Package ‘heatmaps’

April 3, 2024

Title Flexible Heatmaps for Functional Genomics and Sequence Features

Version 1.26.0

Date 2021-11-21

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Depends R (>= 3.4)

Imports methods, grDevices, graphics, stats, Biostrings,
  GenomicRanges, IRanges, KernSmooth, plotrix, Matrix, EBImage,
  RColorBrewer, BiocGenerics, GenomeInfoDb

Suggests BSgenome.Drerio.UCSC.danRer7, knitr, rmarkdown, testthat

biocViews Visualization, SequenceMatching, FunctionalGenomics

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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.

VignetteBuilder knitr

Collate Heatmap-class.R PlotHeatmap.R PlotHeatmapList.R
  PlotPatternDensityMap.R PWMScanHeatmap.R PatternHeatmap.R

NeedsCompilation no

RoxygenNote 6.0.1

git_url https://git.bioconductor.org/packages/heatmaps

git_branch RELEASE_3_18

git_last_commit 6bc363d

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-04-03
R topics documented:

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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'
coords(x) <- value

### Arguments

- **x**
  - A heatmap

- **value**
  - Replacement value

#### Value

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

### Examples

data(HeatmapExamples)
coords(hm) = c(-100, 100)

---

### Description

Generate a Heatmap of coverage

### Usage

CoverageHeatmap(windows, track, ...)

### 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. \( c(-\max(\text{abs}(\text{image}(\text{hm}))), \max(\text{abs}(\text{image}(\text{hm})))) \). 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 \(?\text{getScale}\) 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)

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

```r
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 \( \text{rev(rainbow(9, start=0, end=4/6))} \), so it starts blue and ends with red).

### Value

character, a length-9 color palette
getScale

Examples

  default_color("Blues")
  default_color("Rainbow")

getScale Make an appropriate scale for a heatmap

Description

  Make an appropriate scale for a heatmap

Usage

  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

  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

  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 PWMSanHeatmap

**Examples**

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

---

Heatmap-class

An S4 class to represent a heatmap

**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

```r
data(HeatmapExamples)

hm = new("Heatmap",
    image=mat,
    scale=c(0,max(mat)),
    coords=c(-100L, 100L),
    nseq=100L,
    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)
**heatmapOptions**

- **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**: 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.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**

```r
myOptions = heatmapOptions()
myOptions$color = "Reds"
# plotHeatmap(hm, options=myOptions)
```
### Description

Return or set the image in a Heatmap

```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)))
```

---

### Description

Return or set the label in a Heatmap

```r
label
```

#### Description

Return or set the label in a Heatmap
label

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

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)

```r
## 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

```r
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
**Usage**

```r
nseq(x)
```

## S4 method for signature 'Heatmap'

```r
nseq(x)
```

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

## S4 replacement method for signature 'Heatmap'

```
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**

```r
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)
```
plotHeatmap

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, 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")

plotHeatmap

Plot a Heatmap object to the device

Description

Plot a Heatmap object to the device
plotHeatmapList

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

Description
Plot a list of heatmaps

See Also
heatmapOptions, plotHeatmap
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.

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)
```
**plotPatternDensityMap**

**Arguments**

- **hm_list**: A list of heatmaps
- **binsize**: Integer, size of bins to use in plot
- **colors**: Color to use for each heatmap
- **addReferenceLine**: Logical, add reference line at zero or not

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**

```r
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

This function is a convenient wrapper for plotting many different patterns for the same set of sequences. PatternHeatmap() is applied to the sequence for each pattern in the list, they are passed to smoothHeatmap() with the supplied parameters and finally PlotHeatmapList(). If fine-grained control is desired, or you want to mix other plot types, then more information is available in the vignette.
plot_clusters

### Description
Plot partition in a separate panel

### Usage
```r
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)
**plot_legend**

**See Also**

plotHeatmapList

**Examples**

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

```r
data(HeatmapExamples)
opts = heatmapOptions()
opts$color = "Rainbow"
par(mai= opts$legend.mai)
plot_legend(c(0,1), opts)
```

---

**Description**

Plot a color legend for a heatmap

**Usage**

```r
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.

**Value**

`invisible(0)`

**See Also**

plotHeatmapList

**Examples**

```r
data(HeatmapExamples)
```
PWMScanHeatmap

Generate a Heatmap of PWM Scores in DNA sequence

**Description**

Generate a Heatmap of PWM Scores in DNA sequence

**Usage**

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

## S4 method for signature 'DNAStringSet,matrix'

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

**Arguments**

- `seq` A DNAString of equal length
- `pwm` A PWM
- `...` additional arguments used by methods
  
  This function creates a heatmap where each point is the score of a PWM match starting from that position, which can visualise regions of enrichment or exclusion of certain motifs
- `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

**Reflect a heatmap in the x axis**

#### 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

**Return or set the scale in a Heatmap**

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

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

#### Arguments
- **x**  
  A heatmap
- **value**  
  Replacement value
**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, length 2, (recycled if length 1)

- **output.size**  
  Numeric, length 2

- **algorithm**  
  "kernel" or "blur"
Value

A heatmap

Methods (by class)

- Heatmap: Smooth a heatmap

Examples

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

width,Heatmap-method  

Return the width of sequence represented in a heatmap

Description

Return the width of sequence represented in a heatmap

Usage

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

Arguments

x  A heatmap

Value

integer

xm  

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

Description

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

Usage

xm(x)

## S4 method for signature 'Heatmap'
xm(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 row of the image matrix of a Heatmap

Examples

data(HeatmapExamples)

ym(hm)

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

Description

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

Usage

ym(x)

## S4 method for signature 'Heatmap'

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

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ym(hm)
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