ordinates for the heatmap, defaults to \(c(0, \text{width}(\text{windows}))\)
- **weight**: Passed to `coverage(track)` constructor if `class(track) == "GRanges"`
- **label**: Label for the heatmap
- **nbin**: If set, number of bins to use across each window

**Value**

A Heatmap object

**Methods (by class)**

- `windows = \text{GenomicRanges}, track = \text{GenomicRanges}`: Heatmap of Coverage from 2 GRanges
- `windows = \text{GenomicRanges}, track = \text{RleList}`: Heatmap of Coverage from GRanges + RleList

**Examples**

```r
data(HeatmapExamples)
CoverageHeatmap(windows, rle_list, coords=c(-100, 100), label="Example")
```

---

**default_color**

**Predifined color palettes from RColorBrewer + Rainbow**

**Description**

Predifined color palettes from RColorBrewer + Rainbow

**Usage**

default_color(col)

**Arguments**

- **col**: Character, RColorBrewer colorscheme or "Rainbow"
  
  This function provides a convenient function to all color palettes from RColorBrewer, and a better version of R’s rainbow function (specifically `rev(rainbow(9, start=0, end=4/6))`, so it starts blue and ends with red).

**Value**

character, a length-9 color palette
getScale

Examples

```r
default_color("Blues")
default_color("Rainbow")
```

getScale

Make an appropriate scale for a heatmap

Description

Make an appropriate scale for a heatmap

Usage

```r
getScale(x, y)
```

Arguments

- `x`: Min/max values for the heatmap
- `y`: Min/max values for the heatmap

This function takes min/max values for a heatmap and generates a scale either starting, ending or centered on zero.

Value

numeric, length 2, a new scale

Examples

```r
getScale(0.5, 5) # c(0, 5)
getScale(-6, -2) # c(-6, 6)
getScale(-6, 2) # c(-6, 6)
```

Heatmap

Function to create a heatmap object

Description

Function to create a heatmap object

Usage

```r
Heatmap(image, coords = NULL, label = "", nseq = NULL, scale = NULL, metadata = list())
```
Heatmap-class

Arguments

- **image**: A numeric Matrix
- **coords**: A length-2 integer vector
- **label**: A character vector
- **nseq**: An integer
- **scale**: A length-2 vector
- **metadata**: A list containing arbitrary metadata

Using this function avoids calling 'new' directly or manually setting coords and nseq to integers. Other constructors exist for creating heatmaps from data, rather than a raw matrix.

Value

A Heatmap object

See Also

PatternHeatmap CoverageHeatmap PWMScanHeatmap

Examples

```r
data(HeatmapExamples)
hm = Heatmap(mat, coords=c(-100, 100), label="Test")
```

Description

An S4 class to represent a heatmap

Slots

- **image**: A numeric Matrix
- **scale**: A length-2 vector
- **coords**: A length-2 integer vector
- **nseq**: An integer
- **label**: A character vector
- **metadata**: A list containing arbitrary metadata

A class used to represent a heatmap in a simple, self-contained way

Slots can be accessed and set using getters and setters with the same name.

See Also

CoverageHeatmap PatternHeatmap plotHeatmap plotHeatmapMeta
Examples

data(HeatmapExamples)

hm = new("Heatmap",
    image=mat,
    scale=c(0,max(mat)),
    coords=c(-100L, 100L),
    nseq=1000L,
    label="Test",
    metadata=list())

# or use the constructor:
hm = Heatmap(mat, coords=c(-100, 100), label="Test")

Description

Generated Data for examples
An example heatmap
A second example heatmap
An example matrix
An example RleList
An example DNAStringSet
An example PWM
An example GRanges

Usage

hm

hm2

mat

rle_list

string_set

tata_pwm

windows
Format

An object of class Heatmap of length 500.

Value

invisible("HeatmapExamples")

heatmapOptions

Generate default options for a Heatmap

Description

Generate default options for a Heatmap

Usage

heatmapOptions(...)

Arguments

... options to set manually

Guide to Heatmap options

This is an reference to all the possible options for plotting heatmaps. Some options are handled by heatmaps functions (either plotHeatmap or plotHeatmapList), others are passed directly to plotting functions. Further explanation is available in the vignette. Arguments are numeric if not otherwise stated.

color: A vector of colors or a default color, see ?default_color. plotHeatmap will interpolate between these colors to form a scale.

box.width: width of box around the heatmap, passed to box()

x.ticks: Logical, plot x axis ticks

x.tick.labels: Character, labels to use for x ticks, (default blank)

tcl: Length of x axis ticks

padj: Vertical adjustment of x axis labels

cex.axis: cex for axis labels

scale: Logical, Plot scale or not

scale.label: Character, label for scale

scale.lwd: Width for line around scale

cex.scale: Cex for Scale

label: Logical, plot label or not

label.xpos: x position for label, from left

label.ypos: y position for label, from top

cex.label: cex for axis labels

label.col: Color for label, white is often useful for dark plots

legend: Logical, plot legend (scale indicating values for colors)
legend: Color for label, white is often useful for dark plots
legend.pos: Character, position of legend relative to heatmap: 'l' for left, 'r' for right
legend.ticks: Number of ticks to use on legend.
cex.legend: cex to use for legend marks
refline: Logical, Draw dashed line at coords = 0
label.xpos: x position for label, from left
label.ypos: y position for label, from top
cex.label: cex for axis labels
label.col: Color for label, white is often useful for dark plots
legend: Logical, plot legend (scale indicating values for colors)
legend.pos: Character, position of legend relative to heatmap: 'l' for left, 'r' for right
legend.ticks: Number of ticks to use on legend.
cex.legend: cex to use for legend marks
refline: Logical, Draw dashed line at coords = 0
refline.width: Width of reference line
transform: Function to transform values before plotting
plot.mai: Length-4 numeric, margins around plot
legend.mai: Length-4 numeric, margins around legend
partition: Numeric, relative sizes of clusters
partition.lines: Logical, plot lines delineating clusters
partition.legend: Logical, plot cluster legend in HeatmapList
partition.col: Character, colours to use for plotting clusters. Defaults to RColorBrewer's Set1
hook: Function called after plotting is complete.

Value

A list containing the specified options

See Also

plotHeatmap plotHeatmapList

Examples

myOptions = heatmapOptions()
myOptions$color = "Reds"
# plotHeatmap(hm, options=myOptions)
## image

Return or set the image in a Heatmap

### Description
Return or set the image in a Heatmap

### Usage

```r
## S4 method for signature 'Heatmap'
image(x)

image(x) <- value

## S4 replacement method for signature 'Heatmap'
image(x) <- value
```

### Arguments

- **x** A heatmap
- **value** Replacement value

### Value

matrix, from hm@image

### Examples

```r
data(HeatmapExamples)
image(hm) = log(image(hm))
scale(hm) = c(0, max(image(hm)))
```

## label

Return or set the label in a Heatmap

### Description
Return or set the label in a Heatmap
length,Heatmap-method

Usage

label(x)

## S4 method for signature 'Heatmap'
label(x)

label(x) <- value

## S4 replacement method for signature 'Heatmap'
label(x) <- value

Arguments

x A heatmap
value Replacement value

Value

character, value of hm@label

Examples

data(HeatmapExamples)
label(hm) = "NewLabel"
label(hm) # "NewLabel"

length,Heatmap-method  Return the number of sequences in a heatmap

Description

Return the number of sequences in a heatmap

Usage

## S4 method for signature 'Heatmap'
length(x)

Arguments

x A heatmap

Value

integer, value of x@nseq
metadata

Return or set the metadata in a Heatmap

Description
Store arbitrary metadata in a list, if desired.

Usage
metadata(x)

## S4 method for signature 'Heatmap'
metadata(x)
metadata(x) <- value

## S4 replacement method for signature 'Heatmap'
metadata(x) <- value

Arguments
x A heatmap
value Replacement value

Value
list, value of hm@metadata

Examples
data(HeatmapExamples)
metadata(hm) = list(replicate=1, cell_line="ESC")
metadata(hm)$replicate == 1

nseq

Return or set nseq in a Heatmap

Description
Return or set nseq in a Heatmap
PatternHeatmap

Usage

nseq(x)

## S4 method for signature 'Heatmap'
nseq(x)

nseq(x) <- value

## S4 replacement method for signature 'Heatmap'
nseq(x) <- value

Arguments

x A heatmap

value Replacement value

Value

integer, value of hm@nseq

Examples

data(HeatmapExamples)
nseq(hm) = 1000

---

PatternHeatmap Generate a Heatmap of patterns in DNA sequence

Description

Generate a Heatmap of patterns in DNA sequence

Usage

PatternHeatmap(seq, pattern, ...)

## S4 method for signature 'DNAStringSet,character'
PatternHeatmap(seq, pattern, coords = NULL, 
               min.score = NULL, label = NULL)

## S4 method for signature 'DNAStringSet,matrix'
PatternHeatmap(seq, pattern, coords = NULL, 
               min.score = "80%", label = NULL)
Arguments

seq A DNAString of equal length
pattern A nucleotide pattern or PWM
... additional arguments used by methods

This function creates a Heatmap from a set of DNA sequences. The resulting heatmap will be binary, with 1 representing a match and 0 otherwise. Patterns can be specified as a character vector, e.g. "CTCCC", or as a PWM. These arguments are passed to Biostrings functions, ‘vmatchPattern’ and ‘matchPWM’. Character arguments can contain standard ambiguity codes. PWMs must be 4 by \( n \) matrices with columns names ACGT. "min.score" is specified either as an absolute value, or more commonly as a percentage e.g. "80% for details. PatternHeatmaps often look much better after smoothing.

coords Co-ordinates for the heatmap, defaults to \( c(0, \text{width(windows)}) \)
min.score Minimum score for PWM match
label Label for the heatmap

Value

A heatmap

Methods (by class)

- seq = DNAStringSet, pattern = character: Heatmap of sequence patterns from sequence and character
- seq = DNAStringSet, pattern = matrix: Heatmap of sequence patterns from sequence and matrix

See Also

smoothHeatmap

Examples

data(HeatmapExamples)
PatternHeatmap(string_set, "TA", coords=c(-100, 100), label="TA")
PatternHeatmap(string_set, tata_pwm, coords=c(-100, 100), min.score="80%", label="TATA PWM")

Description

Plot partition in a separate panel
Usage

plot_clusters(options)

Arguments

options     heatmapOptions passed as a list

Two heatmapOptions values are relevant:
* partition Numeric vector containing relative sizes of the clusters * colors Colors to use for clusters, additional colors are discarded

This function plots a vertical color scale (or legend). With the default parameters, it looks good at about 1/5 the width of a heatmap, about 1cm x 10cm. This function only plots the legend, it does not set margin parameters.

Value

invisible(0)

See Also

plotHeatmapList

Examples

data(HeatmapExamples)
opts = heatmapOptions()
opts$partition = c(1,2,3,4)
par(mai=opts$legend.mai)
plot_clusters(opts)

plot_legend         Plot a color legend for a heatmap

Description

Plot a color legend for a heatmap

Usage

plot_legend(scale, options)

Arguments

scale     Numeric vector contain min and max for the scale

options     heatmapOptions passed as a list

This function plots a vertical color scale (or legend). With the default parameters, it looks good at about 1/5 the width of a heatmap, about 1cm x 10cm. This function only plots the legend, it does not set margin parameters.
plotHeatmap

Plot a Heatmap object to the device

Description

Plot a Heatmap object to the device

Usage

plotHeatmap(heatmap, options = NULL, ...)

## S4 method for signature 'Heatmap'
plotHeatmap(heatmap, options = NULL, ...)

Arguments

heatmap A heatmap object
options A list containing plotting options
... Used for passing individual options

This function will take a heatmap and plot it to the device with the specified options. Options can be passed together in a list or individually as additional arguments. If passing options as a list, it's best to first create a list containing the default settings using heatmapOptions() and method then setting options individually.

plotHeatmap() does not control device settings at all, these can be set using plotHeatmapList() and the relevant options in heatmapOptions()

See ?heatmapOptions for a full list of options.

Value

invisible(0)
Methods (by class)

- Heatmap: Plot a Heatmap object to the device

See Also

heatmapOptions, plotHeatmapList

Examples

data(HeatmapExamples)
plotHeatmap(hm, color="Blues")

plotHeatmapList Plot a list of heatmaps

Description

Plot a list of heatmaps

Usage

plotHeatmapList(heatmap_list, groups = 1:length(heatmap_list),
options = heatmapOptions(), ...)

Arguments

  heatmap_list  A list of Heatmaps
  groups       Optionally group heatmaps together
  options      Heatmap options
  ...          Additional options

This function takes a list of one or more heatmaps and plots them to a single
image tiled horizontally.

The "groups" argument specifies heatmaps to be grouped together and plotted
using the same display parameters and a unified scale. plotHeatmapList will try
to guess the best scale, either starting or finishing at zero, or symmetrical around
zero - if this is not the desired behaviour, make sure the scales are identical
before the heatmaps are passed to the function.

Options are specified as for plotHeatmap, but can be specified per group by
passing a list of options instead of a single vector. Note the difference between a
length-2 character vector, c("Reds", "Blues"), and a list containing two length-1
character vectors: list("Reds", "Blues").

These are generally large, complex plots, so it can better to plot straight to a
file. PNG is preferred since pdf files generated can be if the images are not
downsized. The default settings are designed for plots of about 10cm x 20cm per
heatmap, but all of the relevant settings can be tweaked using the options. For
display-quality images, it helps to increase the resolution at to at least 150ppi,
double the default of 72ppi on most systems.
plotHeatmapMeta

Value
 invisible(0)

See Also
 plotHeatmap heatmapOptions plot_legend

Examples

```r
data(HeatmapExamples)
plotHeatmapList(list(hm, hm2), groups=c(1,2), color=list("Reds", "Blues"))
```

---

**plotHeatmapMeta**  
*Plot a Meta-region plot from heatmaps*

Description
 Plot a Meta-region plot from heatmaps

Usage

```r
plotHeatmapMeta(hm_list, binsize = 1, colors = gg_col(length(hm_list)),
               addReferenceLine = FALSE)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>hm_list</td>
<td>A list of heatmaps</td>
</tr>
<tr>
<td>binsize</td>
<td>Integer, size of bins to use in plot</td>
</tr>
<tr>
<td>colors</td>
<td>Color to use for each heatmap</td>
</tr>
<tr>
<td>addReferenceLine</td>
<td>Logical, add reference line at zero or not</td>
</tr>
</tbody>
</table>

This function creates a meta-region plot from 1 or more heatmaps with the same coordinates. A meta-region plot graphs the sum of the signal at each position in each heatmap rather than visualising the signal in two dimensions. Often binning is required to smooth noisy signal.

Value
 invisible(0)

Examples

```r
data(HeatmapExamples)
plotHeatmapMeta(hm, color="steelblue")
```
plotPatternDensityMap  

Plot heatmaps for several patterns in DNA sequence

Description

Plot heatmaps for several patterns in DNA sequence

Usage

plotPatternDensityMap(seq, patterns, ...)

## S4 method for signature 'DNAStringSet'

plotPatternDensityMap(seq, patterns, coords = NULL,
                        min.score = "80%", sigma = c(3, 3), output.size = NULL,
                        options = NULL, ...)

Arguments

seq  DNAStringSet of equal width
patterns A vector or list of patterns
...   Additional Heatmap plotting options
coords Heatmap coords
min.score Minimum score for PWM match
sigma Bandwith for smoothing kernel
output.size Output size of final image
options Heatmap plotting options

Value

invisible(0)

Methods (by class)

- DNAStringSet: Plot heatmaps for several patterns in DNA sequence

See Also

PatternHeatmap plotHeatmapList smoothHeatmap
Examples

```r
data(HeatmapExamples)
plotPatternDensityMap(string_set, c("AT", "CG"), coords=c(-200, 200))
```

---

**PWMScanHeatmap**

*Generate a Heatmap of PWM Scores in DNA sequence*

**Description**

Generate a Heatmap of PWM Scores in DNA sequence

**Usage**

```r
PWMScanHeatmap(seq, pwm, ...)
```

## S4 method for signature 'DNAStringSet,matrix'

```r
PWMScanHeatmap(seq, pwm, coords = NULL,
               label = "")
```

**Arguments**

- `seq` A DNAString of equal length
- `pwm` A PWM
- `...` additional arguments used by methods
- `coords` Co-ordinates for the heatmap, defaults to c(0, width(windows))
- `label` Label for the heatmap

**Value**

A heatmap

**Methods (by class)**

- `seq = DNAStringSet`, `pwm = matrix`: Heatmap of PWM Scores

**See Also**

PatternHeatmap

**Examples**

```r
data(HeatmapExamples)
PatternHeatmap(string_set, tata_pwm, coords=c(-100, 100), label="TATA Scan")
```
rev,Heatmap-method

**Description**

Reflect a heatmap in the x axis

**Usage**

```r
## S4 method for signature 'Heatmap'
rev(x)
```

**Arguments**

- `x` A heatmap

**Value**

A heatmap

---

scale

**Description**

Return or set the scale in a Heatmap

**Usage**

```r
scale(x)
```

```r
## S4 method for signature 'Heatmap'
scale(x)
```

```r
scale(x) <- value
```

```r
## S4 replacement method for signature 'Heatmap'
scale(x) <- value
```

**Arguments**

- `x` A heatmap
- `value` Replacement value
smoothHeatmap

Value

numeric, length 2, the value of hm@scale

Examples

data(HeatmapExamples)
scale(hm) = c(-1000, 1000)

smoothHeatmap Smooth a heatmap

Description

Smooth a heatmap

Usage

smoothHeatmap(heatmap, ...)

## S4 method for signature 'Heatmap'
smoothHeatmap(heatmap, sigma = c(3, 3),
output.size = dim(image(heatmap)), algorithm = NULL)

Arguments

heatmap A heatmap object

... additional arguments to S4 methods

This function smooths a heatmap using either binned kernel density (more efficient for binary heatmaps) or gaussian blur.

Sigma controls the SD of the kernel in both cases, defined in terms of pixels. This means that if you have very different x and y dimensions (e.g. a 200bp heatmap around 10000 promoters) you will need to compensate by setting sigma[2] higher to get the same visual effect in both dimensions.

"output.size" specifies the dimensions of the output matrix. This can be useful to reduce plotting time significantly.

Smoothing can use either a kernel density estimate or a blurring function. The methods implemented are KernSmooth::bkde2D and EBImage::filter2 with a gaussian filter. The kernel based method assumes we are smoothing individual points so the value of these points are ignored. This is most useful for smoothing PatternHeatmaps where each cell in the matrix is either 1 or 0. For non-binary heatmaps, blur is most appropriate. Not setting this parameter will choose the method automatically.

Scaling the output heatmap is handled as in CoverageHeatmap.

sigma Numeric, lengt2, (recycled if length 1)

output.size Numeric, length 2

algorithm "kernel" or "blur"
Methods (by class)

- Heatmap: Smooth a heatmap

Examples

```r
data(HeatmapExamples)
hm_smoothed = smoothHeatmap(hm, sigma=c(5,5), algorithm="blur")
```

Description

Return the width of sequence represented in a heatmap

Usage

```r
## S4 method for signature 'Heatmap'
width(x)
```

Arguments

- `x`: A heatmap

Value

integer

Description

Generate co-ordinates for each row of the image matrix of a Heatmap

Usage

```r
x(x)
```

## S4 method for signature 'Heatmap'

```r
x(x)
```

---

Value

A heatmap

Methods (by class)

- Heatmap: Smooth a heatmap

Examples

```r
data(HeatmapExamples)
hm_smoothed = smoothHeatmap(hm, sigma=c(5,5), algorithm="blur")
```
Arguments

x A Heatmap

Value
numeric, a list of co-ordinates for plotting values in hm@image

Methods (by class)

- Heatmap: Generate co-ordinates for each column of the image matrix of a Heatmap

Examples

```r
data(HeatmapExamples)
ym(hm)
```

Description

Generate co-ordinates for each column of the image matrix of a Heatmap

Usage

```r
ym(x)
```

## S4 method for signature 'Heatmap'

```r
ym(x)
```

Arguments

x A Heatmap

Value
numeric, a list of co-ordinates for plotting values in hm@image

Methods (by class)

- Heatmap: Generate co-ordinates for each column of the matrix

Examples

```r
data(HeatmapExamples)
ym(hm)
```
# Index

* datasets
  HeatmapExamples, 7
  coords, 2
  coords, Heatmap-method (coords), 2
  coords<- (coords), 2
  coords<-, Heatmap-method (coords), 2
  CoverageHeatmap, 3
  CoverageHeatmap, GenomicRanges, GenomicRanges-method (CoverageHeatmap), 3
  CoverageHeatmap, GenomicRanges, RleList-method (CoverageHeatmap), 3
  default_color, 4
  getScale, 5
  Heatmap, 5
  Heatmap-class, 6
  HeatmapExamples, 7
  heatmapOptions, 8
  hm (HeatmapExamples), 7
  hm2 (HeatmapExamples), 7
  image, 10
  image, Heatmap-method (image), 10
  image<- (image), 10
  image<-, Heatmap-method (image), 10
  label, 10
  label, Heatmap-method (label), 10
  label<- (label), 10
  label<-, Heatmap-method (label), 10
  length, Heatmap-method, 11
  mat (HeatmapExamples), 7
  metadata, 12
  metadata, Heatmap-method (metadata), 12
  metadata<- (metadata), 12
  metadata<-, Heatmap-method (metadata), 12
  nseq, 12
  nseq, Heatmap-method (nseq), 12
  nseq<- (nseq), 12
  nseq<-, Heatmap-method (nseq), 12
  PatternHeatmap, 13
  PatternHeatmap, DNAStringSet, character-method (PatternHeatmap), 13
  patternHeatmap, DNAStringSet, matrix-method (PatternHeatmap), 13
  plot_clusters, 14
  plot_legend, 15
  plotHeatmap, 16
  plotHeatmap, Heatmap-method (plotHeatmap), 16
  plotHeatmapList, 17
  plotHeatmapMeta, 18
  plotPatternDensityMap, 19
  plotPatternDensityMap, DNAStringSet-method (plotPatternDensityMap), 19
  PWMScanHeatmap, 20
  PWMScanHeatmap, DNAStringSet, matrix-method (PWMScanHeatmap), 20
  rev, Heatmap-method, 21
  rle_list (HeatmapExamples), 7
  scale, 21
  scale, Heatmap-method (scale), 21
  scale<- (scale), 21
  scale<-, Heatmap-method (scale), 21
  smoothHeatmap, 22
  smoothHeatmap, Heatmap-method (smoothHeatmap), 22
  string_set (HeatmapExamples), 7
  tata_pwm (HeatmapExamples), 7
  width, Heatmap-method, 23
  windows (HeatmapExamples), 7
xm, 23
xm, Heatmap-method (xm), 23

ym, 24
ym, Heatmap-method (ym), 24