

# Package ‘heatmaps’

March 30, 2021

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

**Version** 1.14.0

**Date** 18-01-2016

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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

**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.

**VignetteBuilder** knitr

**Collate** Heatmap-class.R PlotHeatmap.R PlotHeatmapList.R  
PlotPatternDensityMap.R PWMScanHeatmap.R PatternHeatmap.R  
CoverageHeatmap.R SmoothHeatmap.R PlotHeatmapMeta.R Data.R

**NeedsCompilation** no

**RoxygenNote** 6.0.1

**git\_url** <https://git.bioconductor.org/packages/heatmaps>

**git\_branch** RELEASE\_3\_12

**git\_last\_commit** 6e5cabd

**git\_last\_commit\_date** 2020-10-27

**Date/Publication** 2021-03-29

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---

coords	<i>Return or set the coords in a Heatmap</i>
--------	--

---

## Description

Return or set the coords in a Heatmap

## Usage

```
coords(x)
```

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

```
coords(x) <- value
```

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

## Arguments

x	A heatmap
value	Replacement value

**Value**

integer, length 2, value of x@coords

**Examples**

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

---

CoverageHeatmap

*Generate a Heatmap of coverage*

---

**Description**

Generate a Heatmap of coverage

**Usage**

```
CoverageHeatmap(windows, track, ...)

## S4 method for signature 'GenomicRanges,GenomicRanges'
CoverageHeatmap(windows, track,
  coords = NULL, weight = 1, label = NULL, nbin = 0)

## S4 method for signature 'GenomicRanges,RleList'
CoverageHeatmap(windows, track,
  coords = NULL, label = NULL, nbin = 0)
```

**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, ie.  $c(-\max(\text{abs}(\text{image}(\text{hm}))), \max(\text{abs}(\text{image}(\text{hm}))))$ . 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 ?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 $\text{class}(\text{track}) == \text{"GRanges"}$
label	Label for the heatmap
nbin	If set, number of bins to use across each window

**Value**

A Heatmap object

**Methods (by class)**

- windows = GenomicRanges, track = GenomicRanges: Heatmap of Coverage from 2 GRanges
- windows = GenomicRanges, track = RleList: Heatmap of Coverage from GRanges + RleList

**Examples**

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

---

default_color	<i>Predifined color palettes from RColorBrewer + Rainbow</i>
---------------	--

---

**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

**Examples**

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

---

getScale	<i>Make an appropriate scale for a heatmap</i>
----------	--

---

**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	<i>Function to create a heatmap object</i>
---------	--

---

**Description**

Function to create a heatmap object

**Usage**

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

**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**

```
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**

```
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")
```

---

HeatmapExamples	<i>Data for man page examples</i>
-----------------	-----------------------------------

---

**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	<i>Generate default options for a Heatmap</i>
----------------	---

---

**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 heatmap 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: 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

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	<i>Return or set the image in a Heatmap</i>
-------	---

---

### Description

Return or set the image in a Heatmap

### Usage

```

## 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

```

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

```

---

label	<i>Return or set the label in a Heatmap</i>
-------	---

---

**Description**

Return or set the label in a Heatmap

**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	<i>Return the number of sequences in a heatmap</i>
-----------------------	--

---

**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	<i>Return or set the metadata in a Heatmap</i>
----------	--

---

**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	<i>Return or set nseq in a Heatmap</i>
------	--

---

**Description**

Return or set nseq in a Heatmap

**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	<i>Generate a Heatmap of patterns in DNA sequence</i>
----------------	---

---

**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 vectore, eg. "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

**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	<i>Plot a list of heatmaps</i>
-----------------	--------------------------------

---

**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 be 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**

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

---

plotHeatmapMeta	<i>Plot a Meta-region plot from heatmaps</i>
-----------------	--

---

**Description**

Plot a Meta-region plot from heatmaps

**Usage**

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

**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

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

### Arguments

seq	DNAStrngSet 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.
coords	Heatmap coords
min.score	Minimum score for PWM match
sigma	Bandwidth 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**

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

---

plot\_clusters

*Plot partition in a separate panel*


---

**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	<i>Plot a color legend for a heatmap</i>
-------------	--

---

**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.

**Value**

invisible(0)

**See Also**

plotHeatmapList

**Examples**

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

---

PWMScanHeatmap	<i>Generate a Heatmap of PWM Scores in DNA sequence</i>
----------------	---

---

**Description**

Generate a Heatmap of PWM Scores in DNA sequece

**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**

```
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**

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

**Arguments**

x                      A heatmap

**Value**

A heatmap

---

scale	<i>Return or set the scale in a Heatmap</i>
-------	---

---

**Description**

Return or set the scale in a Heatmap

**Usage**

```
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	<i>Smooth a heatmap</i>
---------------	-------------------------

---

**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 (eg. 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 frow of the image matrix of a Heatmap

**Examples**

```
data(HeatmapExamples)
xm(hm)
```

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ym	<i>Generate co-ordinates for each column of the image matrix of a Heatmap</i>
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**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**

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

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