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

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

Imports cowplot, magrittr, GenomeInfoDb, GenomicAlignments, RColorBrewer, zoo, Rsamtools, S4Vectors, parallel, reshape2, methods, graphics, stats

Suggests GenomicFeatures, TxDb.Scerevisiae.UCSC.sacCer3.sgdGene, testthat, covr, knitr, rmarkdown, pkgdown

VignetteBuilder knitr

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R topics documented:

`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)
```

`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))
```

`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, danRer10, 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: • 'libdepth+nloci', e.g. the library depth and the number of loci used to compute the Vmat; • zscore, if relative patterns of fragment density are more important than density per se; • 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

A function to generate a Vplot along chromosome coordinates

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: • 'libdepth+nloci', e.g. the library depth and the number of loci used to compute the Vmat; • zscore, if relative patterns of fragment density are more important than density per se; • 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: • 'libdepth+nloci', e.g. the library depth and the number of loci used to compute the Vmat; • zscore, if relative patterns of fragment density are more important than density per se; • 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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