Package ‘seqsetvis’

May 30, 2024

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).
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Description

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

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---

**.expand_cigar_dt**

Expand intermediate bam fetch by cigar codes

Description

see sam specs for cigar details

Usage

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

Arguments

- `cigar_dt` data.table with 5 required named columns in any order. c("which_label", "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.

Value

data.table with cigar entries expanded
.expand_cigar_dt_recursive

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

Description

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

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

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

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

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

#when colors are named, the names are used rather that just the order
rect_colors = safeBrew(assign_dt$cluster_id)
text_colors = safeBrew(assign_dt$cluster_id, "greys")
p_clusters = add_cluster_annotation(assign_dt$cluster_id, rect_colors = rect_colors, text_colors = text_colors)

#specialized use as plot outside of heatmap
p1 = assemble_heatmap_cluster_bars(plots = list(p_clusters, p_heat), rel_widths = c(1, 3))

#when colors are named, the names are used rather that just the order
#these plots will be identical even though order of colors changes.
rect_colors = rect_colors[c(2, 3, 1)]
text_colors = text_colors[c(3, 1, 2)]
p_clusters = add_cluster_annotation(assign_dt$cluster_id, rect_colors = rect_colors, text_colors = text_colors)

#specialized use as plot outside of heatmap
```
append_ynorm

p2 = assemble_heatmap_cluster_bars(plots = list(p_clusters, p_heat), rel_widths = c(1, 3))
cowplot::plot_grid(p1, p2, ncol = 1)

append_ynorm

append_ynorm

Description

see calc_norm_factors for normalization details.

Usage

append_ynorm(
  full_dt,
  value_ = "y",
  cap_value_ = "y_cap_value",
  norm_value_ = "y_norm",
  by1 = "id",
  by2 = "sample",
  aggFUN1 = max,
  aggFUN2 = function(x) quantile(x, 0.95),
  cap_dt = NULL,
  do_not_cap = FALSE,
  do_not_scaleTo1 = FALSE,
  force_append = FALSE
)

Arguments

full_dt a data.table, as returned by ssvFetch*(..., return_data.table = TRUE).
value_ character, attribute in full_dt to 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.
applyMovingAverage

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))

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

```r
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

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 returned by ssvFetchBigwig

Usage

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

Bcell_peaks  4 random peaks for paired-end data

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

Format
GRanges length 4

Details
this is included only for testing ssvFetchBamPE functions.

calc_norm_factors
calc_norm_factors

Description
Calculate normalization factors in a two step process:

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

Arguments
full_dt a data.table, as returned by ssvFetch*(..., return_data.table. = TRUE)
value_ character, attribute in full_dt to 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.
**centerAtMax**

**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 - i.e. 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))

<table>
<thead>
<tr>
<th>centerAtMax</th>
<th>centers profile of x and y. default is to center by region but across all samples.</th>
</tr>
</thead>
</table>

**Description**

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

**Usage**

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

**Arguments**

dt data.table
x_ the variable name of the x-values. default is 'x'
y_ the variable name of the y-values default is 'y'
by_ optionally, any variables that provide grouping to the data. default is none. see details.

view_size the size in x_ to consider for finding the max of y_. if length(view_size) == 1, range will be c(-view_size, view_size). if length(view_size) > 1, range will be range(view_size). default value of NULL uses complete range of x.

trim_to_valid valid x_ values are those with a set y_ value in all by_ combinations

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

x_precision numerical precision of x, default is 3.

replace_x logical, default TRUE. if TRUE x_ will be replaced with position relative to summit. if FALSE x_ will be preserved and x_summitPosition added.

Details

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>grs</td>
<td>Set of GRanges with inconsistent and/or incorrect size</td>
</tr>
<tr>
<td>fixed_size</td>
<td>The final width of each GRange returned.</td>
</tr>
</tbody>
</table>

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)
```

centerGRangesAtMax

Centers query GRanges at maximum signal in prof_dt.

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>prof_dt</td>
<td>a GRanges or data.table as returned by ssvFetch*.</td>
</tr>
<tr>
<td>qgr</td>
<td>the GRanges used to query ssvFetch* as the qgr argument.</td>
</tr>
<tr>
<td>x_</td>
<td>positional variable. Should almost always be the default, &quot;x&quot;.</td>
</tr>
<tr>
<td>y_</td>
<td>the signal value variable. Likely the default value of &quot;y&quot; but could be &quot;y_norm&quot; if append_ynorm was applied to data.</td>
</tr>
<tr>
<td>by_</td>
<td>region identifier variable. Should almost always be the default, &quot;id&quot;.</td>
</tr>
<tr>
<td>width</td>
<td>Desired width of final regions. Default is 1.</td>
</tr>
</tbody>
</table>

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)
```
chromHMM_demo_bw_states_gr

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

**Description**

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

**Format**

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

**Details**

part of chromHMM_demo_data

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

chromHMM_demo_chain_url

*URL to download hg19ToHg38 liftover chain from UCSC*

**Description**

URL to download hg19ToHg38 liftover chain from UCSC

**Format**

a character containing a URL

**Details**

file is gzipped .txt

part of chromHMM_demo_data
chromHMM state segmentation in the MCF7 cell line

Description

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

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

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

Details

Contains:

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

__chromHMM_demo_overlaps_gr

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

Description

overlap of MCF10A CTCF with MCF7 chromHMM states, hg38.

Format

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

part of `chromHMM_demo_data`

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

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

---

`chromHMM_demo_segmentation_url`

URL to download hg19 MCF7 chromHMM segmentation

---

Description

URL to download hg19 MCF7 chromHMM segmentation

Format

a character containing a URL

Details

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

part of `chromHMM_demo_data`

---

`chromHMM_demo_state_colors`

original state name to color mappings stored in segmentation bed

---

Description

original state name to color mappings stored in segmentation bed

Format

a named character vector mapping states to hex colors

Details

part of `chromHMM_demo_data`
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
clusteringKmeansNestedHclust

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 rowSums. 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.
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

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_mer_gr

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

Value

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

Examples

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

genome_gr = GRanges(dev_dat)
collapse_gr(genome_gr)

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

convert_collapsed_coord

Description

(preliminary implementation, sub-optimal)
copy_clust_info

Usage

convert_collapsed_coord(genome_gr, x)

Arguments

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

Details

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

Value

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

Examples

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

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

#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
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`

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**
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

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

Description

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

Format

A tidy GRanges of 2100 rows and 4 metadata columns
Details

part of CTCF_in_10a_data

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

---

easyLoad_bed 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 narrow-Peak 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**

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

---

easyLoad_FUN  

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

---

**Description**

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

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

**Arguments**

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

**Value**

a named list of results from `load_FUN`

**Examples**

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

---

easyLoad_IDRmerged  

**Description**

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

**Usage**

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

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

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

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
**easyLoad_seacr**

**Examples**

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

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

a named list of GRanges loaded from `file_paths`

**Examples**

```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_10a_overlaps_gr[1:5]
bam_file = system.file("extdata/test.bam", package = "seqsetvis", mustWork = TRUE)
raw_dt = ssvFetchBam(bam_file, qgr, return_unprocessed = TRUE)
expandCigar(raw_dt)
```

---

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

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

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_y_norm 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
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 output 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

```r
bam_file = system.file("extdata/test.bam",
  package = "seqsetvis")
qgr = CTCF_in_10a_overlaps_gr[1:5]
fragLen_calcStranded(bam_file, qgr)
# if plot is included, a list is returned, item 2 is the plot
fragLen_calcStranded(bam_file, qgr,
  include_plot_in_output = TRUE)[[2]]
```
fragLen_fromMacs2Xls  
parse fragLen from MACS2 output

Description
parse fragLen from MACS2 output

Usage
fragLen_fromMacs2Xls(macs2xls_file)

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

Value
numeric fragment length

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

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

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

Usage
gerReadLength(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.
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)

ggellipse

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 rcolors or hex colors or NULL. if null safeBrew of Dark2 is used
- `group_names`: character/factor names of color/fill groups. capital letters by default.
- `line_alpha`: numeric [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),
ycentres = c(2, 1, 1),
r = c(1, 2, 1),
fill_alpha = 0.3,
line_width = 2)
ggellipse(xcentres = c(1, 1, 2),
ycentres = c(2, 1, 1),
r = c(1, 2, 1),
fill_alpha = 0.3,
line_width = 2,
line_alpha = 0.5)
ggellipse(xcentres = c(1, 1, 2),
ycentres = c(2, 1, 1),
r = c(1, 2, 1),
fill_alpha = 0.3,
line_width = 2,
line_alpha = 0.5,
circle_colors = "blue"
```
harmonize_seqlengths

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

---

**Description**

ensures compatibility between seqlength of gr and bam_file based on header

**Usage**

```r
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**

```r
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

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

merge_clusters

Description

merge_clusters

Usage

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

Arguments

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

Value

data.table as output from `ssvSignalClustering`
Examples

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

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

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

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

---

**prepare_fetch_GRanges**  
prepares GRanges for windowed fetching.

**Description**

Deprecated and renamed as `prepare_fetch_GRanges_width`

**Usage**

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

- **qgr**: GRanges to prepare
- **win_size**: numeric window size for fetch
- **min_quantile**: numeric $[0,1]$, 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.

**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**

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

and named GRanges based on input qgr.

Examples

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

```r
prepare_fetch_GRanges_width

prepares GRanges for windowed fetching.
```

Description

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

Usage

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

---

reorder_clusters_hclust

```
reorder_clusters_hclust
```

Description

Applies hierarchical clustering to centroids of clusters to reorder.
Usage

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

Arguments

clust_dt data.table output from \texttt{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 \texttt{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

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

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

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

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

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

```r
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

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

safeBrew

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

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
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**

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

---

**Description**

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

**Usage**

```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
Description

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

Usage

```
split_cluster(
  clust_dt,  # data.table output from ssvSignalClustering
  to_split,  # Cluster to split.
  nclust = 2,  # Number of new clusters to create.
  row_ = "id",  # variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
  column_ = "x",  # variable mapped to column, likely bp position for ngs data. Default is "x" and works with ssvFetch* output.
  fill_ = "y",  # numeric variable to map to fill. Default is "y" and works with ssvFetch* output.
  facet_ = "sample",  # variable name to facet horizontally by. Default is "sample" and works with ssvFetch* output. Set to "" if data is not faceted.
  cluster_ = "cluster_id",  # variable name to use for cluster info. Default is "cluster_id".
  reapply_cluster_names = TRUE  # If TRUE, clusters will be renamed according to new order instead of their original names. Default is 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 contrast 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 absolute 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.
Value

GRanges with metadata columns describing consensus overlap of input grs.

Examples

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

ssvFactorizeMembTable

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

Description

see ssvMakeMembTable

Usage

ssvFactorizeMembTable(object)

Arguments

object

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

Value

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

Examples

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**

```r
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**

```r
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

binary heatmap indicating membership. heatmap is sorted by column left to right. change column order to reveal patterns

Description

binary heatmap indicating membership. heatmap is sorted by column left to right. change column order to reveal patterns

Usage

ssvFeatureBinaryHeatmap(
  object,
  raster_approximation = TRUE,
  true_color = "black",
  false_color = "#EFEFEE",
  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 re-draw 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 "#EFEFEE", 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.
**ssvFeatureEuler**

**Examples**

```r
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**

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

**Arguments**

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

**Value**

`ggplot` of `venneuler` results
**Examples**

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

**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])
```

**Description**

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

```r
ggplot::ggplot( 
  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

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

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
additinal 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'
name_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,
  return_unprocessed = FALSE,
  force_skip_centerFix = FALSE
)

Details

if qgr contains the range chr1:1-100 and win_size is 10, values from positions chr1 15,25,35,45,55,65,75,85, 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" nga{
  library(GenomicRanges)
  bam_f = system.file("extdata/test.bam",
    package = "seqsetvis", mustWork = TRUE)
  bam_files = c("a" = bam_f, "b" = bam_f)
  qgr = CTCF_in_10a_overlaps_gr[1:5]
  bw_gr = ssvFetchBam(bam_files, qgr, win_size = 10)
  bw_gr2 = ssvFetchBam(as.list(bam_files), qgr, win_size = 10)
  bw_dt = ssvFetchBam(bam_files, qgr, win_size = 10, return_data.table = TRUE)
}

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()
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 fetch
win_size 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).
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 &gt;= 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 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()
ssvFetchBamPE

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

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.
\texttt{win\_method} character. one of \texttt{c("sample", "summary")}. Determines if \texttt{viewGRangesWinSample\_dt} or \texttt{viewGRangesWinSummary\_dt} is used to represent each region in \texttt{qgr}.

\texttt{summary\_FUN} function. only relevant if \texttt{win\_method} is "summary". passed to \texttt{viewGRangesWinSummary\_dt}.

\texttt{fragLens} never used by \texttt{ssvFetchBamPE} Ignore.

\texttt{anchor} character, one of \texttt{c("center", "center\_unstranded", "left", "left\_unstranded")}

\texttt{names\_variable} The column name where unique names are stored.

\texttt{return\_data\_table} logical. If \texttt{TRUE} the internal data.table is returned instead of GRanges. Default is \texttt{FALSE}.

\texttt{max\_dupes} numeric \texttt{\geq 1}. duplicate reads by strandd start position over this number are removed, Default is \texttt{Inf}.

\texttt{n\_cores} integer number of cores to use.

\texttt{n\_region\_splits} integer number of splits to apply to \texttt{qgr}. The query GRanges will be split into this many roughly equal parts for increased parallelization. Default is \texttt{1}, no split.

\texttt{min\_isize} integer. Read pairs must have an isize greater than or equal to this value. Default is \texttt{1}.

\texttt{max\_isize} integer. Read pairs must have an isize less than or equal to this value. Default is \texttt{Inf}.

\texttt{return\_unprocessed} boolean. if \texttt{TRUE} returns read alignment in data.table. Default is \texttt{FALSE}.

\texttt{return\_fragSizes} boolean. if \texttt{TRUE} returns fragment sizes for all reads per region.

\texttt{force\_skip\_centerFix} boolean, if \texttt{TRUE} all query ranges will be used "as is". This is already the case by default if \texttt{win\_method \texttt{== "summary"}} but may have applications where \texttt{win\_method \texttt{== "sample"}}.

... passed to \texttt{Rsamtools::ScanBamParam()} Uses \texttt{mc\_cores} option if not supplied.

\textbf{Details}

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

\texttt{ssvFetchBamPE} iteratively calls \texttt{fetchWindowedBam\_single}. See \texttt{ssvFetchBamPE\_single} for more info.

if \texttt{qgr} contains the range \texttt{chr1:1-100} and \texttt{win\_size} is \texttt{10}, values from positions \texttt{chr1 5,15,25...85, and 95} will be retrieved from \texttt{bw\_file}

\textbf{Value}

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

```r
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

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

- `bam_f` character or BamFile to load
- `qgr` GRanges regions to fetch
- `win_size` numeric >=1. pileup grabbed every win_size bp for win_method sample. If win_method is summary, this is the number of windows used (confusing, sorry).
- `win_method` character. one of c("sample", "summary"). Determines if `viewGRangesWinSample_dt` or `viewGRangesWinSummary_dt` is used to represent each region in qgr.
- `summary_FUN` function. only relevant if win_method is "summary". passed to `viewGRangesWinSummary_dt`.
- `anchor` character, one of c("center", "center_unstranded", "left", "left_unstranded")
- `return_data.table` logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.
- `max_dupes` numeric >= 1. duplicate reads by strand and start position over this number are removed, Default is Inf.
- `min_isize` integer. Read pairs must have an isize greater than or equal to this value. Default is 1.
- `max_isize` integer. Read pairs must have an isize less than or equal to this value. Default is Inf.
- `return_unprocessed` boolean. if TRUE returns read alignment in data.table. Default is FALSE.
- `return_fragSizes` boolean. if TRUE returns fragment sizes for all reads per region.
- `force_skip_centerFix` boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".
- ... passed to Rsamtools::ScanBamParam()

**Value**

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

---

**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 additdal 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)
```

**ssvFetchGRanges**

**Arguments**

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

**Details**

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

**Value**

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

---

**ssvFetchGRanges**

*Fetch coverage values for a list of GRanges.*

**Description**

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

**Usage**

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

 Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>grs</td>
<td>a list of GRanges for which to calculate coverage.</td>
</tr>
<tr>
<td>qgr</td>
<td>Set of GRanges to query. For valid results the width of each interval should</td>
</tr>
<tr>
<td></td>
<td>be identical and evenly divisible by win_size.</td>
</tr>
<tr>
<td>file_attribs</td>
<td>data.frame (1 row per item in grs) containing attributes to append to results.</td>
</tr>
<tr>
<td>unique_names</td>
<td>The column name where unique_names are stored. Default is 'sample'</td>
</tr>
<tr>
<td>names_variable</td>
<td>The column name where unique_names are stored. Default is 'sample'</td>
</tr>
<tr>
<td>win_size</td>
<td>The window size that evenly divides widths in qgr.</td>
</tr>
<tr>
<td>win_method</td>
<td>character. one of c(&quot;sample&quot;, &quot;summary&quot;). Determines if viewGRangesWinSample_dt</td>
</tr>
<tr>
<td></td>
<td>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>target_strand</td>
<td>character. if one of &quot;+&quot; or &quot;:&quot;, reads are filtered to match. ignored if any other value.</td>
</tr>
<tr>
<td>use_coverage</td>
<td>boolean or NULL, if TRUE, query regions are scored by the number of intervals overlapping. Default of NULL checks if attrib_var is &quot;score&quot; and uses coverage if so.</td>
</tr>
<tr>
<td>attrib_var</td>
<td>character, column in mcols of GRanges to pull values from. Default of &quot;score&quot;</td>
</tr>
<tr>
<td></td>
<td>is compatible with internal coverage calculation or bedgraph-like files.</td>
</tr>
<tr>
<td>fill_value</td>
<td>numeric or character value to use where queried regions are empty. Default is</td>
</tr>
<tr>
<td></td>
<td>0 and appropriate for both calculated coverage and bedgraph/bigwig like files.</td>
</tr>
<tr>
<td></td>
<td>Will automatically switch to &quot;MISSING&quot; if data is guessed to be qualitative.</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>n_cores</td>
<td>integer number of cores to use. Uses mc.cores option if not supplied.</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

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 additital columns will be used as metadata.
- **qgr**: GRanges of intervals to return from each file
- **unique_names**: unique file ids for each file in file_paths. Default is names of file_paths vector
- **names_variable**: character, variable name for column containing unique_names entries. Default is "sample"
- **file_attribs**: optional data.frame/data.table with one row per item in file paths. Each column will be a variable added to final tidy output.
- **win_size**: numeric/integer window size resolution to load signal at. Default is 50.
- **win_method**: character. one of c("sample", "summary"). Determines if `viewGRangesWinSample_dt` or `viewGRangesWinSummary_dt` is used to represent each region in qgr.
return_data.table  
logical. If TRUE data.table is returned instead of GRanges, the default.

load_signal  
function taking f, nam, and qgr arguments. f is from file_paths, nam is from  
unique_names, and qgr is qgr. See details.

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

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

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

Details

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

Value

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

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)
**svMakeMembTable**

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

**Description**

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

- list of character vectors input
- GRangesList input
- GRanges with mcols input
- DataFrame input
- matrix of logicals, membership table
- data.frame input, final output The final method for all inputs, checks column names and returns logical matrix

**Usage**

```r
svMakeMembTable(object)
```

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

## S4 method for signature 'list'

```r
svMakeMembTable(object)
```

## S4 method for signature 'GRangesList'

```r
svMakeMembTable(object)
```

## S4 method for signature 'GRanges'

```r
svMakeMembTable(object)
```

## S4 method for signature 'DataFrame'

```r
svMakeMembTable(object)
```

## S4 method for signature 'matrix'

```r
svMakeMembTable(object)
```

## S4 method for signature 'data.frame'

```r
svMakeMembTable(object)
```

**Arguments**

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

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

**Examples**

```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)
```

---

**ssvOverlapIntervalSets**

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

**Description**

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

**Usage**

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

**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
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

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

ssvSignalBandedQuantiles

plot profiles from bigwigs

Description

plot profiles from bigwigs

Usage

ssvSignalBandedQuantiles(
bw_data,
y_ = "y",
x_ = "x",
by_ = "fake",
hsv_reverse = FALSE,
hsv_saturation = 1,
hsv_value = 1,
hsv_grayscale = FALSE,
hsv_hue_min = 0,
hsv_hue_max = 0.7,
hsv_symmetric = FALSE,
n_quantile = 18,
quantile_min = 0.05,
quantile_max = 0.95,
return_data = FALSE
)

plot profiles from bigwigs
**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")
```
**ssvSignalClustering**  
*Clustering as for a heatmap.* This is used internally by [ssvSignalHeatmap](#) but can also be run before calling ssvSignalHeatmap for greater control and access to clustering results directly.

---

**Description**

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

**Usage**

```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 facetted.

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

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

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

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

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

within_order_strategy one of "hclust", "sort", "right", "left", "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.ClusterBars for an alternative with more control over where the cluster bars appear.

Usage

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

Arguments

bw_data a GRanges or data.table of bigwig signal. As returned from ssvFetchBam and ssvFetchBigwig
nclust number of clusters
perform_clustering should clustering be done? default is auto. auto considers if row_ has been ordered by being a factor and if cluster_ is a numeric.
row_ variable name mapped to row, likely id or gene name for ngs data. Default is "id" and works with ssvFetch* output.
ssvSignalHeatmap

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, faceted by sample

Examples

#the simplest use
goingToHeatmap(CTCF_in_10a_profiles_gr)
goingToHeatmap(CTCF_in_10a_profiles_gr, show_cluster_bars = FALSE)

#clustering can be done manually beforehand
clust_dt = goingToClustering(CTCF_in_10a_profiles_gr, nclust = 3)
goingToHeatmap(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",
```

**Value**

ggplot heatmap of signal profiles, facetted by 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.
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

```r
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`

Examples

```r
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"
)
```
**color_table**
data.frame with 2 columns, one of which must be named "group" and gets mapped to color. The other column must be the same as by_ parameter and is used for merging.

**value_variable**
variable name that stores numeric values for plotting, default is "y"

**xy_variable**
variable name that stores sample, must contain entries for x_name and y_name

**value_function**
a function to apply to value_variable in all combinations of by_ per x_name and y_name

**by_**
variables that store individual measurement ids

**plot_type**
standard or volcano, default is "standard"

**show_help**
if TRUE overlay labels to aid plot interpretation, default is FALSE

**fixed_coords**
if TRUE coordinate system is 1:1 ratio, default is TRUE

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

---

### Value

ggplot of points comparing signal from 2 samples

### Examples

```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)
```

---

### Description

ssv_mclapply

### Usage

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

X For pbsapply and pblapply, a vector (atomic or list) or an expressions vector
(other objects including classed objects will be coerced by as.list.) For pbapply
an array, including a matrix. For pbtapply an R object for which a split method
exists. Typically vector-like, allowing subsetting with "[".

FUN The function to be applied to each element of X: see apply, sapply, and lapply.
In the case of functions like +, ' 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 down-
stream 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.

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()
    bw_file = system.file("extdata/MCF10A_CTCF_FE_random100.bw",
                          package = "seqsetvis")

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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

```r
viewGRangesWinSummary_dt(
  score_gr,  # GRanges with a "score" metadata column.
  qgr,       # regions to view by window.
  n_tiles = 100,  # numeric >= 1, the number of tiles to use for every region in `qgr`.
  attrib_var = "score",  # character name of attribute to pull data from. Default is "score", compatible with with bigWigs or bam coverage.
  attrib_type = NULL,  # 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 = 0,  # 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 = c("center", "center_unstranded", "left", "left_unstranded")[1],  # character. controls how x value is derived from position for each region in `qgr`. 0 may be the left side or center. If not unstranded, x coordinates are flipped for (-) strand. One of c("center", "center_unstranded", "left", "left_unstranded"). Default is "center".
  summary_FUN = stats::weighted.mean
)
```

### Arguments

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

Details

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

Value
data.table that is GRanges compatible

Examples

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

Description

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

Usage

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

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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