# Package 'VplotR'

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**Type** Package

**Title** Set of tools to make V-plots and compute footprint profiles

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**Description** The pattern of digestion and protection from DNA nucleases such as DNAse I, micrococcal nuclease, and Tn5 transposase can be used to infer the location of associated proteins. This package contains useful functions to analyze patterns of paired-end sequencing fragment density. VplotR facilitates the generation of V-plots and footprint profiles over single or aggregated genomic loci of interest.

**URL** https://github.com/js2264/VplotR

**BugReports** https://github.com/js2264/VplotR/issues

**Depends** R (>= 4.0), GenomicRanges, IRanges, ggplot2

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---

`ABF1_sacCer3` *ABF1_sacCer3*

---

## Description

Genomic loci with a REB1 binding motifs according to http://jaspar.genereg.net/api/v1/matrix/MA0265.1.jaspar. PWM and scanning done with TFBSTools.

## Usage

```
data(ABF1_sacCer3)
```

## Format

An object of class `"GRanges"`.

## References

Rossi, Lai & Pugh 2018 Genome Research

## Examples

```
data(ABF1_sacCer3)
ABF1_sacCer3
```

---

`alignToTSS` *A function to re-align a GRanges object to TSSs*

---

## Description

This function re-aligns ranges (typically regulatory elements) to a set of coordinates, either the TSS column or the TSS.fwd and TSS.rev columns. If none are found, the function assumes the ranges are promoters and that the end or the ranges are the TSSs.

## Usage

```
alignToTSS(granges, upstream = 0, downstream = 1)
```

## Arguments

| | |
|---|---|
| `granges` | A stranded GRanges object with a TSS column or TSS.rev and TSS.fwd columns |
| `upstream` | How many bases upstream of the TSS should the GRanges object by extended by? [Default: 0] |
| `downstream` | How many bases downstream of the TSS should the GRanges object by extended by? [Default: 1] |

## Value

GRanges aligned to the TSS column or to TSS.rev and TSS.fwd columns, and extended by upstream/downstream bp.

## Examples

```
data(ce11_proms)
ce11_proms
alignToTSS(ce11_proms)
```

## ATAC_ce11_Serizay2020 *ATAC_ce11_Serizay2020*

### Description

A sample of ATAC-seq fragments from individual worm tissues (Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv)

### Usage

```
data(ATAC_ce11_Serizay2020)
```

### Format

An object of class `"list"`.

### Examples

```
data(ATAC_ce11_Serizay2020)
ATAC_ce11_Serizay2020
```

## bam_test *bam_test*

### Description

A .bam file sample

### Usage

```
data(bam_test)
```

### Format

An object of class `"GRanges"`.

### Examples

```
data(bam_test)
bam_test
```

ce11_all_REs *ce11_all_REs*

## Description

Regulatory elements annotated in C. elegans (ce11) according to Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv.

## Usage

```
data(ce11_all_REs)
```

## Format

GRanges

## Source

BiorXiv

## References

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv. (DOI)

## Examples

```
data(ce11_all_REs)
table(ce11_all_REs$regulatory_class)
table(ce11_all_REs$which.tissues)
```

ce11_proms *ce11_proms*

## Description

Promoters annotated in C. elegans (ce11) according to Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv.

## Usage

```
data(ce11_proms)
```

## Format

An object of class "GRanges".

## Source

BiorXiv

## References

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv. (DOI)

## Examples

```
data(ce11_proms)
table(ce11_proms$which.tissues)
```

---

# computeNucleosomeEnrichmentOverBackground

*Internal function*

---

## Description

A function to compute nucleosome enrichment of a Vmat

## Usage

```
computeNucleosomeEnrichmentOverBackground(
  Vmat,
  background = NULL,
  plus1_nuc_only = FALSE,
  minus1_nuc = list(c(xmin = -150, xmax = -70), c(ymin = 165, ymax = 260)),
  minus1_nuc_neg = list(c(xmin = -150, xmax = -70), c(ymin = 60, ymax = 145)),
  plus1_nuc = list(c(xmin = 70, xmax = 150), c(ymin = 165, ymax = 260)),
  plus1_nuc_neg = list(c(xmin = 70, xmax = 150), c(ymin = 50, ymax = 145)),
  ...
)
```

## Arguments

| | |
|---|---|
| `Vmat` | A Vmat computed by nucleosomeEnrichment function |
| `background` | a background Vmat |
| `plus1_nuc_only` | Boolean Should compute nucleosome enrichment only for +1 nucleosome? |
| `minus1_nuc` | list where the -1 nucleosome is located |
| `minus1_nuc_neg` | where the background of the -1 nucleosome is located |
| `plus1_nuc` | where the +1 nucleosome is located |
| `plus1_nuc_neg` | where the background of the +1 nucleosome is located |
| `...` | additional parameters |

## Value

list

computeVmat *A function to compute Vplot matrix*

## Description

This function computes the underlying matrix shown as a heatmap in Vplots. For each pair of coordinates (x: distance from fragment midpoint to center of GRanges of interest; y: fragment size), the function computes how many fragments there are.

## Usage

```
computeVmat(
  bam_granges,
  granges,
  cores = 1,
  xlims = c(-250, 250),
  ylims = c(50, 300)
)
```

## Arguments

| | |
|---|---|
| bam_granges | GRanges, paired-end fragments |
| granges | GRanges, regions to map the fragments onto |
| cores | Integer, nb of threads to parallelize fragments subsetting |
| xlims | The x limits of the computed Vmat |
| ylims | The y limits of the computed Vmat |

## Value

A table object

## Examples

```
data(bam_test)
data(ce11_all_REs)
Vmat <- computeVmat(bam_test, ce11_all_REs)
dim(Vmat)
Vmat[seq(1,5), seq(1,10)]
```

CTCF_hg38 *CTCF_hg38*

## Description

high-score CTCF binding motifs, obtained from JASPAR

## Usage

```
data(CTCF_hg38)
```

## Format

An object of class "GRanges".

## Examples

```
data(CTCF_hg38)
CTCF_hg38
```

---

deconvolveBidirectionalPromoters
*A function to duplicate bi-directional GRanges*

---

## Description

This function splits bi-directional ranges into + and - stranded ranges. It duplicates the ranges which are '*'.

## Usage

```
deconvolveBidirectionalPromoters(granges)
```

## Arguments

| | |
|---|---|
| granges | A stranded GRanges object |

## Value

GRanges with only '+' and '-' strands. GRanges with '*' strand have been duplicated and split into forward and reverse strands.

## Examples

```
data(ce11_all_REs)
library(GenomicRanges)
proms <- ce11_all_REs[grepl('prom', ce11_all_REs$regulatory_class)]
proms
table(strand(proms))
proms <- deconvolveBidirectionalPromoters(proms)
proms
table(strand(proms))
```

`getCuts` *Internal function*

## Description

Function to extract cuts (i.e. extremities) of fragments stored as GRanges.

## Usage

```
getCuts(gr)
```

## Arguments

| | |
|---|---|
| `gr` | GRanges Paired-end fragments used to extract their extremities |

## Value

GRanges

`getFragmentsDistribution` *A function to compute sizes distribution for paired-end fragments*

## Description

This function takes fragments and compute the distribution of their sizes over a set or multiple sets of GRanges.

## Usage

```
getFragmentsDistribution(
  fragments,
  granges_list = NULL,
  extend_granges = c(-500, 500),
  limits = c(0, 600),
  roll = 3,
  cores = 1
)
```

## Arguments

| | |
|---|---|
| `fragments` | GRanges object containing paired-end fragments. See importPEBamFiles for more details on how to create such object. |
| `granges_list` | GRanges, can be a list of different sets of GRanges. |
| `extend_granges` | numeric vector of length 2, how the GRanges should be extended. |
| `limits` | numeric vector of length 2, only consider fragments within this window of sizes. |
| `roll` | Integer, apply a moving average of this size |
| `cores` | Integer, number of threads used to compute fragment size distribution |

## Value

A list of tbl, one for each .bam file.

## Examples

```
data(bam_test)
data(ce11_proms)
df <- getFragmentsDistribution(
    bam_test,
    ce11_proms,
    extend_granges = c(-500, 500)
)
head(df)
which.max(df$y)
```

---

`importPEBamFiles` *A function to import paired end bam files as GRanges*

---

## Description

This function takes bam file paths and read them into GRanges objects. Note: Can be quite lengthy for .bam files with 5+ millions fragments.

## Usage

```
importPEBamFiles(
  files,
  genome = NULL,
  where = NULL,
  max_insert_size = 1000,
  shift_ATAC_fragments = FALSE,
  cores = 10,
  verbose = TRUE
)
```

## Arguments

| | |
|---|---|
| `files` | character vector, each element of the vector is the path of an individual .bam file. |
| `genome` | character, genome ID (e.g. "sacCer3", "ce11", "dm6", "mm10" or "hg38"). |
| `where` | GRanges, only import the fragments mapping to the input GRanges (can fasten the import process a lot). |
| `max_insert_size` | Integer, filter out fragments larger than this size. |
| `shift_ATAC_fragments` | Boolean, if the fragments come from ATAC-seq, one might want to shift the extremities by +5 / -4 bp. |
| `cores` | Integer, number of cores to use when indexing bam files |
| `verbose` | Boolean |

## Value

A GRanges object containing fragments from the input .bam file.

## Examples

```
bamfile <- system.file("extdata", "ex1.bam", package = "Rsamtools")
fragments <- importPEBamFiles(
    bamfile,
    shift_ATAC_fragments = TRUE
)
fragments
```

---

`MNase_sacCer3_Henikoff2011`

*MNase_sacCer3_Henikoff2011*

---

## Description

A sample of MNase-seq fragments from yeast (Henikoff et al. 2011, "Epigenome characterization at single base-pair resolution", PNAS)

## Usage

```
data(MNase_sacCer3_Henikoff2011)
```

## Format

An object of class `"GRanges"`.

## Examples

```
data(MNase_sacCer3_Henikoff2011)
MNase_sacCer3_Henikoff2011
```

---

`MNase_sacCer3_Henikoff2011_subset`

*MNase_sacCer3_Henikoff2011_subset*

---

## Description

A sample of fragments from multiple MNase-seq experiments performed in yeast (Henikoff et al. 2011, "Epigenome characterization at single base-pair resolution", PNAS), mapping over chrXV:186,400-187,400.

## Usage

```
data(MNase_sacCer3_Henikoff2011_subset)
```

## Format

An object of class `"GRanges"`.

## Examples

```
data(MNase_sacCer3_Henikoff2011_subset)
MNase_sacCer3_Henikoff2011_subset
```

---

`normalizeVmat` *A function to normalized a Vmat*

---

## Description

This function normalizes a Vmat. Several different approaches have been implemented to normalize the Vmats.

## Usage

```
normalizeVmat(
  Vmat,
  bam_granges,
  granges,
  normFun = c("zscore"),
  s = 0.99,
  roll = 1,
  verbose = TRUE
)
```

## Arguments

| | |
|---|---|
| `Vmat` | A Vmat, usually output of computeVmat |
| `bam_granges` | GRanges, the paired-end fragments |
| `granges` | GRanges, the regions to map the fragments onto |
| `normFun` | character. A Vmat should be scaled either by:<br>• 'libdepth+nloci', e.g. the library depth and the number of loci used to compute the Vmat;<br>• zscore, if relative patterns of fragment density are more important than density per se;<br>• Alternatively, the Vmat can be scaled to a chosen quantile ('quantile') or to the max Vmat value ('max'). |
| `s` | A float indicating which quantile to use if 'quantile' normalization is chosen |
| `roll` | integer, to use as the window to smooth the Vmat rows by rolling mean. |
| `verbose` | Boolean |

## Value

A normalized Vmat object

## Examples

```
data(bam_test)
data(ce11_all_REs)
Vmat <- computeVmat(bam_test, ce11_all_REs)
Vmat <- normalizeVmat(
    Vmat,
    bam_test,
    ce11_all_REs,
    normFun = c('libdepth+nloci')
)
```

---

# nucleosomeEnrichment *A function to compute nucleosome enrichment over a set of GRanges*

---

## Description

A function to compute nucleosome enrichment over a set of GRanges

## Usage

```
nucleosomeEnrichment(x, ...)
```

## Arguments

| | |
|---|---|
| x | a GRanges or Vmat |
| ... | additional parameters |

## Value

list

## Examples

```
data(bam_test)
data(ce11_proms)
n <- nucleosomeEnrichment(bam_test, ce11_proms)
n$fisher_test
n$plot
```

---

# nucleosomeEnrichment.GRanges *A function to compute nucleosome enrichment over a set of GRanges*

---

## Description

A function to compute nucleosome enrichment over a set of GRanges

## Usage

```
## S3 method for class 'GRanges'
nucleosomeEnrichment(x, granges, plus1_nuc_only = FALSE, verbose = TRUE, ...)
```

### Arguments

| | |
|---|---|
| x | GRanges, paired-end fragments |
| granges | GRanges, loci to map the fragments onto |
| plus1_nuc_only | Boolean, should compute nucleosome enrichment only for +1 nucleosome? |
| verbose | Boolean |
| ... | additional parameters |

### Value

list

### Examples

```
data(bam_test)
data(ce11_proms)
n <- nucleosomeEnrichment(bam_test, ce11_proms)
n$fisher_test
n$plot
```

---

## nucleosomeEnrichment.Vmat

*A function to compute nucleosome enrichment over a Vmat*

---

### Description

A function to compute nucleosome enrichment over a Vmat

### Usage

```
## S3 method for class 'Vmat'
nucleosomeEnrichment(x, background, plus1_nuc_only = FALSE, ...)
```

### Arguments

| | |
|---|---|
| x | a computed Vmat. Should be un-normalized. |
| background | a background Vmat. Should be un-normalized. |
| plus1_nuc_only | Boolean, should compute nucleosome enrichment only for +1 nucleosome? |
| ... | additional parameters |

### Value

list

## Examples

```
data(bam_test)
data(ce11_proms)
V <- plotVmat(
    bam_test,
    ce11_proms,
    normFun = '',
    return_Vmat = TRUE
)
V_bg <- plotVmat(
    bam_test,
    sampleGRanges(ce11_proms),
    normFun = '',
    return_Vmat = TRUE
)
n <- nucleosomeEnrichment(V, V_bg)
n$fisher_test
n$plot
```

---

`plotFootprint` *A function to plot footprint of paired-end data at given loci*

---

## Description

This function takes paired-end fragments, extract the "cuts" (i.e. extremities) and plot the footprint profile over a set of GRanges.

## Usage

```
plotFootprint(
  frags,
  targets,
  split_strand = FALSE,
  plot_central = TRUE,
  xlim = c(-75, 75),
  bin = 1,
  verbose = 1
)
```

## Arguments

| | |
|---|---|
| `frags` | GRanges, the paired-end fragments |
| `targets` | GRanges, the loci to map the fragments onto |
| `split_strand` | Boolean, should the + and - strand be splitted? |
| `plot_central` | plot grey rectangle over the loci |
| `xlim` | numeric vector of length 2, the x limits of the computed Vmat |
| `bin` | Integer, bin used to smooth the gootprint profile |
| `verbose` | Integer |

## Value

A footprint ggplot

## Examples

```
data(bam_test)
data(ce11_proms)
plotFootprint(bam_test, ce11_proms)
```

---

`plotProfile` *A function to generate a Vplot along chromosome coordinates*

---

## Description

The paired-end fragments overlapping a locus of interest (e.g., binding sites, provided in the 'loci' argument) are shown in red while the remaining fragments mapping to the genomic window are displayed in black. Marginal curves are also plotted on the side of the distribution plot. They highlight the smoothed distribution of the position of paired-end fragment midpoints (top) or of the paired-end fragment length (right)

## Usage

```
plotProfile(
  fragments,
  window = loc,
  loci = NULL,
  annots = NULL,
  min = 50,
  max = 200,
  alpha = 0.5,
  size = 1,
  with_densities = TRUE,
  verbose = TRUE
)
```

## Arguments

| | |
|---|---|
| `fragments` | GRanges |
| `window` | character, chromosome location |
| `loci` | GRanges, optional genomic locus. Fragments overlapping this locus will be in red. |
| `annots` | GRanges, optional gene annotations |
| `min` | integer, minimum fragment size |
| `max` | integer, maximum fragment size |
| `alpha` | float, transparency value |
| `size` | float, dot size |
| `with_densities` | Boolean, should the densities be plotted? |
| `verbose` | Boolean |

## Value

A ggplot

## Examples

```
data(bam_test)
data(ce11_proms)
V <- plotProfile(
    bam_test,
    'chrI:10000-12000',
    loci = ce11_proms,
    min = 80,
    max = 200
)
```

---

`plotVmat` *A function to generate a Vplot*

---

## Description

See individual methods for further detail

## Usage

```
plotVmat(x, ...)
```

## Arguments

| | |
|---|---|
| `x` | GRanges or list or Vmat |
| `...` | additional parameters |

## Value

A Vmat ggplot

## Examples

```
data(bam_test)
data(ce11_proms)
V <- plotVmat(
    bam_test,
    ce11_proms,
    normFun = 'libdepth+nloci'
)
```

`plotVmat.default` *A function to plot a computed Vmat*

## Description

The default plotVmat method generates a ggplot representing a heatmap of fragment density.

## Usage

```
## Default S3 method:
plotVmat(
  x,
  hm = 90,
  colors = COLORSCALE_VMAT,
  breaks = NULL,
  xlim = c(-250, 250),
  ylim = c(50, 300),
  main = "",
  xlab = "Distance from center of elements",
  ylab = "Fragment length",
  key = "Score",
  ...
)
```

## Arguments

| | |
|---|---|
| `x` | A computed Vmat (ideally, should be normalized) |
| `hm` | Integer, should be between 0 and 100. Used to automatically scale the range of colors (best to keep between 90 and 100) |
| `colors` | a vector of colors |
| `breaks` | a vector of breaks. length(breaks) == length(colors) + 1 |
| `xlim` | vector of two integers, x limits |
| `ylim` | vector of two integers, y limits |
| `main` | character, title of the plot |
| `xlab` | character, x-axis label |
| `ylab` | character, y-axis label |
| `key` | character, legend label |
| `...` | additional parameters |

## Value

A Vmat ggplot

## Examples

```
data(bam_test)
data(ce11_proms)
V <- plotVmat(
    bam_test,
    ce11_proms,
    normFun = 'libdepth+nloci',
    return_Vmat = TRUE
)
plotVmat(V)
```

---

`plotVmat.GRanges` *A function to compute (and plot) a Vmat*

---

## Description

The plotVmat.GRanges() method computes and normalizes a Vmat before passing it to plotVmat.Vmat() method.

## Usage

```
## S3 method for class 'GRanges'
plotVmat(
  x,
  granges,
  xlims = c(-250, 250),
  ylims = c(50, 300),
  normFun = "",
  s = 0.95,
  roll = 3,
  cores = 1,
  return_Vmat = FALSE,
  verbose = 1,
  ...
)
```

## Arguments

| | |
|---|---|
| `x` | GRanges, paired-end fragments |
| `granges` | GRanges, loci to map the fragments onto |
| `xlims` | x limits of the computed Vmat |
| `ylims` | y limits of the computed Vmat |
| `normFun` | character. A Vmat should be scaled either by:<br>• 'libdepth+nloci', e.g. the library depth and the number of loci used to compute the Vmat;<br>• zscore, if relative patterns of fragment density are more important than density per se;<br>• Alternatively, the Vmat can be scaled to a chosen quantile ('quantile') or to the max Vmat value ('max'). |

| | |
|---|---|
| s | A float indicating which quantile to use if 'quantile' normalization is chosen |
| roll | integer, to use as the window to smooth the Vmat rows by rolling mean. |
| cores | Integer, number of threads to parallelize fragments subsetting |
| return_Vmat | Boolean, should the function return the computed Vmat rather than the plot? |
| verbose | Boolean |
| ... | additional parameters |

## Value

A Vmat ggplot

## Examples

```
data(bam_test)
data(ce11_proms)
V <- plotVmat(
    bam_test,
    ce11_proms,
    normFun = 'libdepth+nloci',
    roll = 5
)
```

---

# plotVmat.list *A function to compute (and plot) several Vmats.*

---

## Description

The plotVmat.GRanges() method computes and normalizes multiple Vmats before passing them to plotVmat.VmatList() method.

## Usage

```
## S3 method for class 'list'
plotVmat(
  x,
  cores = 1,
  cores_subsetting = 1,
  nrow = NULL,
  ncol = NULL,
  xlims = c(-250, 250),
  ylims = c(50, 300),
  normFun = "libdepth+nloci",
  s = 0.95,
  roll = 3,
  return_Vmat = FALSE,
  verbose = 1,
  ...
)
```

## Arguments

| | |
|---|---|
| x | list Each element of the list should be a list containing paired-end fragments and GRanges of interest. |
| cores | Integer, number of cores to parallelize the plots |
| cores_subsetting | Integer, number of threads to parallelize fragments subsetting |
| nrow | Integer, how many rows in facet? |
| ncol | Integer, how many cols in facet? |
| xlims | x limits of the computed Vmat |
| ylims | y limits of the computed Vmat |
| normFun | character. A Vmat should be scaled either by:<br>• 'libdepth+nloci', e.g. the library depth and the number of loci used to compute the Vmat;<br>• zscore, if relative patterns of fragment density are more important than density per se;<br>• Alternatively, the Vmat can be scaled to a chosen quantile ('quantile') or to the max Vmat value ('max'). |
| s | A float indicating which quantile to use if 'quantile' normalization is chosen |
| roll | integer, to use as the window to smooth the Vmat rows by rolling mean. |
| return_Vmat | Boolean, should the function return the computed Vmat rather than the plot? |
| verbose | Boolean |
| ... | additional parameters |

## Value

A list of Vmat ggplots

## Examples

```
data(bam_test)
data(ce11_proms)
list_params <- list(
    'germline' = list(
        bam_test,
        ce11_proms[ce11_proms$which.tissues == 'Germline']
    ),
    'muscle' = list(
        bam_test,
        ce11_proms[ce11_proms$which.tissues == 'Muscle']
    )
)
V <- plotVmat(
    list_params,
    normFun = 'libdepth+nloci',
    roll = 5
)
```

## plotVmat.Vmat *A function to plot a computed Vmat*

### Description

The plotVmat.Vmat() method forwards the Vmat to plotVmat.default().

### Usage

```
## S3 method for class 'Vmat'
plotVmat(x, ...)
```

### Arguments

| | |
|---|---|
| x | A computed Vmat (ideally, should be normalized) |
| ... | additional parameters |

### Value

A Vmat ggplot

### Examples

```
data(bam_test)
data(ce11_proms)
V <- plotVmat(
    bam_test,
    ce11_proms,
    normFun = 'libdepth+nloci',
    return_Vmat = TRUE
)
plotVmat(V)
```

## plotVmat.VmatList *A function to plot a computed VmatList*

### Description

The plotVmat.VmatList() method forwards the Vmat to plotVmat.default().

### Usage

```
## S3 method for class 'VmatList'
plotVmat(x, nrow = NULL, ncol = NULL, dir = "v", ...)
```

### Arguments

| | |
|---|---|
| x | A VmatList (output of plotVmat.list()) |
| nrow | Integer, how many rows in facet? |
| ncol | Integer, how many cols in facet? |
| dir | str, direction of facets? |
| ... | additional parameters |

## Value

A Vmat ggplot

## Examples

```
data(bam_test)
data(ce11_proms)
list_params <- list(
    'germline' = list(
        bam_test,
        ce11_proms[ce11_proms$which.tissues == 'Germline']
    ),
    'muscle' = list(
        bam_test,
        ce11_proms[ce11_proms$which.tissues == 'Muscle']
    )
)
V <- plotVmat(
    list_params,
    normFun = 'libdepth+nloci',
    roll = 5
)
```

---

# REB1_sacCer3 *REB1_sacCer3*

---

## Description

Genomic loci with a REB1 binding motifs according to http://jaspar.genereg.net/api/v1/matrix/MA0363.1.jaspar. PWM and scanning done with TFBSTools.

## Usage

```
data(REB1_sacCer3)
```

## Format

An object of class "GRanges".

## References

Rossi, Lai & Pugh 2018 Genome Research

## Examples

```
data(REB1_sacCer3)
REB1_sacCer3
```

## sampleGRanges *A function to sample GRanges from GRanges*

### Description

This function takes a given GRanges and returns another GRanges object. The new GRanges has the same number of ranges and the same chromosome, width and strand distributions than the original GRanges.

### Usage

```
sampleGRanges(
  x,
  n = NULL,
  width = NULL,
  exclude = FALSE,
  avoid_overlap = FALSE
)
```

### Arguments

| | |
|---|---|
| x | GRanges object |
| n | Integer, number of sampled GRanges |
| width | Integer, width of sampled GRanges |
| exclude | Boolean, should the original GRanges be excluded? |
| avoid_overlap | Boolean, should the sampled GRanges not be overlapping? |

### Value

A GRanges object of length n

### Examples

```
data(ce11_proms)
sampleGRanges(ce11_proms, 100)
```

## sampleGRanges.GRanges *A function to sample GRanges within GRanges*

### Description

This function takes a given GRanges and returns another GRanges object. The new GRanges has the same number of ranges and the same chromosome, width and strand distributions than the original GRanges.

### Usage

```
## S3 method for class 'GRanges'
sampleGRanges(
  x,
  n = NULL,
  width = NULL,
  exclude = FALSE,
  avoid_overlap = FALSE
)
```

### Arguments

| | |
|---|---|
| x | GRanges object |
| n | Integer, number of sampled GRanges |
| width | Integer, width of sampled GRanges |
| exclude | Boolean, should the original GRanges be excluded? |
| avoid_overlap | Boolean, should the sampled GRanges not be overlapping? |

### Value

A GRanges object of length n

### Examples

```
data(ce11_proms)
sampleGRanges(ce11_proms, 100)
```

---

## shiftATACGranges *A function to shift GRanges fragments by 5/-4. This is useful when dealing with fragments coming from ATAC-seq.*

---

### Description

A function to shift GRanges fragments by 5/-4. This is useful when dealing with fragments coming from ATAC-seq.

### Usage

```
shiftATACGranges(g, pos_shift = 4, neg_shift = 5)
```

### Arguments

| | |
|---|---|
| g | GRanges of ATAC-seq fragments |
| pos_shift | Integer. How many bases should fragments on direct strand be shifted by? |
| neg_shift | Integer. How many bases should fragments on negative strand be shifted by? |

### Value

A GRanges object containing fragments from the input .bam file.

## Examples

```
data(bam_test)
shiftATACGranges(bam_test)
```

---

`shuffleVmat` *A function to shuffle a Vmat*

---

## Description

This function works on a Vmat (the output of computeVmat()). It shuffles the matrix to randomize the fragment densities.

## Usage

```
shuffleVmat(Vmat)
```

## Arguments

| | |
|---|---|
| `Vmat` | A Vmat, usually output of computeVmat |

## Value

A shuffled Vmat object

## Examples

```
data(bam_test)
data(ce11_all_REs)
Vmat <- computeVmat(bam_test, ce11_all_REs)
Vmat <- shuffleVmat(Vmat)
```

---

`theme_ggplot2` *Personal ggplot2 theming function, adapted from roboto-condensed at https://github.com/hrbrmstr/hrbrthemes/*

---

## Description

Personal ggplot2 theming function, adapted from roboto-condensed at https://github.com/hrbrmstr/hrbrthemes/

## Usage

```
theme_ggplot2(
  grid = TRUE,
  border = TRUE,
  base_family = "",
  base_size = 8,
  plot_title_family = base_family,
  plot_title_size = 12,
  plot_title_face = "plain",
  plot_title_margin = 5,
```

```
  subtitle_size = 11,
  subtitle_face = "plain",
  subtitle_margin = 5,
  strip_text_family = base_family,
  strip_text_size = 10,
  strip_text_face = "bold",
  caption_size = 9,
  caption_face = "plain",
  caption_margin = 3,
  axis_text_size = base_size,
  axis_title_family = base_family,
  axis_title_size = 9,
  axis_title_face = "plain",
  axis_title_just = "rt",
  panel_spacing = grid::unit(2, "lines"),
  grid_col = "#cccccc",
  plot_margin = margin(12, 12, 12, 12),
  axis_col = "#cccccc",
  axis = FALSE,
  ticks = FALSE
)
```

## Arguments

| | |
|---|---|
| grid | panel grid (‘TRUE‘, ‘FALSE‘, or a combination of ‘X‘, ‘x‘, ‘Y‘, ‘y‘) |
| border | border if ‘TRUE‘ add border |
| base_family, base_size | base font family and size |
| plot_title_family, plot_title_face | plot title family, face |
| plot_title_size, plot_title_margin | plot title size and margin |
| subtitle_face, subtitle_size | plot subtitle family, face and size |
| subtitle_margin | plot subtitle margin bottom (single numeric value) |
| strip_text_family, strip_text_face, strip_text_size | facet label font family, face and size |
| caption_face, caption_size, caption_margin | plot caption family, face, size and margin |
| axis_text_size | font size of axis text |
| axis_title_family, axis_title_face, axis_title_size | axis title font family, face and size |
| axis_title_just | axis title font justificationk one of ‘[blmcrt]‘ |
| panel_spacing | panel spacing (use ‘unit()‘) |
| grid_col | grid color |
| plot_margin | plot margin (specify with [ggplot2::margin]) |
| axis_col | axis color |
| axis | add x or y axes? ‘TRUE‘, ‘FALSE‘, "‘xy‘" |
| ticks | ticks if ‘TRUE‘ add ticks |

## Value

theme A ggplot theme

## Examples

```
library(ggplot2)

ggplot(mtcars, aes(mpg, wt)) +
  geom_point() +
  labs(x="Fuel effiency (mpg)", y="Weight (tons)",
       title="Seminal ggplot2 scatterplot example") +
  theme_ggplot2()
```

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