Package ‘seqsetvis’

Type Package
Title Set Based Visualizations for Next-Gen Sequencing Data
Version 1.24.0
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
multiple 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).
License MIT + file LICENSE
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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)**

Maintainer: Joseph R Boyd <jrboyd@uvm.edu>

---

**.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", "seq-names", "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 inserions (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", "seq-names", "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"
)
add_cluster_annotation

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, should 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

#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
pl = assemble_heatmap_cluster_bars(pplots = 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)

Description

see `calc_norm_factors` for normalization details.

Usage

```r
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 normalize.
- `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
append_ynorm(CTCF_in_10a_profiles_dt)
append_ynorm(CTCF_in_10a_profiles_dt,
   aggFUN1 = mean, aggFUN2 = function(x)quantile(x, .5))

describe
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

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 retrieved 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.
assemble_heatmap_cluster_bars

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 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
calc_norm_factors

Examples

```r
plots = ssvSignalHeatmap.ClusterBars(CTCF_in_10a_profiles_gr, return_unassembled_plots = TRUE)
apsemble_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.

calc_norm_factors

Description

Calculate normalization factors in a two step process:

Usage

```r
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 normalize.
- `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) calculate a value to cap each sample to based on regions (default is 95th quantile).

The underlying 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

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

correct_by_dupes default assumption is that there should be one set of x_ for a by_ instance. if this is not the case and you want to disable warnings about this 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

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)
**centerGRangesAtMax**

**Arguments**

- **grs**
  Set of GRanges with inconsistent 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**

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

**Description**

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

**Usage**

```r
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**

```r
centerGRangesAtMax(CTCF_in_10a_profiles_dt, CTCF_in_10a_overlaps_gr)
centerGRangesAtMax(CTCF_in_10a_profiles_gr, CTCF_in_10a_overlaps_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.

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
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.
### chromHMM_demo_state_colors

**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.

---

<table>
<thead>
<tr>
<th>chromHMM_demo_segmentation_url</th>
</tr>
</thead>
<tbody>
<tr>
<td>URL to download hg19 MCF7 chromHMM segmentation</td>
</tr>
</tbody>
</table>

**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

---

<table>
<thead>
<tr>
<th>chromHMM_demo_state_colors</th>
</tr>
</thead>
<tbody>
<tr>
<td>original state name to color mappings stored in segmentation bed</td>
</tr>
</tbody>
</table>

**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
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

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

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 attempt 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 specifying 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 clustering group__ column indicates cluster assignment

Examples

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 = clusteringKmeansNestedHclus(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

gene_gr

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

describe

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

description

(preliminary implementation, sub-optimal)
Usage

convert_collapsed_coord(genome_gr, x)

Arguments

genoeme_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))

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

```r
#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

```r
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 character vector of length 3

**Details**

part of **CTCF_in_10a_data**
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
easyLoad_bed

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 overridden 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 overridden 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
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 overridden 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

eidr_file = system.file("extdata/test_idr.overlapped-peaks.txt", package = "seqsetvis", mustWork = TRUE)
easyLoad_IDRmerged(eidr_file)
easyLoad_IDRmerged(eidr_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 overridden 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
**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 overridden 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**

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

```r
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**

```r
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", "seq-names", "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 insertions (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**

```r
qgr = CTCF_in_l0a_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 strand 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 assumed 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

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

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
fragLen_calcStranded

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 lengths 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

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]]
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.

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)
get_mapped_reads

Examples

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

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)

ggeellipse

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

Description

uses eulerr’s non-exported ellipse drawing coordinate function
Usage

```r
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 `r`colors 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 [0,1] alpha of lines, 1 by default
- `fill_alpha`: numeric [0,1] 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

Value

A ggplot containing ellipses

Examples

```r
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),
```
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

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_  variable 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.
merge_clusters

Value

A wide matrix version of input tidy data.table

Examples

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

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
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
)
prepare_fetch_GRanges_names

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>qgr</td>
<td>GRanges to prepare</td>
</tr>
<tr>
<td>win_size</td>
<td>numeric window size for fetch</td>
</tr>
<tr>
<td>min_quantile</td>
<td>numeric [0,1], lowest possible quantile value. Only relevant if target_size is not specified.</td>
</tr>
<tr>
<td>target_size</td>
<td>numeric final width of qgr if known. Default of NULL leads to quantile based determination of target_size.</td>
</tr>
<tr>
<td>skip_centerFix</td>
<td>boolean, if FALSE (default) all regions will be resized GenomicRanges::resize(x, w, fix = &quot;center&quot;) to a uniform size based on min_quantile to a width divisible by win_size.</td>
</tr>
</tbody>
</table>

**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**

```r
# 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**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>qgr</td>
<td>input GRanges object the set/check names on</td>
</tr>
<tr>
<td>include_id</td>
<td>if TRUE, $id$ is retained. Default is FALSE.</td>
</tr>
</tbody>
</table>
and named GRanges based on input qgr.

Examples

```r
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))
```

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

```r
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 [0,1], 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.
**quantileGRangesWidth**

**Examples**

```r
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**

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

**Arguments**

- **qgr**: GRanges to calculate quantile width for
- **min_quantile**: numeric [0,1] 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**

```r
g = CTCF_in_10a_overlaps_gr
quantileGRangesWidth(g)
quantileGRangesWidth(g, 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 parameters 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_        variable 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

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)
)
Description

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

Usage

```r
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

```r
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**

**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**

```r
defunctionalize {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_`: variable 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 done 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.
reverse_clusters

Value

data.table as output from `ssvSignalClustering`

Examples

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)
)

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_      variable 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.
safeBrew

Value
data.table as output from `ssvSignalClustering`

Examples

```r
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")
)
```

Description

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.

Usage

```r
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 respectively.
- `pal`: palette recognized by RColorBrewer

Details

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**

```r
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**

```r
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**

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

**Description**

orient the relative position of x’s zero value and extends ranges to be contiguous

**Usage**

```r
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

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_ variable 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 faceted.
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

```r
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)
)
```

**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**

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

**Arguments**

- `grs` A list of GRanges
- `ext` An integer specifying how far to extend ranges before merging. in effect, ranges within 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.
- `...` 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.
**ssvFactorizeMembTable**

Convert any object accepted by `ssvMakeMembTable` to a factor to avoid ambiguity.

**Description**

see `ssvMakeMembTable`

**Usage**

```r
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**

```r
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

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**

**Description**

Binary heatmap indicating membership. Heatmap is sorted by column left to right. Change column order to reveal patterns.

**Usage**

```r
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.

**Value**

Ggplot using geom_tile of membership table sorted from left to right.
Examples

```
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

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

Value

ggplot of venn euler results
Examples

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

---

**ssvFeaturePie**

*pie plot of set sizes*

Description

*pie plot of set sizes*

Usage

```r
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

```r
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 upset plot of overlaps.
ssvFeatureUpset

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

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

ssvFeatureVenn 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.

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 [0,1], 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**

```r
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**

```r
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 additional 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 strand 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 assumed 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.
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 assumed 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.

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

```r
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 additional 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 qr.

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 strand 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 qr. 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 qr 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)
}

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,
                      ...)
**ssvFetchBigwig**

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>bam_f</td>
<td>character or BamFile to load</td>
</tr>
<tr>
<td>qgr</td>
<td>GRanges regions to fetchs</td>
</tr>
<tr>
<td>win_size</td>
<td>numeric &gt;=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).</td>
</tr>
<tr>
<td>win_method</td>
<td>character. one of c(&quot;sample&quot;, &quot;summary&quot;). Determines if viewGRangesWinSample_dt or viewGRangesWinSummary_dt is used to represent each region in qgr.</td>
</tr>
<tr>
<td>summary_FUN</td>
<td>function. only relevant if win_method is &quot;summary&quot;. passed to viewGRangesWinSummary_dt.</td>
</tr>
<tr>
<td>anchor</td>
<td>character, one of c(&quot;center&quot;, &quot;center_unstranded&quot;, &quot;left&quot;, &quot;left_unstranded&quot;)</td>
</tr>
<tr>
<td>return_data.table</td>
<td>logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.</td>
</tr>
<tr>
<td>max_dupes</td>
<td>numeric &gt;= 1. duplicate reads by strand and start position over this number are removed, Default is Inf.</td>
</tr>
<tr>
<td>min_isize</td>
<td>integer. Read pairs must have an isize greater than or equal to this value. Default is 1.</td>
</tr>
<tr>
<td>max_isize</td>
<td>integer. Read pairs must have an isize less than or equal to this value. Default is Inf.</td>
</tr>
<tr>
<td>return_unprocessed</td>
<td>boolean. if TRUE returns read alignment in data.table. Default is FALSE.</td>
</tr>
<tr>
<td>return_fragSizes</td>
<td>boolean. if TRUE returns fragment sizes for all reads per region.</td>
</tr>
<tr>
<td>force_skip_centerFix</td>
<td>boolean, if TRUE all query ranges will be used &quot;as is&quot;. This is already the case by default if win_method == &quot;summary&quot; but may have applications where win_method == &quot;sample&quot;.</td>
</tr>
</tbody>
</table>

**Value**

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

---

**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

```r
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 additital 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**

```r
if(Sys.info()
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**

```r
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**

```r
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("x", "+", "-", "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

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

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

```r
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
additinal 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 if return_data.table is TRUE.

Examples

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[1:2]
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

**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**

```r
ssvMakeMembTable(object)
```

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

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

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

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

```r
## S4 method for signature 'matrix'
ssvMakeMembTable(object)
```

```r
## 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
ssvOverlapIntervalSets

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

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

Arguments

- **grs** A list of GRanges
- **ext** An integer specifying how far to extend ranges before merging. In effect, ranges within 2*ext of one another will be joined during the merge

Example usage:

```r
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)
```
**ssvSignalBandedQuantiles**

A logical. If True, instead of merging all grs, only use first and add metadata logicals for others.

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

**Value**

GRanges with metadata columns describing overlap of input grs.

**Examples**

```r
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**

```r
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 [0, 1] saturation for color scale. default 1

hsv_value  
numeric [0, 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**

```r
#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")
```
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

```r
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_**: variable 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 faceted.

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", "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 "reverse" reverses existing order (should only be used after meaningful order imposed).

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 hierarchically clustered; this is controlled via within_order_strategy.

Value
data.table of signal profiles, ready for ssvSignalHeatmap

Examples

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 targeted 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)

clust_dt4 = ssvSignalClustering(CTCF_in_10a_profiles_gr, nclust = 2,
    clustering_col_min = 150, clustering_col_max = 250)
ssvSignalHeatmap(clust_dt4)
**ssvSignalHeatmap**

Heatmap style representation of membership table. Instead of clustering, each column is sorted starting from the left.

**Description**

See **ssvSignalHeatmap.ClustBar** for an alternative with more control over where the cluster bars appear.

**Usage**

```r
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_ variable 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, should 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

#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.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_               variable 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 faceted.
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
### ssvSignalLineplot

**Description**

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

**Usage**

```r
ssvSignalLineplot(
    bw_data,
    x_ = "x",
    y_ = "y",
    color_ = "sample",
    sample_ = "sample",
```

**Examples**

```r
#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")
```
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_ faceting 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 faceting 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

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

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
**Description**

ssv_mclapply

**Usage**

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

**Value**

ggplot of points comparing signal from 2 samples

**Examples**

```r
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)
```
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 +, 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 pbapply normally produces.

mc.cores  Number of cores to use for pbmclapply. Defaults to option mc.cores.

...  passed to pbapply::pblapply or pbmclapply::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.

description

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 meaningful comparison of peak widths can be made.
viewGRangesWinSample_dt

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

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")
}
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, i.e., 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".
within_clust_sort

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

```r
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

```r
within_clust_sort(
  clust_dt,
  row_ = "id",
  column_ = "x",
  fill_ = "y",
  facet_ = "sample",
  cluster_ = "cluster_id",
  within_order_strategy = c("hclust", "sort", "left", "right")[2],
)```
within_clust_sort

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_  variable 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 attempt 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 assignments 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

#clustering by relative value per region does a good job highlighting changes
#however, 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)]
```r
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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