Package 'seqsetvis'

December 24, 2024

Type Package

Title Set Based Visualizations for Next-Gen Sequencing Data

Version 1.26.0

Description seqsetvis enables the visualization and analysis of sets of genomic sites in next gen sequencing data. Although seqsetvis was designed for the comparison of mulitple ChIP-seq samples, this package is domain-agnostic and allows the processing of multiple genomic coordinate files (bed-like files) and signal files (bigwig files pileups from bam file). seqsetvis has multiple functions for fetching data from regions into a tidy format for analysis in data.table or tidyverse and visualization via ggplot2.

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Encoding UTF-8

Suggests BiocFileCache, BiocManager, BiocStyle, ChIPpeakAnno, covr, knitr, rmarkdown, testthat

Depends R (>= 4.3), ggplot2

Imports cowplot, data.table, eulerr, GenomeInfoDb, GenomicAlignments, GenomicRanges, ggplotify, grDevices, grid, IRanges, limma, methods, pbapply, pbmcapply, png, RColorBrewer, Rsamtools, rtracklayer, S4Vectors, scales, stats, UpSetR

RoxygenNote 7.3.1

Roxygen list(markdown = TRUE)

VignetteBuilder knitr

NeedsCompilation no

biocViews Software, ChIPSeq, MultipleComparison, Sequencing, Visualization

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Contents

`seqsetvis-package` *easy awesome peak set vis TESTING seqsetvis allows you to...*

Description

2 steps `ssvOverlapIntervalSets`. `ssvFetchBigwig`. Otherwise refer to the vignettes to see

Author(s)

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`.expand_cigar_dt` *Expand intermediate bam fetch by cigar codes*

Description

see sam specs for cigar details

Usage

```
.expand_cigar_dt(cigar_dt, op_2count = c("M", "D", "=", "X"))
```

Arguments

`cigar_dt`	data.table with 5 required named columns in any order. c("which_label", "seqnames", "strand", "start", "cigar")
`op_2count`	Cigar codes to count. Default is alignment (M), deletion (D), match (=), and mismatch (X). Other useful codes may be skipped regions for RNA splicing (N). The locations of any insterions (I) or clipping/padding (S, H, or P) will be a single bp immediately before the interval.

Value

data.table with cigar entries expanded

`.expand_cigar_dt_recursive` *Expand intermediate bam fetch by cigar codes*

Description

see sam specs for cigar details

Usage

```
.expand_cigar_dt_recursive(cigar_dt)
```

Arguments

cigar_dt	data.table with 5 required named columns in any order. c("which_label", "seqnames", "strand", "start", "cigar")

Value

data.table with cigar entries expanded

.rm_dupes *Remove duplicate reads based on stranded start position. This is an over-simplification. For better duplicate handling, duplicates must be marked in bam and flag passed to fetchBam() ... for ScanBamParam*

Description

flag = scanBamFlag(isDuplicate = FALSE)

Usage

```
.rm_dupes(reads_dt, max_dupes)
```

Arguments

reads_dt	data.table of reads as loaded by fetchBam
max_dupes	maximum allowed positional duplicates

Value

reads_dt with duplicated reads over max_dupes removed

.rm_dupesPE *Remove duplicate paired-end reads based on start and end position. This is an over-simplification. For better duplicate handling, duplicates must be marked in bam and flag passed to fetchBamPE() ... for ScanBamParam*

Description

flag = scanBamFlag(isDuplicate = FALSE)

Usage

```
.rm_dupesPE(reads_dt, max_dupes)
```

Arguments

reads_dt	data.table of reads as loaded by fetchBamPE
max_dupes	maximum allowed positional duplicates

Value

reads_dt with duplicated reads over max_dupes removed

add_cluster_annotation *add_cluster_annotation*

Description

adds rectangle boxes proportional to cluster sizes of heatmap with optional labels.

Usage

```
add_cluster_annotation(
  cluster_ids,
  p = NULL,
  xleft = 0,
  xright = 1,
  rect_colors = c("black", "gray"),
  text_colors = rev(rect_colors),
  show_labels = TRUE,
  label_angle = 0,
  row_ = "id",
  cluster_ = "cluster_id"
)
```

Arguments

cluster_ids	Vector of cluster ids for each item in heatmap. Should be sorted by plot order for heatmap.
p	Optionally an existing ggplot to add annotation to.
xleft	left side of cluster annotation rectangles. Default is 0.
xright	right side of cluster annotation rectangles. Default is 1.
rect_colors	colors of rectangle fill, repeat to match number of clusters. Default is c("black", "gray").
text_colors	colors of text, repeat to match number of clusters. Default is reverse of rect_colors.
show_labels	logical, shoud rectangles be labelled with cluster identity. Default is TRUE.
label_angle	angle to add clusters labels at. Default is 0, which is horizontal.
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* outputs.
cluster_	variable name to use for cluster info. Default is "cluster_id".

Value

A ggplot with cluster annotations added.

Examples

```
data(CTCF_in_10a_profiles_dt)
#simplest uses
add_cluster_annotation(factor(c(rep("A", 3), "B")))
p = ggplot() + coord_cartesian(xlim = c(0,10))
add_cluster_annotation(factor(c(rep("A", 3), "B")), p)

#intended use with ssvSignalHeatmap
clust_dt = ssvSignalClustering(CTCF_in_10a_profiles_dt, nclust = 3)
assign_dt = unique(clust_dt[, .(id, cluster_id)])[order(id)]
p_heat = ssvSignalHeatmap(clust_dt, show_cluster_bars = FALSE)
add_cluster_annotation(assign_dt$cluster_id, p_heat,
  xleft = -500, xright = -360, rect_colors = rainbow(3), text_colors = "gray")

#when colors are named, the names are used rather that just the order
rect_colors = safeBrew(assign_dt$cluster_id)
text_colors = safeBrew(assign_dt$cluster_id, "greys")
p_clusters = add_cluster_annotation(assign_dt$cluster_id,
  rect_colors = rect_colors, text_colors = text_colors)
#specialized use as plot outside of heatmap
p1 = assemble_heatmap_cluster_bars(plots = list(p_clusters, p_heat), rel_widths = c(1, 3))

#when colors are named, the names are used rather that just the order
#these plots will be identical even though order of colors changes.
rect_colors = rect_colors[c(2, 3, 1)]
text_colors = text_colors[c(3, 1, 2)]
p_clusters = add_cluster_annotation(assign_dt$cluster_id,
  rect_colors = rect_colors, text_colors = text_colors)
#specialized use as plot outside of heatmap
p2 = assemble_heatmap_cluster_bars(plots = list(p_clusters, p_heat), rel_widths = c(1, 3))

cowplot::plot_grid(p1, p2, ncol = 1)
```

---

append_ynorm *append_ynorm*

Description

see calc_norm_factors for normalization details.

Usage

```
append_ynorm(
  full_dt,
  value_ = "y",
  cap_value_ = "y_cap_value",
  norm_value_ = "y_norm",
  by1 = "id",
  by2 = "sample",
  aggFUN1 = max,
  aggFUN2 = function(x) quantile(x, 0.95),
  cap_dt = NULL,
```

```
  do_not_cap = FALSE,
  do_not_scaleTo1 = FALSE,
  force_append = FALSE
)
```

Arguments

full_dt	a data.table, as returned by ssvFetch*(..., return_data.table = TRUE).
value_	character, attribute in full_dt to normalzie.
cap_value_	character, new attribute name specifying values to cap to.
norm_value_	character, new attribute name specifying normalized values.
by1	character vector, specifies attributes relevant to step 1.
by2	character vector, specifies attributes relevant to step 1 and 2.
aggFUN1	function called on value_ with by = c(by1, by2) in step 1.
aggFUN2	function called on result of aggFUN1 with by = by2 in step 2.
cap_dt	optionally, provide user generated by2 to cap_value_ mapping
do_not_cap	if TRUE, normalized values are not capped to 1. Default is FALSE.
do_not_scaleTo1	if TRUE, normalized values are not scaled to 1. Default is FALSE.
force_append	if TRUE, any previous cap_value or norm_value is overridden. Default is FALSE.

Value

data.table, full_dt with cap_value_ and norm_value_ values appended.

Examples

```
data(CTCF_in_10a_profiles_dt)
append_ynorm(CTCF_in_10a_profiles_dt)
append_ynorm(CTCF_in_10a_profiles_dt,
  aggFUN1 = mean, aggFUN2 = function(x)quantile(x, .5))
```

---

applyMovingAverage *applyMovingAverage*

Description

http://www.cookbook-r.com/Manipulating_data/Calculating_a_moving_average/

Usage

```
applyMovingAverage(
  dt,
  n,
  centered = TRUE,
  x_ = "x",
  y_ = "y",
  by_ = c("id", "sample"),
  maFun = movingAverage
)
```

Arguments

dt	a tidy data.table containing two-dimensional data
n	the number of samples centered: if FALSE, then average
centered	current sample and previous (n-1) samples if TRUE, then average symmetrically in past and future. (If n is even, use one more sample from future.)
x_	the variable name of the x-values
y_	the variable name of the y-values
by_	optionally, any variables that provide grouping to the data. default is none. see details.
maFun	a function that accepts x, y, and n as arguments and returns a list of length 2 with named elements x and y.

Value

a newly derived data.table where a movingAverage has been applied.

Examples

```
data(CTCF_in_10a_profiles_dt)
agg_dt = CTCF_in_10a_profiles_dt[, list(y = mean(y)), by = list(sample, x)]
ggplot(agg_dt) +
    geom_line(aes(x = x, y = y, color = sample))

ma_smooth = applyMovingAverage(agg_dt, n = 5,
    y_ = 'y', by_ = c('sample'))
ggplot(ma_smooth) +
    geom_line(aes(x = x, y = y, color = sample))

ma_smooth$method = "moving_average"
agg_dt$method = "none"
ggplot(rbind(ma_smooth, agg_dt)) +
    geom_line(aes(x = x, y = y, color = method)) +
    facet_wrap(~sample)
```

---

applySpline *applies a spline smoothing to a tidy data.table containing x and y values.*

Description

applySpline Is intended for two-dimensional tidy data.tables, as retured by ssvFetchBigwig

Usage

```
applySpline(
  dt,
  n,
  x_ = "x",
  y_ = "y",
  by_ = c("id", "sample"),
  splineFun = stats::spline
)
```

Arguments

dt	a tidy data.table containing two-dimensional data
n	the number of interpolation points to use per input point, see ?spline. n must be > 1.
x_	the variable name of the x-values
y_	the variable name of the y-values
by_	optionally, any variables that provide grouping to the data. default is none. see details.
splineFun	a function that accepts x, y, and n as arguments and returns a list of length 2 with named elements x and y. stats::spline by default. see stats::spline for details.

Details

by_ is quite powerful. If by_ = c('gene_id', 'sample_id'), splines will be calculated individually for each gene in each sample. alternatively if by_ = c('gene_id')

Value

a newly derived data.table that is n times longer than original.

See Also

ssvFetchBigwig

Examples

```
data(CTCF_in_10a_profiles_dt)
#data may be blockier than we'd like
ggplot(CTCF_in_10a_profiles_dt[, list(y = mean(y)), by = list(sample, x)]) +
    geom_line(aes(x = x, y = y, color = sample))

#can be smoothed by applying a spline  (think twice about doing so,
#it may look prettier but may also be deceptive or misleading)

splined_smooth = applySpline(CTCF_in_10a_profiles_dt, n = 10,
    y_ = 'y', by_ = c('id', 'sample'))
ggplot(splined_smooth[, list(y = mean(y)), by = list(sample, x)]) +
    geom_line(aes(x = x, y = y, color = sample))
```

---

assemble_heatmap_cluster_bars

assemble_heatmap_cluster_bars

Description

assemble_heatmap_cluster_bars

Usage

```
assemble_heatmap_cluster_bars(plots, ...)
```

Arguments

plots	list of plots as returned from ssvSignalHeatmap.ClusterBars when return_unassembled_plots = TRUE
...	arguments passed to cowplot::plot_grid

Value

A grob produced by cowplot::plot_grid

Examples

```
data(CTCF_in_10a_profiles_gr)
plots = ssvSignalHeatmap.ClusterBars(CTCF_in_10a_profiles_gr, return_unassembled_plots = TRUE)
assemble_heatmap_cluster_bars(plots)
```

Bcell_peaks *4 random peaks for paired-end data*

Description

matches `system.file("extdata/Bcell_PE.mm10.bam", package = "seqsetvis")`

Format

GRanges length 4

Details

this is included only for testing ssvFetchBamPE functions.

Value

GRanges length 4

---

calc_norm_factors *calc_norm_factors*

Description

Calculate normalization factors in a two step process:

Usage

```
calc_norm_factors(
  full_dt,
  value_ = "y",
  cap_value_ = "y_cap_value",
  by1 = "id",
  by2 = "sample",
  aggFUN1 = max,
  aggFUN2 = function(x) quantile(x, 0.95)
)
```

Arguments

full_dt	a data.table, as returned by ssvFetch*(..., return_data.table. = TRUE)
value_	character, attribute in full_dt to normalzie.
cap_value_	character, new attribute name specifying values to cap to.
by1	character vector, specifies attributes relevant to step 1.
by2	character vector, specifies attributes relevant to step 1 and 2.
aggFUN1	function called on value_ with by = c(by1, by2) in step 1.
aggFUN2	function called on result of aggFUN1 with by = by2 in step 2.

Details

1. summarize every region for each sample (default summary function is max)
2. caclulate a value to cap each sample to based on regions (default is 95th quantile).

The uderlying assumption here is that meaningful enrichment is present at the majority of regions provided. If prevalence varies by a specific factor, say ChIP-seq targets with different characteristics - ie. when analyzing TSSes for H3K4me3 and an infrequent transcription factor it is more appropriate to specify appropriate quantile cutoffs per factor.

Value

data.table mapping by2 to cap_value_.

Examples

```
data(CTCF_in_10a_profiles_dt)
calc_norm_factors(CTCF_in_10a_profiles_dt)
calc_norm_factors(CTCF_in_10a_profiles_dt,
  aggFUN1 = mean, aggFUN2 = function(x)quantile(x, .5))
```

---

centerAtMax *centers profile of x and y. default is to center by region but across all samples.*

Description

centerAtMax locates the coordinate x of the maximum in y and shifts x such that it is zero at max y.

Usage

```
centerAtMax(
  dt,
  x_ = "x",
  y_ = "y",
  by_ = "id",
  view_size = NULL,
  trim_to_valid = TRUE,
  check_by_dupes = TRUE,
  x_precision = 3,
  replace_x = TRUE
)
```

Arguments

dt	data.table
x_	the variable name of the x-values. default is 'x'
y_	the variable name of the y-values default is 'y'
by_	optionally, any variables that provide grouping to the data. default is none. see details.
view_size	the size in x_ to consider for finding the max of y_. if length(view_size) == 1, range will be c(-view_size, view_size). if length(view_size) > 1, range will be range(view_size). default value of NULL uses complete range of x.
trim_to_valid	valid x_ values are those with a set y_ value in all by_ combinations
check_by_dupes	default assumption is that there should be on set of x_ for a by_ instance. if this is not the case and you want to disable warnings about set this to FALSE.
x_precision	numerical precision of x, default is 3.
replace_x	logical, default TRUE. if TRUE x_ will be replaced with position relative to summit. if FALSE x_ will be preserved and x_summitPosition added.

Details

character. by_ controls at the level of the data centering is applied. If by_ is "" or NULL, a single max position will be determined for the entire dataset. If by is "id" (the default) then each region will be centered individually across all samples.

Value

data.table with x (or xnew if replace_x is FALSE) shifted such that x = 0 matches the maximum y-value define by by_ grouping

Examples

```
data(CTCF_in_10a_profiles_gr)
centerAtMax(CTCF_in_10a_profiles_gr, y_ = 'y', by_ = 'id',
  check_by_dupes = FALSE)
#it's a bit clearer what's happening with trimming disabled
#but results are less useful for heatmaps etc.
centerAtMax(CTCF_in_10a_profiles_gr, y_ = 'y', by_ = 'id',
  check_by_dupes = FALSE, trim_to_valid = FALSE)
#specify view_size to limit range of x values considered, prevents
#excessive data trimming.
centerAtMax(CTCF_in_10a_profiles_gr, y_ = 'y', view_size = 100, by_ = 'id',
check_by_dupes = FALSE)
```

---

centerFixedSizeGRanges

Transforms set of GRanges to all have the same size.

Description

centerFixedSizeGRanges First calculates the central coordinate of each GRange in grs and extends in both direction by half of fixed_size

Usage

```
centerFixedSizeGRanges(grs, fixed_size = 2000)
```

Arguments

grs	Set of GRanges with incosistent and/or incorrect size
fixed_size	The final width of each GRange returned.

Value

Set of GRanges after resizing all input GRanges, either shortened or lengthened as required to match `fixed_size`

Examples

```
library(GenomicRanges)
grs = GRanges("chr1", IRanges(1:10+100, 1:10*3+100))
centered_grs = centerFixedSizeGRanges(grs, 10)
width(centered_grs)
```

---

centerGRangesAtMax *Centers query GRanges at maximum signal in prof_dt.*

Description

Centers query GRanges at maximum signal in prof_dt.

Usage

```
centerGRangesAtMax(prof_dt, qgr, x_ = "x", y_ = "y", by_ = "id", width = 1)
```

Arguments

prof_dt	a GRanges or data.table as returned by ssvFetch*.
qgr	the GRanges used to query ssvFetch* as the qgr argument.
x_	positional variable. Should almost always be the default, "x".
y_	the signal value variable. Likely the default value of "y" but could be "y_norm" if append_ynorm was applied to data.
by_	region identifier variable. Should almost always be the default, "id".
width	Desired width of final regions. Default is 1.

Value

a GRanges with same mcols as qgr that has been centered based on signal in prof_dt and with regions of specified width.

Examples

```
data(CTCF_in_10a_overlaps_gr)
data(CTCF_in_10a_profiles_gr)
data(CTCF_in_10a_profiles_dt)
centerGRangesAtMax(CTCF_in_10a_profiles_dt, CTCF_in_10a_overlaps_gr)
centerGRangesAtMax(CTCF_in_10a_profiles_gr, CTCF_in_10a_overlaps_gr)
```

---

chromHMM_demo_bw_states_gr

MCF10A CTCF profiles at 20 windows per chromHMM state, hg38.

Description

MCF10A CTCF profiles at 20 windows per chromHMM state, hg38.

Format

a GRanges object of length 4000 with 5 metadata columns sufficient for use with ggplot2

Details

part of chromHMM_demo_data

the result of ssvFetchBigwig() on the MCF10A_CTCF_FE.bw near 20 randomly selected windows per chromHMM state.

Value

a GRanges object of length 4000 with 5 metadata columns sufficient for use with ggplot2

---

chromHMM_demo_chain_url

URL to download hg19ToHg38 liftover chain from UCSC

Description

URL to download hg19ToHg38 liftover chain from UCSC

Format

a character containing a URL

Details

file is gzipped .txt

part of chromHMM_demo_data

Value

a character containing a URL

chromHMM_demo_data *chromHMM state segmentation in the MCF7 cell line*

Description

Vignette data for seqsetvis was downloaded directly from GEO series GSE57498. This data is the state segmentation by chromHMM in the MCF7 cell line. chromHMM creates a hidden markov model by integrating several ChIP-seq samples, in this case:

- MCF7_H3K27ac_ChIP-Seq
- MCF7_H3K27me3_ChIP-Seq
- MCF7_H3K4me1_ChIP-Seq
- MCF7_H3K4me3_ChIP-Seq
- MCF7_RNApolIIp_ChIP-Seq

Data from GEO series GSE57498 is from the publication Taberlay PC et al. 2014

Details

Contains:

- chromHMM_demo_overlaps_gr
- chromHMM_demo_bw_states_gr
- chromHMM_demo_state_total_widths
- chromHMM_demo_state_colors
- chromHMM_demo_segmentation_url
- chromHMM_demo_chain_url

chromHMM_demo_overlaps_gr *overlap of MCF10A CTCF with MCF7 chromHMM states, hg38.*

Description

overlap of MCF10A CTCF with MCF7 chromHMM states, hg38.

Format

a GRanges object of length 98 with 10 logical metadata columns, 1 per state.

Details

part of chromHMM_demo_data

the result of ssvOverlapIntervalSets() on MCF10A CTCF peaks and MCF7 chromHMM states with use_first = TRUE

first (the MCF10A peaks) and no_hit columns have been removed each remaining column represents MCF10A peaks overlapping with a state.

Value

a GRanges object of length 98 with 10 logical metadata columns, 1 per state.

`chromHMM_demo_segmentation_url`
URL to download hg19 MCF7 chromHMM segmentation

Description

URL to download hg19 MCF7 chromHMM segmentation

Format

a character containing a URL

Details

file is gzipped bed with name, score, itemRgb and thick meta columns

part of `chromHMM_demo_data`

Value

a character containing a URL

`chromHMM_demo_state_colors`
original state name to color mappings stored in segmentation bed

---

Description

original state name to color mappings stored in segmentation bed

Format

a named character vector mapping states to hex colors

Details

part of `chromHMM_demo_data`

Value

a named character vector mapping states to hex colors

chromHMM_demo_state_total_widths

state name to total width mappings, hg38

Description

state name to total width mappings, hg38

Format

named numeric of total widths per state

Details

part of chromHMM_demo_data

Value

named numeric of total widths per state

clusteringKmeans

perform kmeans clustering on matrix rows and return reordered matrix along with order matched cluster assignments. clusters are sorted using hclust on centers

Description

perform kmeans clustering on matrix rows and return reordered matrix along with order matched cluster assignments. clusters are sorted using hclust on centers

Usage

```
clusteringKmeans(mat, nclust, centroids = NULL, iter.max = 30)
```

Arguments

mat	numeric matrix to cluster.
nclust	the number of clusters.
centroids	optional matrix with same columns as mat and one centroid per row to base clusters off of. Overrides any setting to nclust. Default of NULL results in randomly initialized k-means.
iter.max	Number of max iterations to allow for k-means. Default is 30.

Value

data.table with group__ variable indicating cluster membership and id__ variable that is a factor indicating order based on within cluster similarity

Examples

```
data(CTCF_in_10a_profiles_dt)
dt = data.table::copy(CTCF_in_10a_profiles_dt)
mat = data.table::dcast(dt, id ~ sample + x, value.var = "y" )
rn = mat$id
mat = as.matrix(mat[,-1])
rownames(mat) = rn
clust_dt = clusteringKmeans(mat, nclust = 3)
dt = merge(dt, clust_dt[, .(id = id__, group = group__)])
dt$id = factor(dt$id, levels = clust_dt$id)
dt[order(id)]
```

`clusteringKmeansNestedHclust` *perform kmeans clustering on matrix rows and return reordered matrix along with order matched cluster assignments clusters are sorted using hclust on centers the contents of each cluster are sorted using hclust*

Description

perform kmeans clustering on matrix rows and return reordered matrix along with order matched cluster assignments clusters are sorted using hclust on centers the contents of each cluster are sorted using hclust

Usage

```
clusteringKmeansNestedHclust(
  mat,
  nclust,
  within_order_strategy = valid_sort_strategies[2],
  centroids = NULL,
  manual_mapping = NULL,
  iter.max = 30
)
```

Arguments

`mat`	A wide format matrix
`nclust`	the number of clusters
`within_order_strategy`	one of "hclust", "sort", "right", "left", "reverse". If "hclust", hierarchical clustering will be used. If "sort", a simple decreasing sort of rosSums. If "left", will atttempt to put high signal on left ("right" is opposite). If "reverse" reverses existing order (should only be used after meaningful order imposed).
`centroids`	optional matrix with same columns as mat and one centroid per row to base clusters off of. Overrides any setting to nclust. Default of NULL results in randomly initialized k-means.
`manual_mapping`	optional named vector manually specifiying cluster assignments. names should be item ids and values should be cluster names the items are assigned to. Default of NULL allows clustering to proceed.
`iter.max`	Number of max iterations to allow for k-means. Default is 30.

Value

data.table with 2 columns of cluster info. id__ column corresponds with input matrix rownames and is sorted within each cluster using hierarchical clusering group__ column indicates cluster assignment

Examples

```
data(CTCF_in_10a_profiles_dt)
dt = data.table::copy(CTCF_in_10a_profiles_dt)
mat = data.table::dcast(dt, id ~ sample + x, value.var = "y" )
rn = mat$id
mat = as.matrix(mat[,-1])
rownames(mat) = rn
clust_dt = clusteringKmeansNestedHclust(mat, nclust = 3)
clust_dt
```

---

col2hex *converts a valid r color name ("black", "red", "white", etc.) to a hex value*

Description

converts a valid r color name ("black", "red", "white", etc.) to a hex value

Usage

```
col2hex(color_name)
```

Arguments

color_name	character. one or more r color names.

Value

hex value of colors coded by colors()

Examples

```
col2hex(c("red", "green", "blue"))
col2hex(c("lightgray", "gray", "darkgray"))
```

collapse_gr *collapse_gr*

Description

collapse non-contiguous regions (i.e. exons) into a contiguous coordinate starting at 1. this is strand sensitive and intended for use with all exons of a single gene.

Usage

```
collapse_gr(genome_gr)
```

Arguments

genome_gr	a GRanges of regions on a single chromosome. Regions are intended to be non-contiguous and may even overlap.

Value

a new GRanges object with same mcols as input with all intervals starting at 1 and no empty space between syntenic regions.

Examples

```
library(data.table)
library(GenomicRanges)
dev_dat = data.table(seqnames = "chrTest",
                     transcript_id = c(1, 1,  2, 2, 3, 3, 3),
                     start = c(5,  30,  8, 30, 2, 30, 40),
                     end = c(10, 35, 15, 38, 7, 35, 45),
                     strand = "+")

genome_gr = GRanges(dev_dat)
collapse_gr(genome_gr)

neg_gr = genome_gr
strand(neg_gr) = "-"
collapse_gr(neg_gr)
```

convert_collapsed_coord *convert_collapsed_coord*

Description

(preliminary implementation, sub-optimal)

Usage

```
convert_collapsed_coord(genome_gr, x)
```

Arguments

genome_gr	non-contiguous regions to collapse a la collapse_gr
x	numeric, positions within genome_gr to convert to collapsed coordinates.

Details

see collapse_gr for explanation of intended uses. this function translates all values of x from original genomic coordinates to new coordinate space created by collapse_gr.

Value

numeric, positions of every value of x within collapse coordinates. values outside of collapsed regions (an intron or outside range) will be NA.

Examples

```
library(data.table)
library(GenomicRanges)
dev_dat = data.table(seqnames = "chrTest",
                     transcript_id = c(1, 1,  2, 2, 3, 3, 3),
                     start = c(5,  30,  8, 30, 2, 30, 40),
                     end = c(10, 35, 15, 38, 7, 35, 45),
                     strand = "+")

genome_gr = GRanges(dev_dat)
convert_collapsed_coord(genome_gr, start(genome_gr))
convert_collapsed_coord(genome_gr, end(genome_gr))
```

---

copy_clust_info *copy_clust_info*

Description

copy_clust_info

Usage

```
copy_clust_info(target, to_copy, row_ = "id", cluster_ = "cluster_id")
```

Arguments

target	A data.table or GRanges returned from ssvFetch*, the target to which cluster info will be added.
to_copy	A data.table or GRanges returned from ssvSignalClustering, from which to copy cluster if.
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
cluster_	variable name to use for cluster info. Default is "cluster_id".

Value

data.table or GRanges (whichever target is) containing row order and cluster assignment derived from to_copy. Suitable for ssvSignalHeatmap and related functions.

Examples

```
data(CTCF_in_10a_narrowPeak_grs)
data(CTCF_in_10a_overlaps_gr)
data(CTCF_in_10a_profiles_dt)
#this takes cluster info from signal and applies to peak hits to
#create a heatmap of peak hits clustered by signal.
clust_dt1 = ssvSignalClustering(CTCF_in_10a_profiles_dt)
peak_hit_gr = ssvFetchGRanges(
  CTCF_in_10a_narrowPeak_grs,
  qgr = CTCF_in_10a_overlaps_gr
)
peak_hit_gr.clust = copy_clust_info(peak_hit_gr, clust_dt1)
peak_hit_gr.clust$hit = peak_hit_gr.clust$y > 0
ssvSignalHeatmap(peak_hit_gr.clust, fill_ = "hit") +
  scale_fill_manual(values = c("FALSE" = "gray90", "TRUE" = "black"))
```

---

crossCorrByRle *Calculate cross correlation by using shiftApply on read coverage Rle*

Description

Calculate cross correlation by using shiftApply on read coverage Rle

Usage

```
crossCorrByRle(
  bam_file,
  query_gr,
  max_dupes = 1,
  fragment_sizes = 50:300,
  read_length = NULL,
  flip_strand = FALSE,
  ...
)
```

Arguments

bam_file	character. Path to .bam file, must have index at .bam.bai.
query_gr	GRanges. Regions to calculate cross correlation for.
max_dupes	integer. Duplicate reads above this value will be removed.
fragment_sizes	integer. fragment size range to search for maximum correlation.
read_length	integer. Any values outside fragment_range that must be searched. If not supplied will be determined from bam_file. Set as NA to disable this behavior.
flip_strand	boolean. if TRUE strands that reads align to are swapped. This is typically only necessary if there was a mismatch between library chemistry and aligner settings. Default is FALSE.
...	arguments passed to ScanBamParam

Value

named list of results

Examples

```
data(CTCF_in_10a_overlaps_gr)
bam_f = system.file("extdata/test.bam",
    package = "seqsetvis", mustWork = TRUE)
query_gr = CTCF_in_10a_overlaps_gr[1:2]
crossCorrByRle(bam_f, query_gr[1:2], fragment_sizes = seq(50, 300, 50))
```

CTCF_in_10a_bigWig_urls

FTP URL path for vignette data.

Description

FE bigWig tracks for CTCF ChIP-seq in a MCF10A progression model. See GEO series GSE98551 for details.

Format

named character vector of length 3

Details

part of CTCF_in_10a_data

CTCF_in_10a_data *CTCF ChIP-seq in breast cancer cell lines*

Description

Vignette data for seqsetvis was downloaded directly from GEO series GSE98551. This data is CTCF ChIP-seq from a model of breast cancer progression derived from the MCF10A cell line.

Data from GEO series GSE98551 is from the publication Fritz AJ et al. 2018

Details

Contains:

- CTCF_in_10a_overlaps_gr
- CTCF_in_10a_profiles_dt
- CTCF_in_10a_bigWig_urls
- CTCF_in_10a_narrowPeak_urls

CTCF_in_10a_narrowPeak_grs

list of GRanges that results in 100 random subset when overlapped

Description

list of GRanges that results in 100 random subset when overlapped

Format

named list of GRanges of length 3

Details

part of CTCF_in_10a_data

Value

named list of GRanges of length 3

CTCF_in_10a_narrowPeak_urls

FTP URL path for vignette data. from

Description

macs2 peak calls for CTCF ChIP-seq in a MCF10A progression model. See GEO series GSE98551 for details.

Format

named character vector of length 3

Details

part of CTCF_in_10a_data

`CTCF_in_10a_overlaps_gr`

100 randomly selected regions from overlapping CTCF peaks in 10a cell ChIP-seq

---

Description

MACS2 narrowPeak calls on pooled biological replicates at pval 1e-5 and then 0.05 IDR filtered. IDR cutoffs determined by comparing top 150,000 pvalue sorted peak in replicates.

Format

GenomicRanges with 3 metadata columns of membership table

Details

See GEO series GSE98551 for details.

part of `CTCF_in_10a_data`

`CTCF_in_10a_profiles_dt`

Profiles for 100 randomly selected regions from overlapping CTCF peaks in 10a cell ChIP-seq Results from fetching bigwigs with CTCF_in_10a_overlaps_gr.

Description

A tidy data.table at window size 50 bp within 350 bp of peak center The variables are as follows:

Format

A tidy data.table of 2100 rows and 9 columns

Details

part of `CTCF_in_10a_data`

1. seqnames. chromosome for GRanges compatibility
2. start. start of interval
3. end. end of interval
4. width. width of interval
5. strand. leftover from GRanges.
6. id. unique identifier
7. y. fold-enrichment over input.
8. x. bp relative to center
9. sample. name of originating sample

CTCF_in_10a_profiles_gr

Profiles for 100 randomly selected regions from overlapping CTCF peaks in 10a cell ChIP-seq Results from CTCF_in_10a_overlaps_gr

Description

A tidy GRanges at window size 50 bp within 350 bp of peak center The variables are as follows:

Format

A tidy GRanges of 2100 rows and 4 metadata columns

Details

part of CTCF_in_10a_data

1. id. unique identifier
2. y. fold-enrichment over input.
3. x. bp relative to center
4. sample. name of originating sample

easyLoad_bed

easyLoad_bed takes a character vector of file paths to bed plus files and returning named list of GRanges.

Description

Mainly a utility function for loading MACS2 narrowPeak and broadPeak.

Usage

```
easyLoad_bed(
  file_paths,
  file_names = NULL,
  extraCols = character(),
  n_cores = getOption("mc.cores", 1)
)
```

Arguments

file_paths	character vector of paths to narrowPeak files. If named, those names will be used in output unless overriden by providing file_names.
file_names	character vector of names for output list. If not NULL will override any existing names for file_paths. Default is NULL.
extraCols	named character vector of classes. passed to rtracklayer::import for format = "BED". default is character().
n_cores	number of cores to use, uses mc.cores option if set or 1.

Value

a named list of GRanges loaded from file_paths

Examples

```
bed_f = system.file("extdata/test_loading.bed",
    package = "seqsetvis", mustWork = TRUE)
easyLoad_bed(bed_f, "my_bed")
```

---

easyLoad_broadPeak *easyLoad_broadPeak takes a character vector of file paths to narrowPeak files from MACS2 and returns a named list of GRanges.*

Description

easyLoad_broadPeak takes a character vector of file paths to narrowPeak files from MACS2 and returns a named list of GRanges.

Usage

```
easyLoad_broadPeak(
  file_paths,
  file_names = NULL,
  n_cores = getOption("mc.cores", 1)
)
```

Arguments

file_paths	character vector of paths to narrowPeak files. If named, those names will be used in output unless overriden by providing file_names.
file_names	character vector of names for output list. If not NULL will override any existing names for file_paths. Default is NULL.
n_cores	number of cores to use, uses mc.cores option if set or 1.

Value

a named list of GRanges loaded from file_paths

Examples

```
bp_f = system.file("extdata/test_loading.broadPeak",
    package = "seqsetvis", mustWork = TRUE)
easyLoad_broadPeak(bp_f, "my_broadPeak")
```

`easyLoad_FUN` *easyLoad_FUN takes a character vector of file paths run an arbitrary function defined in load_FUN*

Description

easyLoad_FUN takes a character vector of file paths run an arbitrary function defined in load_FUN

Usage

```
easyLoad_FUN(
  file_paths,
  load_FUN,
  file_names = NULL,
  n_cores = getOption("mc.cores", 1),
  ...
)
```

Arguments

`file_paths`	character vector of paths to narrowPeak files. If named, those names will be used in output unless overriden by providing file_names.
`load_FUN`	Arbitrary function that takes at least a file path as argument. May take other arguments that should be set in call to easyLoad_FUN.
`file_names`	character vector of names for output list. If not NULL will override any existing names for file_paths. Default is NULL.
`n_cores`	number of cores to use, uses mc.cores option if set or 1.
`...`	extra parameters passed to load_FUN

Value

a named list of results from load_FUN

Examples

```
bed_f = system.file("extdata/test_loading.bed",
    package = "seqsetvis", mustWork = TRUE)
easyLoad_bed(bed_f, "my_bed")
```

`easyLoad_IDRmerged` *easyLoad_IDRmerged loads "overlapped-peaks.txt" from IDR.*

Description

easyLoad_IDRmerged loads "overlapped-peaks.txt" from IDR.

Usage

```
easyLoad_IDRmerged(
  file_paths,
  file_names = NULL,
  n_cores = getOption("mc.cores", 1),
  max_idr = 0.05
)
```

Arguments

file_paths	character vector of paths to narrowPeak files. If named, those names will be used in output unless overriden by providing file_names.
file_names	character vector of names for output list. If not NULL will override any existing names for file_paths. Default is NULL.
n_cores	number of cores to use, uses mc.cores option if set or 1.
max_idr	maximum IDR value allowed

Value

named list of GRanges

Examples

```
idr_file = system.file("extdata/test_idr.overlapped-peaks.txt",
    package = "seqsetvis", mustWork = TRUE)
easyLoad_IDRmerged(idr_file)
easyLoad_IDRmerged(idr_file, max_idr = .01)
```

---

easyLoad_narrowPeak *easyLoad_narrowPeak takes a character vector of file paths to narrowPeak files from MACS2 and returns a named list of GRanges.*

Description

easyLoad_narrowPeak takes a character vector of file paths to narrowPeak files from MACS2 and returns a named list of GRanges.

Usage

```
easyLoad_narrowPeak(
  file_paths,
  file_names = NULL,
  n_cores = getOption("mc.cores", 1)
)
```

Arguments

file_paths	character vector of paths to narrowPeak files. If named, those names will be used in output unless overriden by providing file_names.
file_names	character vector of names for output list. If not NULL will override any existing names for file_paths. Default is NULL.
n_cores	number of cores to use, uses mc.cores option if set or 1.

Value

a named list of GRanges loaded from file_paths

Examples

```
np_f = system.file("extdata/test_loading.narrowPeak",
    package = "seqsetvis", mustWork = TRUE)
easyLoad_narrowPeak(np_f, "my_narrowPeak")
```

---

easyLoad_seacr *easyLoad_seacr takes a character vector of file paths to seacr output bed files and returns a named list of GRanges.*

Description

easyLoad_seacr takes a character vector of file paths to seacr output bed files and returns a named list of GRanges.

Usage

```
easyLoad_seacr(
  file_paths,
  file_names = NULL,
  n_cores = getOption("mc.cores", 1)
)
```

Arguments

file_paths	character vector of paths to seacr bed files. If named, those names will be used in output unless overriden by providing file_names.
file_names	character vector of names for output list. If not NULL will override any existing names for file_paths. Default is NULL.
n_cores	number of cores to use, uses mc.cores option if set or 1.

Value

a named list of GRanges loaded from file_paths

Examples

```
bed_f = system.file("extdata/test_loading.seacr.bed",
    package = "seqsetvis", mustWork = TRUE)
easyLoad_seacr(bed_f, "my_seacr")
```

expandCigar *Expand cigar codes to GRanges*

Description

see sam specs for cigar details

Usage

```
expandCigar(
  cigar_dt,
  op_2count = c("M", "D", "=", "X"),
  return_data.table = FALSE
)
```

Arguments

cigar_dt	data.table with 5 required named columns in any order. c("which_label", "seqnames", "strand", "start", "cigar")
op_2count	Cigar codes to count. Default is alignment (M), deletion (D), match (=), and mismatch (X). Other useful codes may be skipped regions for RNA splicing (N). The locations of any insterions (I) or clipping/padding (S, H, or P) will be a single bp immediately before the interval.
return_data.table	if TRUE, a data.table is returned, else a GRanges. Default is FALSE.

Value

data.table with cigar entries expanded

Examples

```
data(CTCF_in_10a_overlaps_gr)
qgr = CTCF_in_10a_overlaps_gr[1:5]
bam_file = system.file("extdata/test.bam", package = "seqsetvis", mustWork = TRUE)
raw_dt = ssvFetchBam(bam_file, qgr, return_unprocessed = TRUE)
expandCigar(raw_dt)
```

fetchBam *fetch a bam file pileup with the ability to consider read extension to fragment size (fragLen)*

Description

fetch a bam file pileup with the ability to consider read extension to fragment size (fragLen)

Usage

```
fetchBam(
  bam_f,
  qgr,
  fragLen = NULL,
  target_strand = c("*", "+", "-")[1],
  max_dupes = Inf,
  splice_strategy = c("none", "ignore", "add", "only", "splice_count")[1],
  flip_strand = FALSE,
  return_unprocessed = FALSE,
  ...
)
```

Arguments

bam_f	character or BamFile to load
qgr	GRanges regions to fetchs
fragLen	numeric, NULL, or NA. if numeric, supplied value is used. if NULL, value is calculated with fragLen_calcStranded (default) if NA, raw bam pileup with no cross strand shift is returned.
target_strand	character. if one of "+" or "-", reads are filtered to match. ignored if any other value.
max_dupes	numeric >= 1. duplicate reads by strandd start position over this number are removed, Default is Inf.
splice_strategy	character, one of c("none", "ignore", "add", "only"). Default is "none" and split read alignments are asssumed not present. fragLen must be NA for any other value to be valid. "ignore" will not count spliced regions. "add" counts spliced regions along with others, "only" will only count spliced regions and ignore others.
flip_strand	if TRUE, strand alignment is flipped prior to fragLen extension. Default is FALSE.
return_unprocessed	boolean. if TRUE returns read alignment in data.table. Default is FALSE.
...	passed to ScanBamParam(), can't be which or what.

Value

GRanges containing tag pileup values in score meta column. tags are optionally extended to fragment length (fragLen) prior to pile up.

---

findMaxPos *findMaxPos*

Description

findMaxPos

Usage

```
findMaxPos(prof_dt, qgr, x_ = "x", y_ = "y", by_ = "id", width = 1)
```

Arguments

prof_dt	a GRanges or data.table as returned by ssvFetch*.
qgr	the GRanges used to query ssvFetch* as the qgr argument.
x_	positional variable. Should almost always be the default, "x".
y_	the signal value variable. Likely the default value of "y" but could be "y_norm" if append_ynorm was applied to data.
by_	region identifier variable. Should almost always be the default, "id".
width	Desired width of final regions. Default is 1.

Value

data.table of relative x position from center per id

Examples

```
data(CTCF_in_10a_overlaps_gr)
data(CTCF_in_10a_profiles_gr)
data(CTCF_in_10a_profiles_dt)
findMaxPos(CTCF_in_10a_profiles_dt, CTCF_in_10a_overlaps_gr)
findMaxPos(CTCF_in_10a_profiles_gr, CTCF_in_10a_overlaps_gr)
```

---

fragLen_calcStranded *calculate fragLen from a bam file for specified regions*

Description

calculate fragLen from a bam file for specified regions

Usage

```
fragLen_calcStranded(
  bam_f,
  qgr,
  n_regions = 100,
  include_plot_in_output = FALSE,
  test_fragLen = seq(100, 400, 5),
  flip_strand = FALSE,
  ...
)
```

Arguments

bam_f	character or BamFile. bam file to read from. .bai index file must be in same directory
qgr	GRanges. used as which for ScanBamParam. Can be NULL if it's REALLY important to load the entire bam, force_no_which = TRUE also required.
n_regions	numeric (integer) it's generally overkill to pull all regions at this stage and will slow calculation down. Default is 100.
include_plot_in_output	if TRUE ouptut is a list of fragLen and a ggplot showing values considered by calculation. Default is FALSE.
test_fragLen	numeric. The set of fragment lenghts to gather strand cross correlation for.
flip_strand	boolean. if TRUE strands that reads align to are swapped. This is typically only necessary if there was a mismatch between library chemistry and aligner settings. Default is FALSE.
...	passed to Rsamtools::ScanBamParam, can't be which or what.

Value

numeric fragment length

Examples

```
data(CTCF_in_10a_overlaps_gr)
bam_file = system.file("extdata/test.bam",
    package = "seqsetvis")
qgr = CTCF_in_10a_overlaps_gr[1:5]
fragLen_calcStranded(bam_file, qgr)
#if plot is included, a list is returned, item 2 is the plot
fragLen_calcStranded(bam_file, qgr,
  include_plot_in_output = TRUE)[[2]]
```

---

fragLen_fromMacs2Xls *parse fragLen from MACS2 output*

Description

parse fragLen from MACS2 output

Usage

```
fragLen_fromMacs2Xls(macs2xls_file)
```

Arguments

macs2xls_file	character. an xls file output by MACS2 to parse frag length from

Value

numeric fragment length

Examples

```
xls_file = system.file("extdata/test_peaks.xls",
    package = "seqsetvis")
fragLen_fromMacs2Xls(xls_file)
```

---

getReadLength *determine the most common read length for input bam_file. uses 50 randomly selected regions from query_gr. If fewer than 20 reads are present, loads all of query_gr.*

Description

determine the most common read length for input bam_file. uses 50 randomly selected regions from query_gr. If fewer than 20 reads are present, loads all of query_gr.

Usage

```
getReadLength(bam_file, query_gr)
```

Arguments

bam_file	indexed bam file
query_gr	GRanges to read from bam file

Value

numeric of most common read length.

Examples

```
data(CTCF_in_10a_overlaps_gr)
qgr = CTCF_in_10a_overlaps_gr[1:5]
bam_file = system.file("extdata/test.bam", package = "seqsetvis", mustWork = TRUE)
getReadLength(bam_file, qgr)
```

---

get_mapped_reads *get_mapped_reads*

Description

get_mapped_reads

Usage

```
get_mapped_reads(bam_files)
```

Arguments

bam_files	Path to 1 or more bam files. Must be indexed.

Value

the total mapped reads in each bam file as a named numeric vector.

Examples

```
bam_file = system.file("extdata/test.bam", package = "seqsetvis", mustWork = TRUE)
get_mapped_reads(bam_file)
```

---

ggellipse *ggellipse*

Description

returns a ggplot with ellipses drawn using specified parameters used by ssvFeatureVenn and ssvFeatureEuler

Usage

```
ggellipse(
  xcentres,
  ycentres,
  r,
  r2 = r,
  phi = rep(0, length(xcentres)),
  circle_colors = NULL,
  group_names = LETTERS[seq_along(xcentres)],
  line_alpha = 1,
  fill_alpha = 0.3,
  line_width = 2,
  n_points = 200
)
```

Arguments

xcentres	numeric x-coord of centers of ellipses
ycentres	numeric y-coord of centers of ellipses, must have same length as xcentres
r	numeric radius1 of ellipse, must have length of 1 or match length of xcentres
r2	numeric radius2 of ellipse, must have length of 1 or match length of xcentres. same as r by default.
phi	numeric phi of ellipse, must have length of 1 or match length of xcentres. 0 by default.
circle_colors	character of rcolors or hex colors or NULL. if null safeBrew of Dark2 is used
group_names	character/factor names of color/fill groups. capital letters by default.
line_alpha	numeric value from 0 to 1. alpha of lines, 1 by default
fill_alpha	numeric value from 0 to 1. alpha of fill, .3 by default.
line_width	numeric > 0. passed to size. 2 by default
n_points	integer > 1. number of points to approximate circle with. 200 by default

Details

uses eulerr's non-exported ellipse drawing coordinate function

Value

a ggplot containing ellipses

Examples

```
ggellipse(xcentres = c(1, 1, 2),
    ycentres = c(2, 1, 1),
    r = c(1, 2, 1))
ggellipse(xcentres = c(1, 1, 2),
    ycentres = c(2, 1, 1),
    r = c(1, 2, 1),
    fill_alpha = 0,
    group_names = paste("set", 1:3))
ggellipse(xcentres = c(1, 1, 2),
    ycentres = c(2, 1, 1),
    r = c(1, 2, 1),
    circle_colors = c("red", "orange", "yellow"),
    line_alpha = 0,
    group_names = paste("set", 1:3))
```

---

harmonize_seqlengths *harmonize_seqlengths*

Description

ensures compatibility between seqlength of gr and bam_file based on header

Usage

```
harmonize_seqlengths(query_gr, bam_file, force_fix = FALSE)
```

Arguments

query_gr	GRanges, object to harmonize seqlengths for
bam_file	character, a path to a valid bam file
force_fix	Logical, if TRUE incompatible seqnames are removed from the query_gr. Default is FALSE.

Value

GRanges with seqlengths matching bam_file

Examples

```
library(GenomicRanges)
query_gr = GRanges("chr1", IRanges(1, 100))
#seqlengths has not been set
seqlengths(query_gr)
bam = system.file("extdata/test.bam", package = "seqsetvis")
gr2 = harmonize_seqlengths(query_gr, bam)
#seqlengths now set
seqlengths(gr2)
```

`make_clustering_matrix` *make_clustering_matrix*

Description

Create a wide matrix from a tidy data.table more suitable for clustering methods

Usage

```
make_clustering_matrix(
  tidy_dt,
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  max_rows = 500,
  max_cols = 100,
  clustering_col_min = -Inf,
  clustering_col_max = Inf,
  dcast_fill = NA,
  fun.aggregate = "mean"
)
```

Arguments

`tidy_dt`	the tidy data.table to covert to a wide matrix. Must have entries for variables specified by row_, column_, fill_, and facet_.
`row_`	variable name mapped to row, likely peak id or gene name for ngs data
`column_`	varaible mapped to column, likely bp position for ngs data
`fill_`	numeric variable to map to fill
`facet_`	variable name to facet horizontally by
`max_rows`	for speed rows are sampled to 500 by default, use Inf to plot full data
`max_cols`	for speed columns are sampled to 100 by default, use Inf to plot full data
`clustering_col_min`	numeric minimum for col range considered when clustering, default in -Inf
`clustering_col_max`	numeric maximum for col range considered when clustering, default in Inf
`dcast_fill`	value to supply to dcast fill argument. default is NA.

fun.aggregate	Function to aggregate when multiple values present for facet_, row_, and column_. The function should accept a single vector argument or be a character string naming such a function.

Value

A wide matrix version of input tidy data.table

Examples

```
data(CTCF_in_10a_profiles_dt)
mat = make_clustering_matrix(CTCF_in_10a_profiles_dt)
mat[1:5, 1:5]
```

---

merge_clusters *merge_clusters*

Description

merge_clusters

Usage

```
merge_clusters(
  clust_dt,
  to_merge,
  row_ = "id",
  cluster_ = "cluster_id",
  reapply_cluster_names = TRUE
)
```

Arguments

clust_dt	data.table output from ssvSignalClustering
to_merge	Clusters to merge. Must be items in clust_dt variable defined by cluster_ parameter.
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
cluster_	variable name to use for cluster info. Default is "cluster_id".
reapply_cluster_names	If TRUE, clusters will be renamed according to new order instead of their original names. Default is TRUE.

Value

data.table as output from ssvSignalClustering

Examples

```
data(CTCF_in_10a_profiles_dt)
set.seed(0)
clust_dt = ssvSignalClustering(CTCF_in_10a_profiles_dt, nclust = 6)
ssvSignalHeatmap(clust_dt)
agg_dt = clust_dt[, list(y = mean(y)), list(x, cluster_id, sample)]
ggplot(agg_dt, aes(x = x, y = y, color = sample)) +
  geom_path() +
  facet_grid(cluster_id~.)

to_merge = c(2, 3, 5)
# debug(merge_clusters)
new_dt = merge_clusters(clust_dt, c(2, 3, 5), reapply_cluster_names = FALSE)
new_dt.relabel = merge_clusters(clust_dt, c(2, 3, 5), reapply_cluster_names = TRUE)
new_dt.relabel.sort = within_clust_sort(new_dt.relabel, within_order_strategy = "sort")

table(clust_dt$cluster_id)
table(new_dt$cluster_id)

cowplot::plot_grid(
  ssvSignalHeatmap(clust_dt) + labs(title = "original"),
  ssvSignalHeatmap(new_dt) + labs(title = "2,3,5 merged"),
  ssvSignalHeatmap(new_dt.relabel) + labs(title = "2,3,5 merged, renumbered"),
 ssvSignalHeatmap(new_dt.relabel.sort) + labs(title = "2,3,5 merged, renumbered and sorted")
)
```

`prepare_fetch_GRanges` *prepares GRanges for windowed fetching.*

Description

Deprecated and renamed as prepare_fetch_GRanges_width

Usage

```
prepare_fetch_GRanges(
  qgr,
  win_size,
  min_quantile = 0.75,
  target_size = NULL,
  skip_centerFix = FALSE
)
```

Arguments

`qgr`	GRanges to prepare
`win_size`	numeric window size for fetch
`min_quantile`	numeric value from 0 to 1. Lowest possible quantile value. Only relevant if target_size is not specified.

target_size	numeric final width of qgr if known. Default of NULL leads to quantile based determination of target_size.
skip_centerFix	boolean, if FALSE (default) all regions will be resized GenomicRanges::resize(x, w, fix = "center") to a uniform size based on min_quantile to a width divisible by win_size.

Details

output GRanges parallels input with consistent width evenly divisible by win_size. Has warning if GRanges needed resizing, otherwise no warning and input GRanges is returned unchanged.

Value

GRanges, either identical to qgr or with suitable consistent width applied.

Examples

```
data(CTCF_in_10a_overlaps_gr)
#use prepare_fetch_GRanges_width instead:
qgr = prepare_fetch_GRanges_width(CTCF_in_10a_overlaps_gr, win_size = 50)
#no warning if qgr is already valid for windowed fetching
prepare_fetch_GRanges_width(qgr, win_size = 50)
```

---

prepare_fetch_GRanges_names

Creates a named version of input GRanges using the same method seqsetvis uses internally to ensure consistency.

Description

If $id is set, that value is used as name and duplicates are checked for.

Usage

```
prepare_fetch_GRanges_names(qgr, include_id = FALSE)
```

Arguments

qgr	input GRanges object the set/check names on
include_id	if TRUE, $id is retained. Default is FALSE.

Value

and named GRanges based on input qgr.

Examples

```
data(CTCF_in_10a_overlaps_gr)
qgr = CTCF_in_10a_overlaps_gr
names(qgr) = NULL
#default is to paste "region_" and iteration along length of qgr
prepare_fetch_GRanges_names(qgr)
#id gets used is already set
qgr$id = paste0("peak_", rev(seq_along(qgr)), "_of_", length(qgr))
prepare_fetch_GRanges_names(qgr)
```

`prepare_fetch_GRanges_width` *prepares GRanges for windowed fetching.*

Description

output GRanges parallels input with consistent width evenly divisible by win_size. Has warning if GRanges needed resizing, otherwise no warning and input GRanges is returned unchanged.

Usage

```
prepare_fetch_GRanges_width(
  qgr,
  win_size,
  min_quantile = 0.75,
  target_size = NULL,
  skip_centerFix = FALSE
)
```

Arguments

`qgr`	GRanges to prepare
`win_size`	numeric window size for fetch
`min_quantile`	numeric value from 0 to 1. Lowest possible quantile value. Only relevant if target_size is not specified.
`target_size`	numeric final width of qgr if known. Default of NULL leads to quantile based determination of target_size.
`skip_centerFix`	boolean, if FALSE (default) all regions will be resized GenomicRanges::resize(x, w, fix = "center") to a uniform size based on min_quantile to a width divisible by win_size.

Value

GRanges, either identical to qgr or with suitable consistent width applied.

Examples

```
data(CTCF_in_10a_overlaps_gr)
qgr = prepare_fetch_GRanges_width(CTCF_in_10a_overlaps_gr, win_size = 50)
#no warning if qgr is already valid for windowed fetching
prepare_fetch_GRanges_width(qgr, win_size = 50)
```

quantileGRangesWidth *Quantile width determination strategy*

Description

Returns the lowest multiple of win_size greater than min_quantile quantile of width(qgr)

Usage

```
quantileGRangesWidth(qgr, min_quantile = 0.75, win_size = 1)
```

Arguments

qgr	GRanges to calculate quantile width for
min_quantile	numeric value from 0 to 1. The minimum quantile of width in qgr
win_size	numeric/integer >=1, returned value will be a multiple of this

Value

numeric that is >= min_quantile and evenly divisible by win_size

Examples

```
data(CTCF_in_10a_overlaps_gr)
gr = CTCF_in_10a_overlaps_gr
quantileGRangesWidth(gr)
quantileGRangesWidth(gr, min_quantile = .5, win_size = 100)
```

reorder_clusters_hclust *reorder_clusters_hclust*

Description

Applies hierarchical clustering to centroids of clusters to reorder.

Usage

```
reorder_clusters_hclust(
  clust_dt,
  hclust_result = NULL,
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  cluster_ = "cluster_id",
  reapply_cluster_names = TRUE,
  return_hclust = FALSE
)
```

Arguments

clust_dt	data.table output from ssvSignalClustering
hclust_result	hclust result returned by a previous call of this function with identical paramters when return_hclust = TRUE.
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
column_	varaible mapped to column, likely bp position for ngs data. Default is "x" and works with ssvFetch* output.
fill_	numeric variable to map to fill. Default is "y" and works with ssvFetch* output.
facet_	variable name to facet horizontally by. Default is "sample" and works with ssvFetch* output. Set to "" if data is not facetted.
cluster_	variable name to use for cluster info. Default is "cluster_id".
reapply_cluster_names	If TRUE, clusters will be renamed according to new order instead of their original names. Default is TRUE.
return_hclust	If TRUE, return the result of hclust instead of the reordered clustering data.table. Default is FALSE. Ignored if hclust_result is supplied.

Value

data.table as output from ssvSignalClustering

Examples

```
data(CTCF_in_10a_profiles_dt)
clust_dt = ssvSignalClustering(CTCF_in_10a_profiles_dt, nclust = 10)
new_dt = reorder_clusters_hclust(clust_dt)
cowplot::plot_grid(
    ssvSignalHeatmap(clust_dt),
    ssvSignalHeatmap(new_dt)
)
```

---

reorder_clusters_manual

reorder_clusters_manual

Description

Manually applies a new order (top to bottom) for cluster using the result of ssvSignalClustering.

Usage

```
reorder_clusters_manual(
  clust_dt,
  manual_order,
  row_ = "id",
  cluster_ = "cluster_id",
  reapply_cluster_names = TRUE
)
```

Arguments

clust_dt	data.table output from ssvSignalClustering
manual_order	New order for clusters Does not need to include all clusters. Any colors not included will be at the bottom in their original order.
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
cluster_	variable name to use for cluster info. Default is "cluster_id".
reapply_cluster_names	If TRUE, clusters will be renamed according to new order instead of their original names. Default is TRUE.

Value

data.table as output from ssvSignalClustering

Examples

```
data(CTCF_in_10a_profiles_dt)
clust_dt = ssvSignalClustering(CTCF_in_10a_profiles_dt, nclust = 3)
new_dt = reorder_clusters_manual(clust_dt = clust_dt, manual_order = 2)
cowplot::plot_grid(
    ssvSignalHeatmap(clust_dt),
    ssvSignalHeatmap(new_dt)
)
```

---

reorder_clusters_stepdown

reorder_clusters_stepdown

Description

Attempts to reorder clusters so that rows with highest signal on the left relative to the right appear at the top. Signal should have a roughly diagonal pattern in a "stepdown" pattern.

Usage

```
reorder_clusters_stepdown(
  clust_dt,
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  cluster_ = "cluster_id",
  reapply_cluster_names = TRUE,
  step_by_column = TRUE,
  step_by_facet = FALSE
)
```

Arguments

clust_dt	data.table output from ssvSignalClustering
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
column_	varaible mapped to column, likely bp position for ngs data. Default is "x" and works with ssvFetch* output.
fill_	numeric variable to map to fill. Default is "y" and works with ssvFetch* output.
facet_	variable name to facet horizontally by. Default is "sample" and works with ssvFetch* output. Set to "" if data is not facetted.
cluster_	variable name to use for cluster info. Default is "cluster_id".
reapply_cluster_names	If TRUE, clusters will be renamed according to new order instead of their original names. Default is TRUE.
step_by_column	If TRUE, column is considered for left-right cluster balance. Default is TRUE.
step_by_facet	If TRUE, facet is considered for left-right cluster balance. Default is FALSE.

Details

This can be down by column (step_by_column = TRUE) which averages across facets. By facet (step_by_column = FALSE, step_by_facet = TRUE) which averages all columns per facet. Or both column and facet (step_by_column = TRUE, step_by_facet = TRUE), which does no averaging so it looks at the full matrix as plotted.

Value

data.table as output from ssvSignalClustering

Examples

```
data(CTCF_in_10a_profiles_dt)
clust_dt = ssvSignalClustering(CTCF_in_10a_profiles_dt, nclust = 10)
new_dt = reorder_clusters_stepdown(clust_dt)
cowplot::plot_grid(
    ssvSignalHeatmap(clust_dt),
    ssvSignalHeatmap(new_dt)
)
```

---

reverse_clusters *reverse_clusters*

Description

reverse_clusters

Usage

```
reverse_clusters(
  clust_dt,
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  cluster_ = "cluster_id",
  reverse_rows_within = TRUE,
  reapply_cluster_names = TRUE
)
```

Arguments

clust_dt	data.table output from ssvSignalClustering
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
column_	varaible mapped to column, likely bp position for ngs data. Default is "x" and works with ssvFetch* output.
fill_	numeric variable to map to fill. Default is "y" and works with ssvFetch* output.
facet_	variable name to facet horizontally by. Default is "sample" and works with ssvFetch* output. Set to "" if data is not facetted.
cluster_	variable name to use for cluster info. Default is "cluster_id".
reverse_rows_within	If TRUE, rows within clusters will be reversed as well. Default is TRUE.
reapply_cluster_names	If TRUE, clusters will be renamed according to new order instead of their original names. Default is TRUE.

Value

data.table as output from ssvSignalClustering

Examples

```
data(CTCF_in_10a_profiles_dt)
set.seed(0)
clust_dt = ssvSignalClustering(CTCF_in_10a_profiles_dt, nclust = 3)
rev_dt = reverse_clusters(clust_dt)
rev_dt.no_relabel = reverse_clusters(clust_dt, reapply_cluster_names = FALSE)
rev_dt.not_rows = reverse_clusters(clust_dt, reverse_rows_within = FALSE)
cowplot::plot_grid(nrow = 1,
  ssvSignalHeatmap(clust_dt) + labs(title = "original"),
  ssvSignalHeatmap(rev_dt) + labs(title = "reversed"),
  ssvSignalHeatmap(rev_dt.no_relabel) + labs(title = "reversed, no relabel"),
  ssvSignalHeatmap(rev_dt.not_rows) + labs(title = "reversed, not rows")
)
```

safeBrew *safeBrew*

Description

Allows RColorBrew to handle n values less than 3 and greater than 8 without warnings and return expected number of colors.

Usage

```
safeBrew(n, pal = "Dark2")
```

Arguments

n	integer value of number of colors to make palette for. Alternatively a character or factor, in which case palette will be generated for each unique item or factor level repsectively.
pal	palette recognized by RColorBrewer

Details

For convenience, instead of the number n requested, n may be a character or factor vector and outputs will be appropriately named for use with scale_color/fill_manual.

Additionally, accepts pal as "gg", "ggplot", or "ggplot2" to reproduce default ggplot colors in the same way.

Value

a character vector of hex coded colors of length n from the color brewer palette pal. If n is supplied as character or factor, output will be named accordingly.

Examples

```
plot(1:2, rep(0, 2),  col = safeBrew(2, "dark2"), pch = 16, cex = 6)
plot(1:12, rep(0, 12),  col = safeBrew(12, "set1"), pch = 16, cex = 6)
plot(1:12, rep(0, 12),  col = safeBrew(12, "set2"), pch = 16, cex = 6)
plot(1:12, rep(0, 12),  col = safeBrew(12, "set3"), pch = 16, cex = 6)
```

set_list2memb *convert a list of sets, each list item should be a character vector denoting items in sets*

Description

convert a list of sets, each list item should be a character vector denoting items in sets

Usage

```
set_list2memb(set_list)
```

Arguments

set_list	a list of character vectors. default names will be added if missing

Value

converts list of characters/numeric to membership table matrix

---

shift_anchor *orients the relative position of x's zero value and extends ranges to be contiguous*

Description

orients the relative position of x's zero value and extends ranges to be contiguous

Usage

```
shift_anchor(score_dt, window_size, anchor)
```

Arguments

score_dt	data.table, GRanges() sufficient
window_size	numeric, window size used to generate score_dt
anchor	character, one of c("center", "center_unstranded", "left", "left_unstranded")

Value

score_dt with x values shifted appropriately and start and end extended to make ranges contiguous

---

split_cluster *split_cluster*

Description

Splits one specified cluster in number of new clusters determined by nclust

Usage

```
split_cluster(
  clust_dt,
  to_split,
  nclust = 2,
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  cluster_ = "cluster_id",
  reapply_cluster_names = TRUE
)
```

Arguments

clust_dt	data.table output from ssvSignalClustering
to_split	Cluster to split.
nclust	Number of new clusters to create.
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
column_	varaible mapped to column, likely bp position for ngs data. Default is "x" and works with ssvFetch* output.
fill_	numeric variable to map to fill. Default is "y" and works with ssvFetch* output.
facet_	variable name to facet horizontally by. Default is "sample" and works with ssvFetch* output. Set to "" if data is not facetted.
cluster_	variable name to use for cluster info. Default is "cluster_id".
reapply_cluster_names	If TRUE, clusters will be renamed according to new order instead of their original names. Default is TRUE.

Value

data.table as output from ssvSignalClustering

Examples

```
data(CTCF_in_10a_profiles_dt)
set.seed(0)
clust_dt = ssvSignalClustering(CTCF_in_10a_profiles_dt, nclust = 3)
split_dt = split_cluster(clust_dt, to_split = 2, nclust = 3)
split_dt.no_rename = split_cluster(
  clust_dt,
  to_split = 2,
  nclust = 3,
  reapply_cluster_names = FALSE
)
cowplot::plot_grid(nrow = 1,
  ssvSignalHeatmap(clust_dt),
  ssvSignalHeatmap(split_dt),
  ssvSignalHeatmap(split_dt.no_rename)
)
```

---

ssvAnnotateSubjectGRanges

ssvAnnotateSubjectGRanges

Description

ssvAnnotateSubjectGRanges

Usage

```
ssvAnnotateSubjectGRanges(
  annotation_source,
  subject_gr,
  annotation_name = NULL,
  multi_resolver_FUN = "default"
)

## S4 method for signature 'GRanges'
ssvAnnotateSubjectGRanges(
  annotation_source,
  subject_gr,
  annotation_name = NULL,
  multi_resolver_FUN = "default"
)

## S4 method for signature 'list'
ssvAnnotateSubjectGRanges(
  annotation_source,
  subject_gr,
  annotation_name = NULL,
  multi_resolver_FUN = "default"
)

## S4 method for signature 'GRangesList'
ssvAnnotateSubjectGRanges(
  annotation_source,
  subject_gr,
  annotation_name = NULL,
  multi_resolver_FUN = "default"
)
```

Arguments

annotation_source	A single GRanges, a list of GRanges, or a GRangesList
subject_gr	The base GRanges to add annotation mcols to.
annotation_name	Optional name for single GRanges. Required for list inputs if list does not have names.
multi_resolver_FUN	Optional function to resolve multiple overlapping annotation source regions per subject region. This function must accept 2 arguments. x is the values in a single mcol attribute and variable.name is the name of variable. A single value must be returned or an error will be generated. The default of "default" can handle numeric, logical, character, and factor types.

Value

GRanges with the same regions as subject_gr but with addtional mcols added from annotation_source.

Examples

```
library(GenomicRanges)
data(CTCF_in_10a_narrowPeak_grs)
np_grs = CTCF_in_10a_narrowPeak_grs
olap_gr = ssvOverlapIntervalSets(np_grs)
# annotating with a signle GRanges is OK
ssvAnnotateSubjectGRanges(np_grs$MCF10A_CTCF, olap_gr)
# provide a name if that's useful
ssvAnnotateSubjectGRanges(np_grs$MCF10A_CTCF, olap_gr,
  annotation_name = "MCF10A")
# a named list adds each annotation
ssvAnnotateSubjectGRanges(np_grs, olap_gr)
# overriding list names is an option
ssvAnnotateSubjectGRanges(np_grs, olap_gr, LETTERS[1:3])
# GRangeList are handled like a standard list
ssvAnnotateSubjectGRanges(GRangesList(np_grs), olap_gr, LETTERS[1:3])
```

`ssvConsensusIntervalSets` *Intersect a list of GRanges to create a single GRanges object of merged ranges including metadata describing overlaps per input GRanges.*

Description

In constrast to ssvOverlapIntervalSets, only regions where a consensus of input grs are present are preserved and annotated.

Usage

```
ssvConsensusIntervalSets(
  grs,
  ext = 0,
  min_number = 2,
  min_fraction = 0.5,
  preserve_mcols = FALSE,
  ...
)
```

Arguments

`grs`	A list of GRanges
`ext`	An integer specifying how far to extend ranges before merging. in effect, ranges withing 2*ext of one another will be joined during the merge
`min_number`	An integer number specifying the absloute minimum of input grs that must overlap for a site to be considered consensus.
`min_fraction`	A numeric between 0 and 1 specifying the fraction of grs that must overlap to be considered consensus.
`preserve_mcols`	Controls carrying forward mcols metadata from input list of GRanges. If TRUE, all mcols will be carried forward with the item name appended. If a character vector, only those attributes will be carried and all must be present in all GRanges. The default of FALSE will carry nothing forward and only membership table will be generated. ssvAnnotateSubjectGRanges is used internally.

... arguments passed to IRanges::findOverlaps, i.e. maxgap, minoverlap, type, select, invert.

Details

Only the most stringent of min_number or min_fraction will be applied.

Value

GRanges with metadata columns describing consensus overlap of input grs.

Examples

```
library(GenomicRanges)
a = GRanges("chr1", IRanges(1:7*10, 1:7*10))
b = GRanges("chr1", IRanges(5:10*10, 5:10*10))
ssvConsensusIntervalSets(list(a, b))
```

---

ssvFactorizeMembTable *Convert any object accepted by ssvMakeMembTable to a factor To avoid ambiguity,*

Description

see ssvMakeMembTable

Usage

```
ssvFactorizeMembTable(object)
```

Arguments

object a valid object for conversion to a membership table and then factor

Value

a 2 column ("id" and "group") data.frame. "id" is factor of item names if any or simply order of items. "group" is a factor of set combinations

Examples

```
data(CTCF_in_10a_overlaps_gr)
ssvFactorizeMembTable(CTCF_in_10a_overlaps_gr)
ssvFactorizeMembTable(list(1:4, 2:3, 4:6))
```

ssvFeatureBars *bar plots of set sizes*

Description

bar plots of set sizes

Usage

```
ssvFeatureBars(
  object,
  show_counts = TRUE,
  bar_colors = NULL,
  counts_text_colors = NULL,
  return_data = FALSE,
  count_label_size = 8
)
```

Arguments

object	passed to ssvMakeMembTable for conversion to membership table
show_counts	logical. should counts be displayed at the center of each bar. default is TRUE
bar_colors	character. rcolor or hex colors. default of NULL uses RColorBrewer Dark2. Will repeat to match number of samples.
counts_text_colors	character. rcolor or hex colors. default of NULL uses RColorBrewer Dark2. Will repeat to match number of samples.
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.
count_label_size	Font size bar count labels. Default is 8.

Value

ggplot of bar plot of set sizes

Examples

```
data(CTCF_in_10a_overlaps_gr)
ssvFeatureBars(list(1:3, 2:6))
ssvFeatureBars(CTCF_in_10a_overlaps_gr, count_label_size = 10)
ssvFeatureBars(S4Vectors::mcols(CTCF_in_10a_overlaps_gr)[,2:3])
```

ssvFeatureBinaryHeatmap *ssvFeatureBinaryHeatmap*

Description

Outputs a ggplot binary heatmap, where color indicates TRUE and the other indicates FALSE in a membership table. The heatmap is sorted, TRUE at the top, by column left to right. Changes to column order can reveal different patterns.

Usage

```
ssvFeatureBinaryHeatmap(
  object,
  raster_approximation = TRUE,
  true_color = "black",
  false_color = "#EFEFEF",
  raster_width_min = 1000,
  raster_height_min = 1000,
  return_data = FALSE
)
```

Arguments

object	passed to ssvMakeMembTable
raster_approximation	If TRUE, instead of standard ggplot, write temporary raster png image and redraw that as plot background. default is FALSE
true_color	character. rcolor or hex color used for TRUE values. default is "black".
false_color	character. rcolor or hex color used for TRUE values. default is "#EFEFEF", a gray.
raster_width_min	raster width will be minimum multiple of number of columns over this number. ignored if raster_approximation is FALSE.
raster_height_min	raster height will be minimum multiple of number of rows over this number ignored if raster_approximation is FALSE
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is TRUE

Details

As a svg output, the final plot can be unwieldy. The default of raster_approximation = TRUE is easier to work with, especially for larger membership tables.

Value

ggplot using geom_tile of membership table sorted from left to right.

Examples

```
data(CTCF_in_10a_overlaps_gr)
ssvFeatureBinaryHeatmap(list(1:3, 2:6))
# horizontal version
ssvFeatureBinaryHeatmap(list(1:3, 2:6)) + coord_flip() +
  theme(axis.text.x = element_blank(), axis.text.y = element_text())
ssvFeatureBinaryHeatmap(CTCF_in_10a_overlaps_gr)
ssvFeatureBinaryHeatmap(S4Vectors::mcols(CTCF_in_10a_overlaps_gr)[,2:3])
ssvFeatureBinaryHeatmap(S4Vectors::mcols(CTCF_in_10a_overlaps_gr)[,3:2])
```

---

ssvFeatureEuler *Try to load a bed-like file and convert it to a GRanges object*

Description

Try to load a bed-like file and convert it to a GRanges object

Usage

```
ssvFeatureEuler(
  object,
  line_width = 2,
  shape = c("circle", "ellipse")[1],
  n_points = 200,
  fill_alpha = 0.3,
  line_alpha = 1,
  circle_colors = NULL,
  return_data = FALSE
)
```

Arguments

object	A membership table
line_width	numeric, passed to size aesthetic to control line width
shape	shape argument passed to eulerr::euler
n_points	number of points to use for drawing ellipses, passed to eulerr:::ellipse
fill_alpha	numeric value from 0 to 1. Alpha value for circle fill
line_alpha	numeric value from 0 to 1. Alpha value for circle line
circle_colors	colors to choose from for circles. passed to ggplot2 color scales.
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

Value

ggplot of venneuler results

Examples

```
data(CTCF_in_10a_overlaps_gr)
ssvFeatureEuler(list(1:3, 2:6))
ssvFeatureEuler(CTCF_in_10a_overlaps_gr)
ssvFeatureEuler(S4Vectors::mcols(CTCF_in_10a_overlaps_gr)[,2:3])
```

ssvFeaturePie *ssvFeaturePie*

Description

Generate a ggplot pie plot of set sizes.

Usage

```
ssvFeaturePie(object, slice_colors = NULL, return_data = FALSE)
```

Arguments

object	object that ssvMakeMembTable can convert to logical matrix membership
slice_colors	colors to use for pie slices
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

Value

ggplot pie graph of set sizes

Examples

```
data(CTCF_in_10a_overlaps_gr)
ssvFeaturePie(list(1:3, 2:6))
ssvFeaturePie(CTCF_in_10a_overlaps_gr)
ssvFeaturePie(S4Vectors::mcols(CTCF_in_10a_overlaps_gr)[,2:3])
```

ssvFeatureUpset *ssvFeatureUpset*

Description

Uses the UpSetR package to create an UpSetR::upset plot of region overlaps.

Usage

```
ssvFeatureUpset(
  object,
  return_UpSetR = FALSE,
  nsets = NULL,
  nintersects = 15,
  order.by = "freq",
  ...
)
```

Arguments

object	will be passed to ssvMakeMembTable for conversion to membership matrix
return_UpSetR	If TRUE, return the UpSetR object, The default is FALSE and results in a ggplotified version compatible with cowplot etc.
nsets	Number of sets to look at
nintersects	Number of intersections to plot. If set to NA, all intersections will be plotted.
order.by	How the intersections in the matrix should be ordered by. Options include frequency (entered as "freq"), degree, or both in any order.
...	Additional parameters passed to upset in the UpSetR package.

Value

ggplot version of UpSetR plot

Examples

```
data(CTCF_in_10a_overlaps_gr)
ssvFeatureUpset(list(1:3, 2:6))
ssvFeatureUpset(CTCF_in_10a_overlaps_gr)
ssvFeatureUpset(S4Vectors::mcols(CTCF_in_10a_overlaps_gr)[,2:3])
```

---

ssvFeatureVenn *ssvFeatureVenn*

Description

ggplot implementation of vennDiagram from limma package. Currently limited at 3 sets. ssvFeatureUpset and ssvFeatureBinaryHeatmap are good options for more than 3 sets. ssvFeatureEuler can work too but can take a very long time to run for more than 5 or so.

Usage

```
ssvFeatureVenn(
  object,
  group_names = NULL,
  counts_txt_size = 5,
  counts_as_labels = FALSE,
  show_outside_count = FALSE,
  line_width = 3,
  circle_colors = NULL,
  fill_alpha = 0.3,
  line_alpha = 1,
  counts_color = NULL,
  counts_as_percent = FALSE,
  percentage_digits = 1,
  percentage_suffix = "%",
  n_points = 200,
  return_data = FALSE
)
```

Arguments

object	will be passed to ssvMakeMembTable for conversion to membership matrix
group_names	useful if names weren't provided or were lost in creating membership matrix
counts_txt_size	font size for count numbers
counts_as_labels	if TRUE, geom_label is used instead of geom_text. can be easier to read.
show_outside_count	if TRUE, items outside of all sets are counted outside. can be confusing.
line_width	uses size aesthetic to control line width of circles.
circle_colors	colors to use for circle line colors. Uses Dark2 set from RColorBrewer by default.
fill_alpha	alpha value to use for fill, defaults to .3.
line_alpha	numeric value from 0 to 1. Alpha value for circle line
counts_color	character. single color to use for displaying counts
counts_as_percent	if TRUE, convert counts to percentages in plots.
percentage_digits	The number of digits to round percentages to, default is 1.
percentage_suffix	The character to append to percentages, default is "%".
n_points	integer. number of points to approximate circle with. default is 200.
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

Value

ggplot venn diagram

Examples

```
data(CTCF_in_10a_overlaps_gr)
ssvFeatureVenn(list(1:3, 2:6))
ssvFeatureVenn(CTCF_in_10a_overlaps_gr)
ssvFeatureVenn(S4Vectors::mcols(CTCF_in_10a_overlaps_gr)[,2:3])

ssvFeatureVenn(list(1:3, 2:6),
  counts_as_percent = TRUE,
  percentage_digits = 2)

ssvFeatureVenn(list(1:3, 2:6),
  counts_as_percent = TRUE,
  percentage_digits = 0,
  percentage_suffix = " %",
  counts_txt_size = 12)
```

ssvFetchBam	*Iterates a character vector (ideally named) and calls* ssvFetchBam.single *on each. Appends grouping variable to each resulting data.table and uses rbindlist to efficiently combine results*

Description

ssvFetchBam iteratively calls fetchWindowedBam.single. See ssvFetchBam.single for more info.

Usage

```
ssvFetchBam(
  file_paths,
  qgr,
  unique_names = NULL,
  names_variable = "sample",
  file_attribs = NULL,
  win_size = 50,
  win_method = c("sample", "summary")[1],
  summary_FUN = stats::weighted.mean,
  fragLens = "auto",
  target_strand = c("*", "+", "-", "both")[1],
  flip_strand = FALSE,
  anchor = c("left", "left_unstranded", "center", "center_unstranded")[3],
  return_data.table = FALSE,
  max_dupes = Inf,
  splice_strategy = c("none", "ignore", "add", "only", "splice_count")[1],
  n_cores = getOption("mc.cores", 1),
  n_region_splits = 1,
  return_unprocessed = FALSE,
  force_skip_centerFix = FALSE,
  ...
)
```

Arguments

file_paths	character vector of file_paths to load from. Alternatively, file_paths can be a data.frame or data.table whose first column is a character vector of paths and additial columns will be used as metadata.
qgr	Set of GRanges to query. For valid results the width of each interval should be identical and evenly divisible by win_size.
unique_names	names to use in final data.table to designate source bigwig. Default is 'sample'
names_variable	The column name where unique_names are stored.
file_attribs	optional data.frame/data.table with one row per item in file paths. Each column will be a variable added to final tidy output.
win_size	The window size that evenly divides widths in qgr.
win_method	character. one of c("sample", "summary"). Determines if viewGRangesWinSample_dt or viewGRangesWinSummary_dt is used to represent each region in qgr.

summary_FUN function. only relevant if win_method is "summary". passed to viewGRangesWinSummary_dt.

fragLens numeric. The fragment length to use to extend reads. The default value "auto" causes an automatic calculation from 100 regions in qgr. NA causes no extension of reads to fragment size.

target_strand character. One of c("", "+", "-"). *Controls filtering of reads by strand. Default of* "" combines both strands.

flip_strand boolean. if TRUE strands are flipped.

anchor character, one of c("center", "center_unstranded", "left", "left_unstranded")

return_data.table logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.

max_dupes numeric >= 1. duplicate reads by strandd start position over this number are removed, Default is Inf.

splice_strategy character, one of c("none", "ignore", "add", "only", "splice_count"). Default is "none" and spliced alignment are asssumed not present. fragLen will be forced to be NA for any other value. "ignore" will not count spliced regions. add" counts spliced regions along with others, "only" will only count spliced regions and ignore others.

n_cores integer number of cores to use. Uses mc.cores option if not supplied.

n_region_splits integer number of splits to apply to qgr. The query GRanges will be split into this many roughly equal parts for increased parallelization. Default is 1, no split.

return_unprocessed boolean. if TRUE returns read alignment in data.table. Default is FALSE.

force_skip_centerFix boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".

... passed to Rsamtools::ScanBamParam()

Details

if qgr contains the range chr1:1-100 and win_size is 10, values from positions chr1 5,15,25...85, and 95 will be retrieved from bw_file

Value

A tidy formatted GRanges (or data.table if specified) containing fetched values.

Examples

```
if(Sys.info()['sysname'] != "Windows"){
data(CTCF_in_10a_overlaps_gr)
library(GenomicRanges)
bam_f = system.file("extdata/test.bam",
    package = "seqsetvis", mustWork = TRUE)
bam_files = c("a" = bam_f, "b" = bam_f)
qgr = CTCF_in_10a_overlaps_gr[1:5]
bw_gr = ssvFetchBam(bam_files, qgr, win_size = 10)
bw_gr2 = ssvFetchBam(as.list(bam_files), qgr, win_size = 10)
```

```
bw_dt = ssvFetchBam(bam_files, qgr, win_size = 10,
    return_data.table = TRUE)
}
```

`ssvFetchBam.single` *fetch a windowed version of a bam file, returns GRanges*

Description

fetch a windowed version of a bam file, returns GRanges

Usage

```
ssvFetchBam.single(
  bam_f,
  qgr,
  win_size = 50,
  win_method = c("sample", "summary")[1],
  summary_FUN = stats::weighted.mean,
  fragLen = NULL,
  target_strand = c("*", "+", "-", "both")[1],
  anchor = c("left", "left_unstranded", "center", "center_unstranded")[3],
  return_data.table = FALSE,
  max_dupes = Inf,
  splice_strategy = c("none", "ignore", "add", "only", "splice_count")[1],
  flip_strand = FALSE,
  return_unprocessed = FALSE,
  force_skip_centerFix = FALSE,
  ...
)
```

Arguments

`bam_f`	character or BamFile to load
`qgr`	GRanges regions to fetchs
`win_size`	numeric >=1. pileup grabbed every win_size bp for win_method sample. If win_method is summary, this is the number of windows used (confusing, sorry).
`win_method`	character. one of c("sample", "summary"). Determines if `viewGRangesWinSample_dt` or `viewGRangesWinSummary_dt` is used to represent each region in qgr.
`summary_FUN`	function. only relevant if win_method is "summary". passed to `viewGRangesWinSummary_dt`.
`fragLen`	numeric, NULL, or NA. if numeric, supplied value is used. if NULL, value is calculated with fragLen_calcStranded if NA, raw bam pileup with no cross strand shift is returned.
`target_strand`	character. if one of "+" or "-", reads are filtered accordingly. ignored if any other value.
`anchor`	character, one of c("center", "center_unstranded", "left", "left_unstranded")
`return_data.table`	logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.

max_dupes numeric >= 1. duplicate reads by strandd start position over this number are removed, Default is Inf.

splice_strategy
character, one of c("none", "ignore", "add", "only", "splice_count"). Default is "none" and spliced alignment are asssumed not present. fragLen must be NA for any other value to be valid. "ignore" will not count spliced regions. add" counts spliced regions along with others, "only" will only count spliced regions and ignore others.

flip_strand if TRUE, strand alignment is flipped prior to fragLen extension. Default is FALSE.

return_unprocessed
boolean. if TRUE returns read alignment in data.table. Default is FALSE.

force_skip_centerFix
boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".

... passed to Rsamtools::ScanBamParam()

Value

tidy GRanges (or data.table if specified) with pileups from bam file. pileup is calculated only every win_size bp.

---

ssvFetchBamPE *ssvFetchBam for paired-end ChIP-seq files. Only concordant reads are considered, but this has been minimally tested, please verify.*

Description

Iterates a character vector (ideally named) and calls `ssvFetchBamPE.single` on each. Appends grouping variable to each resulting data.table and uses rbindlist to efficiently combine results

Usage

```
ssvFetchBamPE(
  file_paths,
  qgr,
  unique_names = NULL,
  win_size = 50,
  win_method = c("sample", "summary")[1],
  summary_FUN = stats::weighted.mean,
  fragLens = "not_used",
  anchor = c("left", "left_unstranded", "center", "center_unstranded")[3],
  names_variable = "sample",
  return_data.table = FALSE,
  max_dupes = Inf,
  n_cores = getOption("mc.cores", 1),
  n_region_splits = 1,
  min_isize = 1,
  max_isize = Inf,
```

```
  return_unprocessed = FALSE,
  return_fragSizes = FALSE,
  force_skip_centerFix = FALSE,
  ...
)
```

Arguments

file_paths	character vector of file_paths to load from. Alternatively, file_paths can be a data.frame or data.table whose first column is a character vector of paths and additial columns will be used as metadata.
qgr	Set of GRanges to query. For valid results the width of each interval should be identical and evenly divisible by win_size.
unique_names	names to use in final data.table to designate source bigwig. Default is 'sample'
win_size	The window size that evenly divides widths in qgr.
win_method	character. one of c("sample", "summary"). Determines if viewGRangesWinSample_dt or viewGRangesWinSummary_dt is used to represent each region in qgr.
summary_FUN	function. only relevant if win_method is "summary". passed to viewGRangesWinSummary_dt.
fragLens	never used by ssvFetchBamPE Ignore.
anchor	character, one of c("center", "center_unstranded", "left", "left_unstranded")
names_variable	The column name where unique_names are stored.
return_data.table	logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.
max_dupes	numeric >= 1. duplicate reads by strandd start position over this number are removed, Default is Inf.
n_cores	integer number of cores to use.
n_region_splits	integer number of splits to apply to qgr. The query GRanges will be split into this many roughly equal parts for increased parallelization. Default is 1, no split.
min_isize	integer. Read pairs must have an isize greater than or equal to this value. Default is 1.
max_isize	integer. Read pairs must have an isize less than or equal to this value. Default is Inf.
return_unprocessed	boolean. if TRUE returns read alignment in data.table. Default is FALSE.
return_fragSizes	boolean. if TRUE returns fragment sizes for all reads per region.
force_skip_centerFix	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".
...	passed to Rsamtools::ScanBamParam() Uses mc.cores option if not supplied.

Details

#' In contrast to ssvFetchBam, extension of reads to estimated fragment size is not an issue as each read pair represents a fragment of exact size.

ssvFetchBamPE iteratively calls fetchWindowedBam.single. See ssvFetchBamPE.single for more info.

if qgr contains the range chr1:1-100 and win_size is 10, values from positions chr1 5,15,25...85, and 95 will be retrieved from bw_file

Value

A tidy formatted GRanges (or data.table if specified) containing fetched values.

Examples

```
if(Sys.info()['sysname'] != "Windows"){
library(GenomicRanges)
bam_f = system.file("extdata/Bcell_PE.mm10.bam",
    package = "seqsetvis", mustWork = TRUE)
bam_files = c("a" = bam_f, "b" = bam_f)
data("Bcell_peaks")
qgr = Bcell_peaks
bw_gr = ssvFetchBamPE(bam_files, qgr, win_size = 10)
bw_gr2 = ssvFetchBamPE(as.list(bam_files), qgr, win_size = 10)

bw_dt = ssvFetchBamPE(bam_files, qgr, win_size = 10,
    return_data.table = TRUE)
}
```

---

ssvFetchBamPE.RNA *ssvFetchBamPE.RNA*

Description

ssvFetchBamPE.RNA

Usage

```
ssvFetchBamPE.RNA(
  file_paths,
  qgr,
  unique_names = NULL,
  win_size = 50,
  target_strand = "both",
  absolute_strand = FALSE,
  splice_strategy = "ignore",
  return_data.table = FALSE,
  win_method = "sample",
  max_dupes = Inf,
  flip_strand = FALSE,
  sum_reads = TRUE,
  n_cores = getOption("mc.cores", 1),
```

```
  force_skip_centerFix = TRUE,
  n_region_splits = 1
)
```

Arguments

file_paths	character vector of file_paths to load from. Alternatively, file_paths can be a data.frame or data.table whose first column is a character vector of paths and additial columns will be used as metadata.
qgr	Set of GRanges to query. For valid results the width of each interval should be identical and evenly divisible by win_size.
unique_names	names to use in final data.table to designate source bigwig. Default is 'sample'
win_size	The window size that evenly divides widths in qgr.
target_strand	character. if one of "+" or "-", reads are filtered to match. ignored if any other value.
absolute_strand	If TRUE, strandedness of qgr will be ignored. This is useful when creating tracks for similar.
splice_strategy	character, one of c("none", "ignore", "add", "only", "splice_count"). Default is "none" and spliced alignment are asssumed not present. fragLen must be NA for any other value to be valid. "ignore" will not count spliced regions. add" counts spliced regions along with others, "only" will only count spliced regions and ignore others.
return_data.table	logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.
win_method	character. one of c("sample", "summary"). "sample" selects values at intervals and "summary" applies a weight mean function to all values in window.
max_dupes	numeric >= 1. duplicate reads by strandd start position over this number are removed, Default is Inf.
flip_strand	logical. if TRUE strands are flipped.
sum_reads	logical. If true R1 and R2 reads are added together. If FALSE they are returned separately, identified by the "read" attribute.
n_cores	integer number of cores to use. Uses mc.cores option if not supplied.
force_skip_centerFix	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".
n_region_splits	integer number of splits to apply to qgr. The query GRanges will be split into this many roughly equal parts for increased parallelization. Default is 1, no split.

Value

A tidy formatted GRanges (or data.table if specified) containing fetched values.

Examples

```
library(GenomicRanges)
pkg_dir = system.file(package = "seqsetvis", "extdata", mustWork = TRUE)
bam_files_esr1 = dir(pkg_dir, pattern = "H1.+R1.ESR1_RNA.+bam$", full.names = TRUE)
names(bam_files_esr1) = sub("_R.+", "", basename(bam_files_esr1))
query_gr = GenomicRanges::GRanges("chr6:151656691-152129619:+")

strand(query_gr) = "+"

prof_dt = ssvFetchBamPE.RNA(bam_files_esr1, query_gr, return_data.table = TRUE)
```

`ssvFetchBamPE.single` *fetch a windowed version of a paired-end bam file, returns GRanges In contrast to ssvFetchBam, extension of reads to estimated fragment size is not an issue as each read pair represents a fragment of exact size.*

Description

fetch a windowed version of a paired-end bam file, returns GRanges In contrast to ssvFetchBam, extension of reads to estimated fragment size is not an issue as each read pair represents a fragment of exact size.

Usage

```
ssvFetchBamPE.single(
  bam_f,
  qgr,
  win_size = 50,
  win_method = c("sample", "summary")[1],
  summary_FUN = stats::weighted.mean,
  anchor = c("left", "left_unstranded", "center", "center_unstranded")[3],
  return_data.table = FALSE,
  max_dupes = Inf,
  min_isize = 1,
  max_isize = Inf,
  return_unprocessed = FALSE,
  return_fragSizes = FALSE,
  force_skip_centerFix = FALSE,
  ...
)
```

Arguments

`bam_f`	character or BamFile to load
`qgr`	GRanges regions to fetchs
`win_size`	numeric >=1. pileup grabbed every win_size bp for win_method sample. If win_method is summary, this is the number of windows used (confusing, sorry).
`win_method`	character. one of c("sample", "summary"). Determines if `viewGRangesWinSample_dt` or `viewGRangesWinSummary_dt` is used to represent each region in qgr.

summary_FUN function. only relevant if win_method is "summary". passed to viewGRangesWinSummary_dt.

anchor character, one of c("center", "center_unstranded", "left", "left_unstranded")

return_data.table logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.

max_dupes numeric >= 1. duplicate reads by strandd start position over this number are removed, Default is Inf.

min_isize integer. Read pairs must have an isize greater than or equal to this value. Default is 1.

max_isize integer. Read pairs must have an isize less than or equal to this value. Default is Inf.

return_unprocessed boolean. if TRUE returns read alignment in data.table. Default is FALSE.

return_fragSizes boolean. if TRUE returns fragment sizes for all reads per region.

force_skip_centerFix boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".

... passed to Rsamtools::ScanBamParam()

Value

tidy GRanges (or data.table if specified) with pileups from bam file. pileup is calculated only every win_size bp.

---

ssvFetchBigwig *Iterates a character vector (ideally named) and calls* ssvFetchBigwig.single *on each. Appends grouping variable to each resulting data.table and uses rbindlist to efficiently combine results.*

Description

ssvFetchBigwig iteratively calls fetchWindowedBigwig.single. See ssvFetchBigwig.single for more info.

Usage

```
ssvFetchBigwig(
  file_paths,
  qgr,
  unique_names = NULL,
  names_variable = "sample",
  win_size = 50,
  win_method = c("sample", "summary")[1],
  summary_FUN = stats::weighted.mean,
  fragLens = "not_used",
  anchor = c("left", "left_unstranded", "center", "center_unstranded")[3],
```

```
  return_data.table = FALSE,
  n_cores = getOption("mc.cores", 1),
  n_region_splits = 1,
  force_skip_centerFix = FALSE
)
```

Arguments

file_paths	character vector of file_paths to load from. Alternatively, file_paths can be a data.frame or data.table whose first column is a character vector of paths and additial columns will be used as metadata.
qgr	Set of GRanges to query. For valid results the width of each interval should be identical and evenly divisible by win_size.
unique_names	names to use in final data.table to designate source bigwig.
names_variable	The column name where unique_names are stored. Default is 'sample'
win_size	The window size that evenly divides widths in qgr.
win_method	character. one of c("sample", "summary"). Determines if viewGRangesWinSample_dt or viewGRangesWinSummary_dt is used to represent each region in qgr.
summary_FUN	function. only relevant if win_method is "summary". passed to viewGRangesWinSummary_dt.
fragLens	never used by ssvFetchBigwig. Ignore.
anchor	character, one of c("center", "center_unstranded", "left", "left_unstranded")
return_data.table	logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.
n_cores	integer number of cores to use. Uses mc.cores option if not supplied.
n_region_splits	integer number of splits to apply to qgr. The query GRanges will be split into this many roughly equal parts for increased parallelization. Default is 1, no split.
force_skip_centerFix	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".

Details

if qgr contains the range chr1:1-100 and win_size is 10, values from positions chr1 5,15,25...85, and 95 will be retrieved from bw_file

Value

A tidy formatted GRanges (or data.table if specified) containing fetched values.

Examples

```
if(Sys.info()['sysname'] != "Windows"){
library(GenomicRanges)
bw_f = system.file("extdata/test_loading.bw",
    package = "seqsetvis", mustWork = TRUE)
bw_files = c("a" = bw_f, "b" = bw_f)
qgr = GRanges("chrTest", IRanges(1, 30))
bw_gr = ssvFetchBigwig(bw_files, qgr, win_size = 10)
```

```
bw_gr2 = ssvFetchBigwig(as.list(bw_files), qgr, win_size = 10)

bw_dt = ssvFetchBigwig(bw_files, qgr, win_size = 10,
    return_data.table = TRUE)
}
```

`ssvFetchBigwig.single` *Fetch values from a bigwig appropriate for heatmaps etc.*

Description

`ssvFetchBigwig.single` Gets values for each region of the query GRanges (`qgr`). Values correspond to the center of each window of size `win_size`. A tidy formatted data.table object is returned suitable for plotting using ggplots.

Usage

```
ssvFetchBigwig.single(
  bw_file,
  qgr,
  win_size = 50,
  win_method = c("sample", "summary")[1],
  summary_FUN = stats::weighted.mean,
  anchor = c("left", "left_unstranded", "center", "center_unstranded")[3],
  return_data.table = FALSE,
  force_skip_centerFix = FALSE
)
```

Arguments

`bw_file`	The character vector path to bigwig files to read from.
`qgr`	Set of GRanges to query. For valid results the width of each interval should be identical and evenly divisible by `win_size`.
`win_size`	The window size that evenly divides widths in `qgr`.
`win_method`	character. one of c("sample", "summary"). Determines if `viewGRangesWinSample_dt` or `viewGRangesWinSummary_dt` is used to represent each region in qgr.
`summary_FUN`	function. only relevant if win_method is "summary". passed to `viewGRangesWinSummary_dt`.
`anchor`	character, one of c("center", "center_unstranded", "left", "left_unstranded")
`return_data.table`	logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.
`force_skip_centerFix`	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".

Details

if `qgr` contains the range chr1:1-100 and `win_size` is 10, values from positions chr1 5,15,25...85, and 95 will be retrieved from `bw_file`

Value

A GRanges (or data.table if specified) containing fetched values.

`ssvFetchGRanges` *Fetch coverage values for a list of GRanges.*

Description

`ssvFetchGRanges` Gets coverage values for each region of the query GRanges (`qgr`). Values correspond to the center of each window of size `win_size`. A tidy formatted data.table object is returned suitable for plotting using ggplots.

Usage

```
ssvFetchGRanges(
  grs,
  qgr,
  file_attribs = data.frame(matrix(0, nrow = length(grs), ncol = 0)),
  unique_names = names(grs),
  names_variable = "sample",
  win_size = 50,
  win_method = c("sample", "summary")[1],
  summary_FUN = function(x, w) max(x),
  target_strand = c("*", "+", "-", "both")[1],
  use_coverage = NULL,
  attrib_var = "score",
  fill_value = 0,
  anchor = c("left", "left_unstranded", "center", "center_unstranded")[3],
  return_data.table = FALSE,
  n_cores = getOption("mc.cores", 1),
  force_skip_centerFix = FALSE
)
```

Arguments

`grs`	a list of GRanges for which to calculate coverage.
`qgr`	Set of GRanges to query. For valid results the width of each interval should be identical and evenly divisible by `win_size`.
`file_attribs`	data.frame (1 row per item in grs) containing attributes to append to results.
`unique_names`	The column name where unique_names are stored. Default is 'sample'
`names_variable`	The column name where unique_names are stored. Default is 'sample'
`win_size`	The window size that evenly divides widths in `qgr`.
`win_method`	character. one of c("sample", "summary"). Determines if `viewGRangesWinSample_dt` or `viewGRangesWinSummary_dt` is used to represent each region in qgr.
`summary_FUN`	function. only relevant if win_method is "summary". passed to `viewGRangesWinSummary_dt`.
`target_strand`	character. if one of "+" or "-", reads are filtered to match. ignored if any other value.

use_coverage boolean or NULL, if TRUE, query regions are scored by the number of intervals overlapping. Default of NULL checks if attrib_var is "score" and uses coverage if so.

attrib_var character, column in mcols of GRanges to pull values from. Default of "score" is compatible with internal coverage calculation or bedgraph-like files.

fill_value numeric or character value to use where queried regions are empty. Default is 0 and appropriate for both calculated coverage and bedgraph/bigwig like files. Will automatically switch to "MISSING" if data is guessed to be qualitative.

anchor character, one of c("center", "center_unstranded", "left", "left_unstranded")

return_data.table logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.

n_cores integer number of cores to use. Uses mc.cores option if not supplied.

force_skip_centerFix boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".

Value

A tidy formatted GRanges (or data.table if specified) containing fetched values.

Examples

```
data(CTCF_in_10a_narrowPeak_grs)
data(CTCF_in_10a_overlaps_gr)
ssvFetchGRanges(CTCF_in_10a_narrowPeak_grs, CTCF_in_10a_overlaps_gr, win_size = 200)
```

---

ssvFetchSignal *signal loading framework*

Description

Does nothing unless load_signal is overridden to carry out reading data from file_paths (likely via the appropriate ssvFetch* function, ie. ssvFetchBigwig or ssvFetchBam

Usage

```
ssvFetchSignal(
  file_paths,
  qgr,
  unique_names = NULL,
  names_variable = "sample",
  file_attribs = NULL,
  win_size = 50,
  win_method = c("sample", "summary")[1],
  return_data.table = FALSE,
  load_signal = function(f, nam, qgr) {
     warning("nothing happened, ",
    "supply a function to", "load_signal parameter.")
```

```
 },
  n_cores = getOption("mc.cores", 1),
  n_region_splits = 1,
  force_skip_centerFix = FALSE
)
```

Arguments

file_paths	character vector of file_paths to load from. Alternatively, file_paths can be a data.frame or data.table whose first column is a character vector of paths and additial columns will be used as metadata.
qgr	GRanges of intervals to return from each file
unique_names	unique file ids for each file in file_paths. Default is names of file_paths vector
names_variable	character, variable name for column containing unique_names entries. Default is "sample"
file_attribs	optional data.frame/data.table with one row per item in file paths. Each column will be a variable added to final tidy output.
win_size	numeric/integer window size resolution to load signal at. Default is 50.
win_method	character. one of c("sample", "summary"). Determines if viewGRangesWinSample_dt or viewGRangesWinSummary_dt is used to represent each region in qgr.
return_data.table	logical. If TRUE data.table is returned instead of GRanges, the default.
load_signal	function taking f, nam, and qgr arguments. f is from file_paths, nam is from unique_names, and qgr is qgr. See details.
n_cores	integer number of cores to use. Uses mc.cores option if not supplied.
n_region_splits	integer number of splits to apply to qgr. The query GRanges will be split into this many roughly equal parts for increased parallelization. Default is 1, no split.
force_skip_centerFix	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".

Details

load_signal is passed f, nam, and qgr and is executed in the environment where load_signal is defined. See ssvFetchBigwig and ssvFetchBam for examples.

Value

A GRanges with values read from file_paths at intervals of win_size. Originating file is coded by unique_names and assigned to column of name names_variable. Output is data.table is return_data.table is TRUE.

Examples

```
library(GenomicRanges)
data(CTCF_in_10a_overlaps_gr)
bam_f = system.file("extdata/test.bam",
    package = "seqsetvis", mustWork = TRUE)
bam_files = c("a" = bam_f, "b" = bam_f)
```

```
qgr = CTCF_in_10a_overlaps_gr[1:2]
qgr = resize(qgr, 500, "center")
load_bam = function(f, nam, qgr) {
    message("loading ", f, " ...")
    dt = seqsetvis:::ssvFetchBam.single(bam_f = f,
                      qgr = qgr,
                      win_size = 50,
                      fragLen = NULL,
                      target_strand = "*",
                      return_data.table = TRUE)

    data.table::set(dt, j = "sample", value = nam)
    message("finished loading ", nam, ".")
    dt
}
ssvFetchSignal(bam_files, qgr, load_signal = load_bam)
```

`ssvMakeMembTable` *generic for methods to convert various objects to a logical matrix indicating membership of items (rows) in sets (columns)*

Description

generic for methods to convert various objects to a logical matrix indicating membership of items (rows) in sets (columns)

list of character vectors input

GRangesList input

GRanges with mcols input

DataFrame input

matrix of logicals, membership table

data.frame input, final output The final method for all inputs, checks column names and returns logical matrix

Usage

```
ssvMakeMembTable(object)

## S4 method for signature 'list'
ssvMakeMembTable(object)

## S4 method for signature 'GRangesList'
ssvMakeMembTable(object)

## S4 method for signature 'GRanges'
ssvMakeMembTable(object)

## S4 method for signature 'DataFrame'
ssvMakeMembTable(object)

## S4 method for signature 'matrix'
```

```
ssvMakeMembTable(object)

## S4 method for signature 'data.frame'
ssvMakeMembTable(object)
```

Arguments

object	the object to convert. Supported types: list (of character or GRanges), GRanges with membership table metadata, GRangesList, data.frame/matrix/DataFrame of membership table

Value

a logical matrix indicating membership of items (rows) in sets (columns)

Examples

```
char_list = list(letters[1:3], letters[2:4])
ssvMakeMembTable(char_list)
library(GenomicRanges)
gr_list = list(GRanges("chr1", IRanges(1:3*2, 1:3*2)),
    GRanges("chr1", IRanges(2:4*2, 2:4*2)))
ssvMakeMembTable(gr_list)
library(GenomicRanges)
gr_list = list(GRanges("chr1", IRanges(1:3*2, 1:3*2)),
    GRanges("chr1", IRanges(2:4*2, 2:4*2)))
ssvMakeMembTable(GRangesList(gr_list))
gr = GRanges("chr1", IRanges(1:3*2, 1:3*2))
gr$set_a = c(TRUE, TRUE, FALSE)
gr$set_b = c(FALSE, TRUE, TRUE)
ssvMakeMembTable(gr)
gr = GRanges("chr1", IRanges(1:3*2, 1:3*2))
gr$set_a = c(TRUE, TRUE, FALSE)
gr$set_b = c(FALSE, TRUE, TRUE)
ssvMakeMembTable(mcols(gr))
memb_mat =  matrix(c(TRUE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, FALSE),
    ncol = 2, byrow = FALSE)
ssvMakeMembTable(memb_mat)
memb_df = data.frame(a = c(TRUE, TRUE, FALSE, FALSE),
    b = c(TRUE, FALSE, TRUE, FALSE))
ssvMakeMembTable(memb_df)
```

---

ssvOverlapIntervalSets

Intersect a list of GRanges to create a single GRanges object of merged ranges including metadata describing overlaps per input GRanges

---

Description

Intersect a list of GRanges to create a single GRanges object of merged ranges including metadata describing overlaps per input GRanges

Usage

```
ssvOverlapIntervalSets(
  grs,
  ext = 0,
  use_first = FALSE,
  preserve_mcols = FALSE,
  ...
)
```

Arguments

grs	A list of GRanges
ext	An integer specifying how far to extend ranges before merging. in effect, ranges withing 2*ext of one another will be joined during the merge
use_first	A logical. If True, instead of merging all grs, only use first and add metadata logicals for others.
preserve_mcols	Controls carrying forward mcols metadata from input list of GRanges. If TRUE, all mcols will be carried forward with the item name appended. If a character vector, only those attributes will be carried and all must be present in all GRanges. The default of FALSE will carry nothing forward and only membership table will be generated. ssvAnnotateSubjectGRanges is used internally.
...	arguments passed to IRanges::findOverlaps, i.e. maxgap, minoverlap, type, select, invert.

Value

GRanges with metadata columns describing overlap of input grs.

Examples

```
library(GenomicRanges)
a = GRanges("chr1", IRanges(1:7*10, 1:7*10))
b = GRanges("chr1", IRanges(5:10*10, 5:10*10))
ssvOverlapIntervalSets(list(a, b))
```

---

ssvSignalBandedQuantiles

plot profiles from bigwigs

Description

plot profiles from bigwigs

Usage

```
ssvSignalBandedQuantiles(
  bw_data,
  y_ = "y",
  x_ = "x",
  by_ = "fake",
```

```
  hsv_reverse = FALSE,
  hsv_saturation = 1,
  hsv_value = 1,
  hsv_grayscale = FALSE,
  hsv_hue_min = 0,
  hsv_hue_max = 0.7,
  hsv_symmetric = FALSE,
  n_quantile = 18,
  quantile_min = 0.05,
  quantile_max = 0.95,
  return_data = FALSE
)
```

Arguments

bw_data	a GRanges or data.table of bigwig signal. As returned from ssvFetchBam and ssvFetchBigwig
y_	the variable name in bw_data for y axis in plot
x_	the variable name in bw_data for x axis in plot
by_	the variable name in bw_data to facet on
hsv_reverse	logical, should color scale be reversed? default FALSE
hsv_saturation	numeric value from 0 to 1. Saturation for color scale. default 1
hsv_value	numeric value from 0 to 1. Value for color scale. default 1
hsv_grayscale	logical, if TRUE gray() is used instead of rainbow(). default FALSE
hsv_hue_min	numeric [0, hsv_hue_max) hue min of color scale
hsv_hue_max	numeric (hsv_hue_min, 1] hue max of color scale
hsv_symmetric	if TRUE, colorscale is symmetrical, default FALSE.
n_quantile	number of evenly size quantile bins
quantile_min	the lowest quantile start
quantile_max	the highest quantile end
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

Value

ggplot object using ribbon plots to show quantile distributions

Examples

```
data(CTCF_in_10a_profiles_gr)
#rainbow colors
qgr = CTCF_in_10a_profiles_gr
ssvSignalBandedQuantiles(qgr)
#grayscale
ssvSignalBandedQuantiles(qgr, hsv_grayscale = TRUE,
    hsv_symmetric = TRUE, hsv_reverse = TRUE)
#using "by_" per sample
ssvSignalBandedQuantiles(qgr, hsv_grayscale = TRUE,
    hsv_symmetric = TRUE, hsv_reverse = TRUE, by_ = "sample")
#adding spline smoothing
```

```
splined = applySpline(qgr, n = 10,
    by_ = c("id", "sample"))
ssvSignalBandedQuantiles(splined, n_quantile = 50,
    quantile_min = .25, quantile_max = .75,
    hsv_symmetric = TRUE, hsv_reverse = TRUE, by_ = "sample")
```

---

ssvSignalClustering *Clustering as for a heatmap. This is used internally by* ssvSignalHeatmap *but can also be run before calling ssvSignalHeatmap for greater control and access to clustering results directly.*

Description

Clustering is via k-means by default. The number of clusters is determined by nclust. Optionally, k-means can be initialized with a data.frame provided to k_centroids. As an alternative to k-means, a membership table from ssvMakeMembTable can be provided to determine logical clusters.

Usage

```
ssvSignalClustering(
  bw_data,
  nclust = NULL,
  k_centroids = NULL,
  memb_table = NULL,
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  cluster_ = "cluster_id",
  max_rows = 500,
  max_cols = 100,
  clustering_col_min = -Inf,
  clustering_col_max = Inf,
  within_order_strategy = valid_sort_strategies[2],
  dcast_fill = NA,
  iter.max = 30,
  fun.aggregate = "mean"
)
```

Arguments

bw_data	a GRanges or data.table of bigwig signal. As returned from ssvFetchBam and ssvFetchBigwig
nclust	Number of clusters. Defaults to 6 if nclust, k_centroids, and memb_table are not set.
k_centroids	data.frame of centroids for k-means clusters. Incompatible with nclust or memb_table.
memb_table	Membership table as from ssvMakeMembTable. Logical groups from membership table will be clusters. Incompatible with nclust or k_centroids.
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.

column_	varaible mapped to column, likely bp position for ngs data. Default is "x" and works with ssvFetch* output.
fill_	numeric variable to map to fill. Default is "y" and works with ssvFetch* output.
facet_	variable name to facet horizontally by. Default is "sample" and works with ssvFetch* output. Set to "" if data is not facetted.
cluster_	variable name to use for cluster info. Default is "cluster_id".
max_rows	for speed rows are sampled to 500 by default, use Inf to plot full data
max_cols	for speed columns are sampled to 100 by default, use Inf to plot full data
clustering_col_min	numeric minimum for col range considered when clustering, default in -Inf
clustering_col_max	numeric maximum for col range considered when clustering, default in Inf
within_order_strategy	one of "hclust", "sort", "right", "left", "none", "reverse". If "hclust", hierarchical clustering will be used. If "sort", a simple decreasing sort of rosSums. If "left", will attempt to put high signal on left ("right" is opposite). If "none", existing order is preserved. If "reverse" reverses existing order.
dcast_fill	value to supply to dcast fill argument. default is NA.
iter.max	Number of max iterations to allow for k-means. Default is 30.
fun.aggregate	Function to aggregate when multiple values present for facet_, row_, and column_. The function should accept a single vector argument or be a character string naming such a function.

Details

Within each cluster, items will either be sorted by decreasing average signal or hierachically clustered; this is controlled via within_order_strategy.

Value

data.table of signal profiles, ready for ssvSignalHeatmap

Examples

```
data(CTCF_in_10a_profiles_gr)
clust_dt = ssvSignalClustering(CTCF_in_10a_profiles_gr)
ssvSignalHeatmap(clust_dt)

clust_dt2 = ssvSignalClustering(CTCF_in_10a_profiles_gr, nclust = 2)
ssvSignalHeatmap(clust_dt2)

#clustering can be targetted to a specific part of the region
clust_dt3 = ssvSignalClustering(CTCF_in_10a_profiles_gr, nclust = 2,
    clustering_col_min = -250, clustering_col_max = -150)
ssvSignalHeatmap(clust_dt3)

# there are also multiple sorting strategies to apply within each cluster
clust_dt4 = ssvSignalClustering(
  CTCF_in_10a_profiles_gr,
  nclust = 2,
  within_order_strategy = "left"
)
```

```
ssvSignalHeatmap(clust_dt4)

clust_dt5 = ssvSignalClustering(
  CTCF_in_10a_profiles_gr,
  nclust = 2,
  within_order_strategy = "sort"
)
ssvSignalHeatmap(clust_dt5)
```

`ssvSignalHeatmap` *heatmap style representation of membership table. instead of clustering, each column is sorted starting from the left.*

Description

See `ssvSignalHeatmap.ClusterBars` for an alternative with more control over where the cluster bars appear.

Usage

```
ssvSignalHeatmap(
  bw_data,
  nclust = 6,
  perform_clustering = c("auto", "yes", "no")[1],
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  cluster_ = "cluster_id",
  max_rows = 500,
  max_cols = 100,
  fill_limits = NULL,
  clustering_col_min = -Inf,
  clustering_col_max = Inf,
  within_order_strategy = c("hclust", "sort")[2],
  dcast_fill = NA,
  return_data = FALSE,
  show_cluster_bars = TRUE,
  rect_colors = c("black", "gray"),
  text_colors = rev(rect_colors),
  show_labels = TRUE,
  label_angle = 0,
  fun.aggregate = "mean"
)
```

Arguments

`bw_data`	a GRanges or data.table of bigwig signal. As returned from `ssvFetchBam` and `ssvFetchBigwig`
`nclust`	number of clusters

perform_clustering
: should clustering be done? default is auto. auto considers if row_ has been ordered by being a factor and if cluster_ is a numeric.

row_
: variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.

column_
: varaible mapped to column, likely bp position for ngs data. Default is "x" and works with ssvFetch* output.

fill_
: numeric variable to map to fill. Default is "y" and works with ssvFetch* output.

facet_
: variable name to facet horizontally by. Default is "sample" and works with ssvFetch* output. Set to "" if data is not facetted.

cluster_
: variable name to use for cluster info. Default is "cluster_id".

max_rows
: for speed rows are sampled to 500 by default, use Inf to plot full data

max_cols
: for speed columns are sampled to 100 by default, use Inf to plot full data

fill_limits
: limits for fill legend. values will be cropped to this range if set. Default of NULL uses natural range of fill_.

clustering_col_min
: numeric minimum for col range considered when clustering, default in -Inf

clustering_col_max
: numeric maximum for col range considered when clustering, default in Inf

within_order_strategy
: one of "hclust" or "sort". if hclust, hierarchical clustering will be used. if sort, a simple decreasing sort of rosSums.

dcast_fill
: value to supply to dcast fill argument. default is NA.

return_data
: logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

show_cluster_bars
: if TRUE, show bars indicating cluster membership.

rect_colors
: colors of rectangle fill, repeat to match number of clusters. Default is c("black", "gray").

text_colors
: colors of text, repeat to match number of clusters. Default is reverse of rect_colors.

show_labels
: logical, shoud rectangles be labelled with cluster identity. Default is TRUE.

label_angle
: angle to add clusters labels at. Default is 0, which is horizontal.

fun.aggregate
: Function to aggregate when multiple values present for facet_, row_, and column_. Affects both clustering and plotting. The function should accept a single vector argument or be a character string naming such a function.

Value

ggplot heatmap of signal profiles, facetted by sample

Examples

```
data(CTCF_in_10a_profiles_gr)

#the simplest use
ssvSignalHeatmap(CTCF_in_10a_profiles_gr)
ssvSignalHeatmap(CTCF_in_10a_profiles_gr, show_cluster_bars = FALSE)
```

```
#clustering can be done manually beforehand
clust_dt = ssvSignalClustering(CTCF_in_10a_profiles_gr, nclust = 3)
ssvSignalHeatmap(clust_dt)

ssvSignalHeatmap(clust_dt, max_rows = 20, max_cols = 7)

# aggregation, when facet_ is shared by multiple samples
prof_gr = CTCF_in_10a_profiles_gr
prof_gr$mark = "CTCF"
clust_gr = ssvSignalClustering(
  prof_gr,
  facet_ = "mark",
  fun.aggregate = function(x)as.numeric(x > 10)
)
table(clust_gr$y)
ssvSignalHeatmap(prof_gr, facet_ = "mark",
  fun.aggregate = function(x)as.numeric(x > 10))
ssvSignalHeatmap(prof_gr, facet_ = "mark",
  fun.aggregate = max)
ssvSignalHeatmap(prof_gr, facet_ = "mark",
  fun.aggregate = min)
```

`ssvSignalHeatmap.ClusterBars` *heatmap style representation of membership table. instead of clustering, each column is sorted starting from the left.*

Description

Compared to ssvSignalHeatmap, cluster_bars are displayed on the left once instead of for each facet

Usage

```
ssvSignalHeatmap.ClusterBars(
  bw_data,
  nclust = 6,
  perform_clustering = c("auto", "yes", "no")[1],
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  cluster_ = "cluster_id",
  FUN_format_heatmap = NULL,
  max_rows = 500,
  max_cols = 100,
  fill_limits = NULL,
  clustering_col_min = -Inf,
  clustering_col_max = Inf,
  within_order_strategy = c("hclust", "sort")[2],
  dcast_fill = NA,
  return_data = FALSE,
  return_unassembled_plots = FALSE,
  rel_widths = c(1, 9),
```

```
  rect_colors = c("black", "gray"),
  text_colors = rev(rect_colors),
  show_labels = TRUE,
  label_angle = 0,
  fun.aggregate = "mean",
  ...
)
```

Arguments

bw_data	a GRanges or data.table of bigwig signal. As returned from ssvFetchBam and ssvFetchBigwig
nclust	number of clusters
perform_clustering	should clustering be done? default is auto. auto considers if row_ has been ordered by being a factor and if cluster_ is a numeric.
row_	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
column_	varaible mapped to column, likely bp position for ngs data. Default is "x" and works with ssvFetch* output.
fill_	numeric variable to map to fill. Default is "y" and works with ssvFetch* output.
facet_	variable name to facet horizontally by. Default is "sample" and works with ssvFetch* output. Set to "" if data is not facetted.
cluster_	variable name to use for cluster info. Default is "cluster_id".
FUN_format_heatmap	optional function to modify main ggplot (labels, themes, scales, etc.). Take a ggplot and returns a ggplot. Default is NULL.
max_rows	for speed rows are sampled to 500 by default, use Inf to plot full data
max_cols	for speed columns are sampled to 100 by default, use Inf to plot full data
fill_limits	limits for fill legend. values will be cropped to this range if set. Default of NULL uses natural range of fill_.
clustering_col_min	numeric minimum for col range considered when clustering, default in -Inf
clustering_col_max	numeric maximum for col range considered when clustering, default in Inf
within_order_strategy	one of "hclust" or "sort". if hclust, hierarchical clustering will be used. if sort, a simple decreasing sort of rosSums.
dcast_fill	value to supply to dcast fill argument. default is NA.
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.
return_unassembled_plots	logical. If TRUE, return list of heatmap and cluster-bar ggplots. Can be customized and passed to assemble_heatmap_cluster_bars
rel_widths	numeric of length 2. Passed to cowplot::plot_grid. Default is c(1, 9).
rect_colors	colors of rectangle fill, repeat to match number of clusters. Default is c("black", "gray").

text_colors	colors of text, repeat to match number of clusters. Default is reverse of rect_colors.
show_labels	logical, shoud rectangles be labelled with cluster identity. Default is TRUE.
label_angle	angle to add clusters labels at. Default is 0, which is horizontal.
fun.aggregate	Function to aggregate when multiple values present for facet_, row_, and column_. Affects both clustering and plotting. The function should accept a single vector argument or be a character string naming such a function.
...	addtional arguments passed to cowplot::plot_grid

Value

ggplot heatmap of signal profiles, facetted by sample

Examples

```
data(CTCF_in_10a_profiles_gr)

#the simplest use
ssvSignalHeatmap.ClusterBars(CTCF_in_10a_profiles_gr)
ssvSignalHeatmap.ClusterBars(CTCF_in_10a_profiles_gr, rel_widths = c(1, 5))

#clustering can be done manually beforehand
clust_dt = ssvSignalClustering(data.table::as.data.table(CTCF_in_10a_profiles_gr), nclust = 3)
ssvSignalHeatmap.ClusterBars(clust_dt)

# aggregation, when facet_ is shared by multiple samples
prof_gr = CTCF_in_10a_profiles_gr
prof_gr$mark = "CTCF"
ssvSignalHeatmap.ClusterBars(prof_gr, facet_ = "mark", fun.aggregate = mean)
ssvSignalHeatmap.ClusterBars(prof_gr, facet_ = "mark", fun.aggregate = "sum")
```

---

ssvSignalLineplot *construct line type plots where each region in each sample is represented*

Description

construct line type plots where each region in each sample is represented

Usage

```
ssvSignalLineplot(
  bw_data,
  x_ = "x",
  y_ = "y",
  color_ = "sample",
  sample_ = "sample",
  region_ = "id",
  group_ = "auto_grp",
  line_alpha = 1,
  facet_ = "auto_facet",
  facet_method = facet_wrap,
  spline_n = NULL,
  return_data = FALSE
)
```

Arguments

bw_data	a GRanges or data.table of bigwig signal. As returned from ssvFetchBam and ssvFetchBigwig
x_	variable name mapped to x aesthetic, x by default.
y_	variable name mapped to y aesthetic, y by default.
color_	variable name mapped to color aesthetic, sample by default.
sample_	variable name, along with region_ used to group and facet by default, change group_ or facet_ to override.
region_	variable name, along with sample_ used to group and facet by default, change group_ or facet_ to override.
group_	group aesthetic keeps lines of geom_path from mis-connecting. auto_grp by default which combines sample_ and region_. probably shouldn't change.
line_alpha	alpha value for lines. default is 1.
facet_	facetting divides up plots. auto_facet by default which combines sample_ and region_. if overriding facet_method with facet_grid, make sure to include ~ between two variables, ie. "a~b", ".~b", "a~."
facet_method	ggplot2 facetting method or wrapper for same, facet_wrap by default.
spline_n	if not NULL, applySpline will be called with n = spline_n. default is NULL.
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

Value

ggplot of signal potentially facetted by region and sample

Examples

```
data(CTCF_in_10a_profiles_gr)

bw_gr = CTCF_in_10a_profiles_gr
ssvSignalLineplot(subset(bw_gr, bw_gr$id %in% seq_len(3)), facet_ = "sample")
ssvSignalLineplot(subset(bw_gr, bw_gr$id %in% seq_len(3)),
    facet_ = "sample~.",
    facet_method = facet_grid)
ssvSignalLineplot(subset(bw_gr, bw_gr$id %in% seq_len(3)),
    facet_ = paste("sample", "~", "id"), facet_method = facet_grid)
ssvSignalLineplot(subset(bw_gr, bw_gr$id %in% seq_len(3)))
ssvSignalLineplot(subset(bw_gr, bw_gr$id %in% seq_len(3)), facet_ = "id")
ssvSignalLineplot(subset(bw_gr, bw_gr$id %in% seq_len(3)),
    facet_ = "id", spline_n = 10)
```

---

ssvSignalLineplotAgg *aggregate line signals in a single line plot*

Description

aggregate line signals in a single line plot

Usage

```
ssvSignalLineplotAgg(
  bw_data,
  x_ = "x",
  y_ = "y",
  sample_ = "sample",
  color_ = sample_,
  group_ = sample_,
  agg_fun = mean,
  spline_n = NULL,
  return_data = FALSE
)
```

Arguments

bw_data	a GRanges or data.table of bigwig signal. As returned from ssvFetchBam and ssvFetchBigwig
x_	variable name mapped to x aesthetic, x by default.
y_	variable name mapped to y aesthetic, y by default.
sample_	variable name, along with region_ used to group by default,
color_	variable name mapped to color aesthetic, sample_ by default. change group_ to override.
group_	group aesthetic keeps lines of geom_path from mis-connecting. Most useful if you need to supply a variable to later facet upon. Defaults to value of sample_.
agg_fun	the aggregation function to apply by sample_ and x_, default is mean
spline_n	if not NULL, applySpline will be called with n = spline_n. default is NULL.
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

Value

ggplot of signal aggregated with agg_fun() by sample.

Examples

```
data(CTCF_in_10a_profiles_gr)
bw_gr = CTCF_in_10a_profiles_gr
ssvSignalLineplotAgg(bw_gr) +
    labs(title = "agg regions by sample.")
ssvSignalLineplotAgg(CTCF_in_10a_profiles_gr, spline_n = 10) +
    labs(title = "agg regions by sample, with spline smoothing.")
ssvSignalLineplotAgg(subset(bw_gr, bw_gr$id %in% seq_len(10)),
    sample_ = "id", color_ = "id") +
    labs(title = "agg samples by region id (weird)")
ssvSignalLineplotAgg(subset(bw_gr, bw_gr$id %in% seq_len(10)), sample_ = "id",
    color_ = "id", spline_n = 10) +
    labs(title = "agg samples by region id (weird), with spline smoothing")
```

`ssvSignalScatterplot` *maps signal from 2 sample profiles to the x and y axis. axes are standard or "volcano" min XY vs fold-change Y/X*

Description

maps signal from 2 sample profiles to the x and y axis. axes are standard or "volcano" min XY vs fold-change Y/X

Usage

```
ssvSignalScatterplot(
  bw_data,
  x_name,
  y_name,
  color_table = NULL,
  value_variable = "y",
  xy_variable = "sample",
  value_function = max,
  by_ = "id",
  plot_type = c("standard", "volcano")[1],
  show_help = FALSE,
  fixed_coords = TRUE,
  return_data = FALSE
)
```

Arguments

`bw_data`	a GRanges or data.table of bigwig signal. As returned from `ssvFetchBam` and `ssvFetchBigwig`
`x_name`	sample name to map to x-axis, must be stored in variable specified in `xy_variable`
`y_name`	sample name to map to y-axis, must be stored in variable specified in `xy_variable`
`color_table`	data.frame with 2 columns, one of which must be named "group" and gets mapped to color. The other column must be the same as by_ parameter and is used for merging.
`value_variable`	variable name that stores numeric values for plotting, default is "y"
`xy_variable`	variable name that stores sample, must contain entires for `x_name` and `y_name`
`value_function`	a function to apply to `value_variable` in all combintations of `by_` per `x_name` and `y_name`
`by_`	variables that store individual measurement ids
`plot_type`	standard or volcano, default is "standard"
`show_help`	if TRUE overlay labels to aid plot interpretation, default is FALSE
`fixed_coords`	if TRUE coordinate system is 1:1 ratio, default is TRUE
`return_data`	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

Value

ggplot of points comparing signal from 2 samples

Examples

```
data(CTCF_in_10a_profiles_gr)
ssvSignalScatterplot(CTCF_in_10a_profiles_gr,
    x_name = "MCF10A_CTCF", y_name = "MCF10AT1_CTCF")
ssvSignalScatterplot(CTCF_in_10a_profiles_gr,
    x_name = "MCF10A_CTCF", y_name = "MCF10CA1_CTCF")

ssvSignalScatterplot(CTCF_in_10a_profiles_gr,
    x_name = "MCF10A_CTCF", y_name = "MCF10AT1_CTCF",
    value_function = median) + labs(title = "median FE in regions")

ssvSignalScatterplot(CTCF_in_10a_profiles_gr,
    x_name = "MCF10A_CTCF", y_name = "MCF10AT1_CTCF",
    plot_type = "volcano")

ssvSignalScatterplot(CTCF_in_10a_profiles_gr,
    x_name = "MCF10A_CTCF", y_name = "MCF10AT1_CTCF",
    plot_type = "volcano", show_help = TRUE)
```

`ssv_mclapply` *ssv_mclapply*

Description

ssv_mclapply

Usage

```
ssv_mclapply(X, FUN, mc.cores = getOption("mc.cores", 1), ...)
```

Arguments

`X`	For pbsapply and pblapply, a vector (atomic or list) or an expressions vector (other objects including classed objects will be coerced by as.list.) For pbapply an array, including a matrix. For pbtapply an R object for which a split method exists. Typically vector-like, allowing subsetting with "[".
`FUN`	The function to be applied to each element of X: see apply, sapply, and lapply. In the case of functions like +, '%*%', etc., the function name must be backquoted or quoted. If FUN is NULL, pbtapply returns a vector which can be used to subscript the multi-way array pbtapply normally produces.
`mc.cores`	Number of cores to use for pbmclapply. Defaults to option mc.cores.
`...`	passed to pbapply::pblapply or pbmcapply::pbmclapply

Value

result of either pblapply or pbmclapply

test_peaks *4 random peaks for single-end data and 4 control regions 30kb downstream from each peak.*

Description

matches `system.file("extdata/test_peaks.bam", package = "seqsetvis")`

Format

GRanges length 8

Details

this is included only for testing ssvFetchBam functions.

Value

GRanges length 8

viewGRangesWinSample_dt *get a windowed sampling of score_gr*

Description

This method is appropriate when all GRanges in qgr are identical width and when it is practical to use a window_size smaller than features in genomic signal. For instance, when retrieving signal around peaks or promoters this method maintains a fixed genomic scale across regions. This allows meaingful comparison of peak widths can be made.

Usage

```
viewGRangesWinSample_dt(
  score_gr,
  qgr,
  window_size,
  attrib_var = "score",
  fill_value = 0,
  anchor = c("center", "center_unstranded", "left", "left_unstranded")[1]
)
```

Arguments

score_gr	GRanges with a "score" metadata column.
qgr	regions to view by window.
window_size	qgr will be represented by value from score_gr every window_size bp.
attrib_var	character name of attribute to pull data from. Default is "score", compatible with with bigWigs or bam coverage.

fill_value	numeric or character value to use where queried regions are empty. Default is 0 and appropriate for both calculated coverage and bedgraph/bigwig like files. Will automatically switch to "MISSING" if data is guessed to be qualitative.
anchor	character. controls how x value is derived from position for each region in qgr. 0 may be the left side or center. If not unstranded, x coordinates are flipped for (-) strand. One of c("center", "center_unstranded", "left", "left_unstranded"). Default is "center".

Details

Summarizes score_gr by grabbing value of "score" every window_size bp. Columns in output data.table are: standard GRanges columns: seqnames, start, end, width, strand id - matched to names(score_gr). if names(score_gr) is missing, added as 1:length(score_gr). y - value of score from score_gr. x - relative bp position.

Value

data.table that is GRanges compatible

Examples

```
data(CTCF_in_10a_overlaps_gr)
bam_file = system.file("extdata/test.bam",
    package = "seqsetvis")
qgr = CTCF_in_10a_overlaps_gr[seq_len(5)]
qgr = GenomicRanges::resize(qgr, width = 500, fix = "center")
bam_gr = seqsetvis:::fetchBam(bam_file, qgr)
bam_dt = viewGRangesWinSample_dt(bam_gr, qgr, 50)

if(Sys.info()['sysname'] != "Windows"){
    bw_file = system.file("extdata/MCF10A_CTCF_FE_random100.bw",
        package = "seqsetvis")
    bw_gr = rtracklayer::import.bw(bw_file, which = qgr)
    bw_dt = viewGRangesWinSample_dt(bw_gr, qgr, 50)
}
```

---

viewGRangesWinSummary_dt

Summarizes signal in bins. The same number of bins per region in qgr is used and widths can vary in qgr, in contrast to viewGRangesWinSample_dt *where width must be constant across regions.*

Description

This function is most appropriate where features are expected to vary greatly in size and feature boundaries are important, ie. gene bodies, enhancers or TADs.

Usage

```
viewGRangesWinSummary_dt(
  score_gr,
  qgr,
  n_tiles = 100,
  attrib_var = "score",
  attrib_type = NULL,
  fill_value = 0,
  anchor = c("center", "center_unstranded", "left", "left_unstranded")[1],
  summary_FUN = stats::weighted.mean
)
```

Arguments

score_gr	GRanges with a "score" metadata column.
qgr	regions to view by window.
n_tiles	numeric >= 1, the number of tiles to use for every region in qgr.
attrib_var	character name of attribute to pull data from. Default is "score", compatible with with bigWigs or bam coverage.
attrib_type	one of NULL, qualitative or quantitative. If NULL will attempt to guess by casting attrib_var attribute to character or factor. Default is NULL.
fill_value	numeric or character value to use where queried regions are empty. Default is 0 and appropriate for both calculated coverage and bedgraph/bigwig like files. Will automatically switch to "MISSING" if data is guessed to be qualitative.
anchor	character. controls how x value is derived from position for each region in qgr. 0 may be the left side or center. If not unstranded, x coordinates are flipped for (-) strand. One of c("center", "center_unstranded", "left", "left_unstranded"). Default is "center".
summary_FUN	function. used to aggregate score by tile. must accept x=score and w=width numeric vectors as only arguments. default is weighted.mean. limma::weighted.median is a good alternative.

Details

Columns in output data.table are: standard GRanges columns: seqnames, start, end, width, strand id - matched to names(score_gr). if names(score_gr) is missing, added as seq_along(score_gr). y - value of score from score_gr x - relative bp position

Value

data.table that is GRanges compatible

Examples

```
data(CTCF_in_10a_overlaps_gr)
bam_file = system.file("extdata/test.bam",
    package = "seqsetvis")
qgr = CTCF_in_10a_overlaps_gr[1:5]
# unlike viewGRangesWinSample_dt, width is not fixed
# qgr = GenomicRanges::resize(qgr, width = 500, fix = "center")
bam_gr = seqsetvis:::fetchBam(bam_file, qgr)
```

```
bam_dt = viewGRangesWinSummary_dt(bam_gr, qgr, 50)

if(Sys.info()['sysname'] != "Windows"){
    bw_file = system.file("extdata/MCF10A_CTCF_FE_random100.bw",
        package = "seqsetvis")
    bw_gr = rtracklayer::import.bw(bw_file, which = qgr)
    bw_dt = viewGRangesWinSummary_dt(bw_gr, qgr, 50)
}
```

`within_clust_sort` *within_clust_sort*

Description

Without modifying cluster assignments, modify the order of rows within each cluster based on within_order_strategy.

Usage

```
within_clust_sort(
  clust_dt,
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  cluster_ = "cluster_id",
 within_order_strategy = c("hclust", "sort", "left", "right", "none", "reverse")[2],
  clustering_col_min = -Inf,
  clustering_col_max = Inf,
  dcast_fill = NA
)
```

Arguments

`clust_dt`	data.table output from `ssvSignalClustering`
`row_`	variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
`column_`	varaible mapped to column, likely bp position for ngs data. Default is "x" and works with ssvFetch* output.
`fill_`	numeric variable to map to fill. Default is "y" and works with ssvFetch* output.
`facet_`	variable name to facet horizontally by. Default is "sample" and works with ssvFetch* output. Set to "" if data is not facetted.
`cluster_`	variable name to use for cluster info. Default is "cluster_id".
`within_order_strategy`	one of "hclust", "sort", "right", "left", "reverse". If "hclust", hierarchical clustering will be used. If "sort", a simple decreasing sort of rosSums. If "left", will atttempt to put high signal on left ("right" is opposite). If "reverse" reverses existing order (should only be used after meaningful order imposed).
`clustering_col_min`	numeric minimum for col range considered when clustering, default in -Inf

clustering_col_max
: numeric maximum for col range considered when clustering, default in Inf

dcast_fill
: value to supply to dcast fill argument. default is NA.

Details

This is particularly useful when you want to sort within each cluster by a different variable from cluster assignment. Also if you've imported cluster assigments but want to sort within each for the new data for a prettier heatmap.

TODO refactor shared code with clusteringKmeansNestedHclust

Value

data.table matching input clust_dt save for the reassignment of levels of row_ variable.

Examples

```
data(CTCF_in_10a_profiles_dt)
#clustering by relative value per region does a good job highlighting changes
#when then plotting raw values the order within clusters is not smooth
#this is a good situation to apply a separate sort within clusters.
prof_dt = CTCF_in_10a_profiles_dt
prof_dt = append_ynorm(prof_dt)
prof_dt[, y_relative := y_norm / max(y_norm), list(id)]

clust_dt = ssvSignalClustering(prof_dt, fill_ = "y_relative")
clust_dt.sort = within_clust_sort(clust_dt)

cowplot::plot_grid(
  ssvSignalHeatmap(clust_dt) +
    labs(title = "clustered by relative, sorted by relative"),
  ssvSignalHeatmap(clust_dt.sort) +
    labs(title = "clustered by relative, sorted by raw value")
)
```

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