

# Package ‘seqsetvis’

October 17, 2020

**Type** Package

**Title** Set Based Visualizations for Next-Gen Sequencing Data

**Version** 1.8.0

**Description** seqsetvis enables the visualization and analysis of multiple genomic samples. 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 or bam pileups).

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**Encoding** UTF-8

**LazyData** true

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

**Depends** R (>= 3.5), ggplot2

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**R topics documented:**

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---

seqsetvis-package	<i>easy awesome peak set vis TESTING seqsetvis allows you to...</i>
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---

## Description

2 steps [ssvOverlapIntervalSets](#). [ssvFetchBigwig](#). Otherwise refer to the vignettes to see

## Author(s)

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

---

.expand_cigar_dt	<i>Expand intermediate bam fetch by cigar codes</i>
------------------	---

---

## 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
```

*Expand intermediate bam fetch by cigar codes*

---

**Description**

see [sam specs](#) for cigar details

**Usage**

```
.expand_cigar_dt_recursive(cigar_dt)
```

**Arguments**

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

**Value**

data.table with cigar entries expanded

---

```
.rm_dupes
```

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

---

**Description**

```
flag = scanBamFlag(isDuplicate = FALSE)
```

**Usage**

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

**Arguments**

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

**Value**

reads\_dt with duplicated reads over max\_dupes removed

---

.rm_dupesPE	<i>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</i>
-------------	--

---

**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

---

append_ynorm	<i>append_ynorm</i>
--------------	---------------------

---

**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,
  force_append = FALSE
)
```

**Arguments**

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

**Value**

data.table, full\_dt with cap\_value\_ and norm\_value\_ values appended.

**Examples**

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

---

applySpline	<i>applies a spline smoothing to a tidy data.table containing x and y values.</i>
-------------	---

---

**Description**

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

**Usage**

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

**Arguments**

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

## Details

by\_ is quite powerful. If by\_ = c('gene\_id', 'sample\_id'), splines will be calculated individually for each gene in each sample. alternatively if by\_ = c('gene\_id')

## Value

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

## See Also

[ssvFetchBigwig](#)

## Examples

```
#data 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))
```

---

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 normalzie.
cap_value_	character, new attribute name specifying values to cap to.
by1	character vector, specifies attributes relevant to step 1.
by2	character vector, specifies attributes relevant to step 1 and 2.
aggFUN1	function called on value_ with by = c(by1, by2) in step 1.
aggFUN2	function called on result of aggFUN1 with by = by2 in step 2.

## Details

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

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

## Value

data.table mapping by2 to cap\_value\_.

## Examples

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



---

centerAtMax	<i>centers profile of x and y. default is to center by region but across all samples.</i>
-------------	---

---

### Description

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

### Usage

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

### Arguments

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

### Details

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

### Value

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

**Examples**

```

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

```

---

centerFixedSizeGRanges

*Transforms set of GRanges to all have the same size.*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

Set of GRanges after resizing all input GRanges, either shortened or lengthened as required to match fixed\_size

**Examples**

```

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

```

---

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\_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](#)

---

chromHMM\_demo\_state\_total\_widths

*state name to total width mappings, hg38*

---

**Description**

state name to total width mappings, hg38

**Format**

named numeric of total widths per state

**Details**

part of [chromHMM\\_demo\\_data](#)

---

clusteringKmeans	<i>perform kmeans clustering on matrix rows and return reordered matrix along with order matched cluster assignments. clusters are sorted using hclust on centers</i>
------------------	---

---

### 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, seed = NULL)
```

### Arguments

mat	numeric matrix to cluster
nclust	the number of clusters
seed	DEPRECATED. Call set.seed() prior to this function to allow reproducibility.

### Value

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

### Examples

```
dt = data.table::copy(CTCF_in_10a_profiles_dt)
mat = data.table::dcast(dt, id ~ sample + x, value.var = "y" )
rn = mat$id
mat = as.matrix(mat[,-1])
rownames(mat) = rn
clust_dt = clusteringKmeans(mat, nclust = 3)
dt = merge(dt, clust_dt)
dt$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 = c("hclust", "sort")[2],
  seed = NULL
)
```

**Arguments**

mat	A wide format matrix
nclust	the number of clusters
within_order_strategy	one of "hclust" or "sort". if hclust, hierarchical clustering will be used. if sort, a simple decreasing sort of rosSums.
seed	passed to set.seed() to allow reproducibility

**Value**

data.table with 2 columns of cluster info. id column corresponds with input matrix rownames and is sorted within each cluster using hierarchical clustering group column indicates cluster assignment

**Examples**

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

---

col2hex	<i>converts a valid r color name ("black", "red", "white", etc.) to a hex value</i>
---------	---

---

**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	<i>collapse_gr</i>
-------------	--------------------

---

**Description**

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

**Usage**

```
collapse_gr(genome_gr)
```

**Arguments**

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

**Value**

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

**Examples**

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

genome_gr = GRanges(dev_dat)
collapse_gr(genome_gr)

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



---

```
convert_collapsed_coord
      convert_collapsed_coord
```

---

### Description

(preliminary implementation, sub-optimal)

### Usage

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

### Arguments

`genome_gr` non-contiguous regions to collapse a la [collapse\\_gr](#)  
`x` numeric, positions within `genome_gr` to convert to collapsed coordinates.

### Details

see [collapse\\_gr](#) for explanation of intended uses. this function translates all values of `x` from original genomic coordinates to new coordinate space created by [collapse\\_gr](#).

### Value

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

### Examples

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

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

---

```
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**

<code>bam_file</code>	character. Path to .bam file, must have index at .bam.bai.
<code>query_gr</code>	GRanges. Regions to calculate cross correlation for.
<code>max_dupes</code>	integer. Duplicate reads above this value will be removed.
<code>fragment_sizes</code>	integer. fragment size range to search for maximum correlation.
<code>read_length</code>	integer. Any values outside <code>fragment_range</code> that must be searched. If not supplied will be determined from <code>bam_file</code> . Set as NA to disable this behavior.
<code>flip_strand</code>	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.
<code>...</code>	arguments passed to <code>ScanBamParam</code>

**Value**

named list of results

**Examples**

```

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

```

---

CTCF\_in\_10a\_bigWig\_urls

*FTP URL path for vignette data.*

---

**Description**

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

**Format**

named character vector of length 3

**Details**

part of [CTCF\\_in\\_10a\\_data](#)

---

CTCF\_in\_10a\_data      *CTCF ChIP-seq in breast cancer cell lines*

---

**Description**

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

Data from GEO series [GSE98551](#) is from the publication [Fritz AJ et al. 2018](#)

**Details**

Contains:

- [CTCF\\_in\\_10a\\_overlaps\\_gr](#)
- [CTCF\\_in\\_10a\\_profiles\\_dt](#)
- [CTCF\\_in\\_10a\\_bigWig\\_urls](#)
- [CTCF\\_in\\_10a\\_narrowPeak\\_urls](#)

---

CTCF\_in\_10a\_narrowPeak\_grs  
*list of GRanges that results in 100 random subset when overlapped*

---

**Description**

list of GRanges that results in 100 random subset when overlapped

**Format**

named character vector of length 3

**Details**

part of [CTCF\\_in\\_10a\\_data](#)

---

CTCF\_in\_10a\_narrowPeak\_urls  
*FTP URL path for vignette data. from*

---

**Description**

macs2 peak calls for CTCF ChIP-seq in a MCF10A progression model. See GEO series [GSE98551](#) for details.

**Format**

named character vector of length 3

**Details**

part of [CTCF\\_in\\_10a\\_data](#)

---

CTCF\_in\_10a\_overlaps\_gr

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

---

### Description

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

### Format

GenomicRanges with 3 metadata columns of membership table

### Details

See GEO series GSE98551 for details.

part of [CTCF\\_in\\_10a\\_data](#)

---

CTCF\_in\_10a\_profiles\_dt

*Profiles for 100 randomly selected regions from overlapping CTCF peaks in 10a cell ChIP-seq Results from fetching bigwigs with CTCF\_in\_10a\_overlaps\_gr.*

---

### Description

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

### Format

A tidy data.table of 2100 rows and 9 columns

### Details

part of [CTCF\\_in\\_10a\\_data](#)

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

---

 CTCF\_in\_10a\_profiles\_gr

*Profiles for 100 randomly selected regions from overlapping CTCF peaks in 10a cell ChIP-seq Results from CTCF\_in\_10a\_overlaps\_gr*

---

### Description

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

### Format

A tidy GRanges of 2100 rows and 4 metadata columns

### Details

part of [CTCF\\_in\\_10a\\_data](#)

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

---

 easyLoad\_bed

*easyLoad\_bed takes a character vector of file paths to bed plus files and returning named list of GRanges. Mainly a utility function for loading MACS2 narrowPeak and broadPeak.*

---

### Description

easyLoad\_bed takes a character vector of file paths to bed plus files and returning named list of GRanges. Mainly a utility function for loading MACS2 narrowPeak and broadPeak.

### Usage

```
easyLoad_bed(file_paths, file_names = NULL, extraCols = character())
```

### 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().                           |

### 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	<i>easyLoad_broadPeak takes a character vector of file paths to narrowPeak files from MACS2 and returns a named list of GRanges.</i>
--------------------	--

---

**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)
```

**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.

**Value**

a named list of GRanges loaded from file\_paths

**Examples**

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

---

easyLoad_narrowPeak	<i>easyLoad_narrowPeak takes a character vector of file paths to narrowPeak files from MACS2 and returns a named list of GRanges.</i>
---------------------	---

---

**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)
```

**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.

**Value**

a named list of GRanges loaded from `file_paths`

**Examples**

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

---

expandCigar

*Expand cigar codes to GRanges*

---

**Description**

see [sam specs](#) for cigar details

**Usage**

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

**Arguments**

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

```
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	<i>fetch a bam file pileup with the ability to consider read extension to fragment size (fragLen)</i>
----------	---

---

### Description

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

### Usage

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

### Arguments

bam_f	character or BamFile to load
qgr	GRanges regions to fetchs
fragLen	numeric, NULL, or NA. if numeric, supplied value is used. if NULL, value is calculated with fragLen_calcStranded (default) if NA, raw bam pileup with no cross strand shift is returned.
target_strand	character. if one of "+" or "-", reads are filtered to match. ignored if any other value.
max_dupes	numeric >= 1. duplicate reads by strandd start position over this number are removed, Default is Inf.
splice_strategy	character, one of c("none", "ignore", "add", "only"). Default is "none" and split read alignments are 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.



---

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

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

---

```
fragLen_fromMacs2Xls  parse fragLen from MACS2 output
```

---

**Description**

parse fragLen from MACS2 output

**Usage**

```
fragLen_fromMacs2Xls(macs2xls_file)
```

**Arguments**

macs2xls\_file character. an xls file output by MACS2 to parse frag length from

**Value**

numeric fragment length

**Examples**

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

---

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

---

**Description**

determine the most common read length for input bam\_file. uses 50 randomly selected regions from query\_gr. If fewer than 20 reads are present, loads all of query\_gr.

**Usage**

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

**Arguments**

bam\_file indexed bam file  
 query\_gr GRanges to read from bam file

**Value**

numeric of most common read length.

---

ggellipse	<i>returns a ggplot with ellipses drawn using specified parameters used by ssvFeatureVenn and ssvFeatureEuler</i>
-----------	---

---

### Description

uses eulerr's non-exported ellipse drawing coordinate function

### Usage

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

### Arguments

xcentres	numeric x-coord of centers of ellipses
ycentres	numeric y-coord of centers of ellipses, must have same length as xcentres
r	numeric radius1 of ellipse, must have length of 1 or match length of xcentres
r2	numeric radius2 of ellipse, must have length of 1 or match length of xcentres. same as r by default.
phi	numeric phi of ellipse, must have length of 1 or match length of xcentres. 0 by default.
circle_colors	character of rcolors or hex colors or NULL. if null safeBrew of Dark2 is used
group_names	character/factor names of color/fill groups. capital letters by default.
line_alpha	numeric [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**

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

---

```
harmonize_seqlengths  harmonize_seqlengths
```

---

**Description**

ensures compatibility between seqlength of gr and bam\_file based on header

**Usage**

```
harmonize_seqlengths(gr, bam_file)
```

**Arguments**

gr	GRanges, object to harmonize seqlengths for
bam_file	character, a path to a valid bam file

**Value**

gr with seqlengths matching bam\_file

**Examples**

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

---

prepare\_fetch\_GRanges *prepares GRanges for windowed fetching.*

---

### Description

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

### Usage

```
prepare_fetch_GRanges(
  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.

### Examples

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

---

quantileGRangesWidth *Quantile width determination strategy*

---

### Description

Returns the lowest multiple of win\_size greater than min\_quantile quantile of width(qgr)

### Usage

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

### Arguments

qgr                    GRanges to calculate quantile width for  
min\_quantile        numeric [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

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

---

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

---

### Description

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

### Usage

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

### Arguments

n                         integer value of number of colors to make palette for  
pal                        palette recognized by RColorBrewer

### Value

a character vector of hex coded colors of length n from the color brewer palette pal

**Examples**

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

---

set_list2memb	<i>convert a list of sets, each list item should be a character vector denoting items in sets</i>
---------------	---

---

**Description**

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

**Usage**

```
set_list2memb(set_list)
```

**Arguments**

set\_list            a list of character vectors. default names will be added if missing

**Value**

converts list of characters/numeric to membership table matrix

---

shift_anchor	<i>orients the relative position of x's zero value and extends ranges to be contiguous</i>
--------------	--

---

**Description**

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

**Usage**

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

**Arguments**

score\_dt            data.table, GRanges() sufficient  
window\_size        numeric, window size used to generate score\_dt  
anchor              character, one of c("center", "center\_unstranded", "left", "left\_unstranded")

**Value**

score\_dt with x values shifted appropriately and start and end extended to make ranges contiguous

---

`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

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

### 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.

`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 bar plot of set sizes

**Examples**

```
ssvFeatureBars(list(1:3, 2:6))
ssvFeatureBars(CTCF_in_10a_overlaps_gr)
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 = FALSE,
  true_color = "black",
  false_color = "#EFEFEF",
  raster_width_min = 1000,
  raster_height_min = 1000,
  return_data = FALSE
)
```

**Arguments**

object	passed to ssvMakeMembTable
raster_approximation	If TRUE, instead of standard ggplot, write temporary raster png image and 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 "#EFEFEF", a gray.
raster_width_min	raster width will be minimum multiple of number of columns over this number. ignored if raster_approximation is FALSE.
raster_height_min	raster height will be minimum multiple of number of rows over this number ignored if raster_approximation is FALSE
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

**Value**

ggplot using geom\_tile of membership table sorted from left to right.

**Examples**

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

---

ssvFeatureEuler

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


---

**Description**

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

**Usage**

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

**Arguments**

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**

```

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

```

---

ssvFeaturePie	<i>pie plot of set sizes</i>
---------------	------------------------------

---

**Description**

pie plot of set sizes

**Usage**

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

**Arguments**

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

**Value**

ggplot pie graph of set sizes

**Examples**

```

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

```

---

ssvFeatureVenn	<i>ggplot implementation of vennDiagram from limma package. currently limited at 3 sets</i>
----------------	---

---

**Description**

ggplot implementation of vennDiagram from limma package. currently limited at 3 sets

**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,
  n_points = 200,
  return_data = FALSE
)

```

**Arguments**

<code>object</code>	will be passed to <a href="#">ssvMakeMembTable</a> for conversion to membership matrix
<code>group_names</code>	useful if names weren't provided or were lost in creating membership matrix
<code>counts_txt_size</code>	font size for count numbers
<code>counts_as_labels</code>	if TRUE, <code>geom_label</code> is used instead of <code>geom_text</code> . can be easier to read.
<code>show_outside_count</code>	if TRUE, items outside of all sets are counted outside. can be confusing.
<code>line_width</code>	uses size aesthetic to control line width of circles.
<code>circle_colors</code>	colors to use for circle line colors. Uses Dark2 set from RColorBrewer by default.
<code>fill_alpha</code>	alpha value to use for fill, defaults to .3.
<code>line_alpha</code>	numeric [0,1], alpha value for circle line
<code>counts_color</code>	character. single color to use for displaying counts
<code>n_points</code>	integer. number of points to approximate circle with. default is 200.
<code>return_data</code>	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**

```

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

```

---

ssvFetchBam	<i>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</i>
-------------	---

---

## Description

ssvFetchBam iteratively calls `fetchWindowedBam.single`. See [ssvFetchBam.single](#) for more info.

## Usage

```
ssvFetchBam(
  file_paths,
  qgr,
  unique_names = 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],
  names_variable = "sample",
  return_data.table = FALSE,
  max_dupes = Inf,
  splice_strategy = c("none", "ignore", "add", "only", "splice_count")[1],
  n_cores = getOption("mc.cores", 1),
  return_unprocessed = FALSE,
  force_skip_centerFix = FALSE,
  ...
)
```

## Arguments

<code>file_paths</code>	character vector of <code>file_paths</code> to load from. Alternatively, <code>file_paths</code> can be a <code>data.frame</code> or <code>data.table</code> whose first column is a character vector of paths and additional columns will be used as metadata.
<code>qgr</code>	Set of GRanges to query. For valid results the width of each interval should be identical and evenly divisible by <code>win_size</code> .
<code>unique_names</code>	names to use in final <code>data.table</code> to designate source bigwig. Default is 'sample'
<code>win_size</code>	The window size that evenly divides widths in <code>qgr</code> .
<code>win_method</code>	character. one of <code>c("sample", "summary")</code> . Determines if <a href="#">viewGRangesWinSample_dt</a> or <a href="#">viewGRangesWinSummary_dt</a> is used to represent each region in <code>qgr</code> .
<code>summary_FUN</code>	function. only relevant if <code>win_method</code> is "summary". passed to <a href="#">viewGRangesWinSummary_dt</a> .
<code>fragLens</code>	numeric. The fragment length to use to extend reads. The default value "auto" causes an automatic calculation from 100 regions in <code>qgr</code> . 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")

names\_variable The column name where unique\_names are stored.

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

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

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.

n\_cores integer number of cores to use. Uses mc.cores option if not supplied.

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

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

... passed to Rsamtools::ScanBamParam()

### Details

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

### Value

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

### Examples

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

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

---

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

---

## Description

fetch a windowed version of a bam file, returns GRanges

## Usage

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

## Arguments

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

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

flip\_strand if TRUE, strand alignment is flipped prior to fragLen extension. Default is FALSE.

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

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

... passed to Rsamtools::ScanBamParam()

### Value

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

---

ssvFetchBamPE

*ssvFetchBam for paired-end ChIP-seq files.*

---

### 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,
  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),
  min_isize = 1,
  max_isize = Inf,
  return_unprocessed = FALSE,
  force_skip_centerFix = FALSE,
  ...
)
```



**Arguments**

<code>file_paths</code>	character vector of <code>file_paths</code> to load from. Alternatively, <code>file_paths</code> can be a <code>data.frame</code> or <code>data.table</code> whose first column is a character vector of paths and additional columns will be used as metadata.
<code>qgr</code>	Set of GRanges to query. For valid results the width of each interval should be identical and evenly divisible by <code>win_size</code> .
<code>unique_names</code>	names to use in final <code>data.table</code> to designate source bigwig. Default is 'sample'
<code>win_size</code>	The window size that evenly divides widths in <code>qgr</code> .
<code>win_method</code>	character. one of <code>c("sample", "summary")</code> . Determines if <code>viewGRangesWinSample_dt</code> or <code>viewGRangesWinSummary_dt</code> is used to represent each region in <code>qgr</code> .
<code>summary_FUN</code>	function. only relevant if <code>win_method</code> is "summary". passed to <code>viewGRangesWinSummary_dt</code> .
<code>anchor</code>	character, one of <code>c("center", "center_unstranded", "left", "left_unstranded")</code>
<code>names_variable</code>	The column name where <code>unique_names</code> are stored.
<code>return_data.table</code>	logical. If TRUE the internal <code>data.table</code> is returned instead of GRanges. Default is FALSE.
<code>max_dupes</code>	numeric $\geq 1$ . duplicate reads by strand and start position over this number are removed, Default is Inf.
<code>n_cores</code>	integer number of cores to use.
<code>min_isize</code>	integer. Read pairs must have an <code>isize</code> greater than or equal to this value. Default is 1.
<code>max_isize</code>	integer. Read pairs must have an <code>isize</code> less than or equal to this value. Default is Inf.
<code>return_unprocessed</code>	boolean. if TRUE returns read alignment in <code>data.table</code> . Default is FALSE.
<code>force_skip_centerFix</code>	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if <code>win_method == "summary"</code> but may have applications where <code>win_method == "sample"</code> .
<code>...</code>	passed to <code>Rsamtools::ScanBamParam()</code> Uses <code>mc.cores</code> option if not supplied.

**Details**

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

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

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

**Value**

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

**Examples**

```

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

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

```

---

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

---

**Description**

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

**Usage**

```

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

```

**Arguments**

bam_f	character or BamFile to load
qgr	GRanges regions to fetchs
win_size	numeric >=1. pileup grabbed every win_size bp for win_method sample. If win_method is summary, this is the number of windows used (confusing, sorry).

win_method	character. one of c("sample", "summary"). Determines if <a href="#">viewGRangesWinSample_dt</a> or <a href="#">viewGRangesWinSummary_dt</a> is used to represent each region in qgr.
summary_FUN	function. only relevant if win_method is "summary". passed to <a href="#">viewGRangesWinSummary_dt</a> .
anchor	character, one of c("center", "center_unstranded", "left", "left_unstranded")
return_data.table	logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.
max_dupes	numeric >= 1. duplicate reads by strandd start position over this number are removed, Default is Inf.
min_isize	integer. Read pairs must have an isize greater than or equal to this value. Default is 1.
max_isize	integer. Read pairs must have an isize less than or equal to this value. Default is Inf.
return_unprocessed	boolean. if TRUE returns read alignment in data.table. Default is FALSE.
force_skip_centerFix	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".
...	passed to Rsamtools::ScanBamParam()

**Value**

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

---

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

---

**Description**

ssvFetchBigwig iteratively calls [fetchWindowedBigwig.single](#). See [ssvFetchBigwig.single](#) for more info.

**Usage**

```
ssvFetchBigwig(
  file_paths,
  qgr,
  unique_names = NULL,
  names_variable = "sample",
  win_size = 50,
  win_method = c("sample", "summary")[1],
  summary_FUN = stats::weighted.mean,
  anchor = c("left", "left_unstranded", "center", "center_unstranded")[3],
  return_data.table = FALSE,
  n_cores = getOption("mc.cores", 1),
  force_skip_centerFix = FALSE
)
```

**Arguments**

<code>file_paths</code>	character vector of <code>file_paths</code> to load from. Alternatively, <code>file_paths</code> can be a <code>data.frame</code> or <code>data.table</code> whose first column is a character vector of paths and additional columns will be used as metadata.
<code>qgr</code>	Set of GRanges to query. For valid results the width of each interval should be identical and evenly divisible by <code>win_size</code> .
<code>unique_names</code>	names to use in final <code>data.table</code> to designate source bigwig.
<code>names_variable</code>	The column name where <code>unique_names</code> are stored. Default is 'sample'
<code>win_size</code>	The window size that evenly divides widths in <code>qgr</code> .
<code>win_method</code>	character. one of <code>c("sample", "summary")</code> . Determines if <code>viewGRangesWinSample_dt</code> or <code>viewGRangesWinSummary_dt</code> is used to represent each region in <code>qgr</code> .
<code>summary_FUN</code>	function. only relevant if <code>win_method</code> is "summary". passed to <code>viewGRangesWinSummary_dt</code> .
<code>anchor</code>	character, one of <code>c("center", "center_unstranded", "left", "left_unstranded")</code>
<code>return_data.table</code>	logical. If TRUE the internal <code>data.table</code> is returned instead of GRanges. Default is FALSE.
<code>n_cores</code>	integer number of cores to use. Uses <code>mc.cores</code> option if not supplied.
<code>force_skip_centerFix</code>	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if <code>win_method == "summary"</code> but may have applications where <code>win_method == "sample"</code> .

**Details**

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

**Value**

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

**Examples**

```
if(Sys.info()['sysname'] != "Windows"){
  library(GenomicRanges)
  bw_f = system.file("extdata/test_loading.bw",
    package = "seqsetvis", mustWork = TRUE)
  bw_files = c("a" = bw_f, "b" = bw_f)
  qgr = GRanges("chrTest", IRanges(1, 30))
  bw_gr = ssvFetchBigwig(bw_files, qgr, win_size = 10)
  bw_gr2 = ssvFetchBigwig(as.list(bw_files), qgr, win_size = 10)

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

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Details

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

## Value

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

---

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

---

### Description

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

### Usage

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

### Arguments

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

attrib_var	character, column in mcols of GRanges to pull values from. Default of "score" is compatible with internal coverage calculation or bedgraph-like files.
fill_value	numeric or character value to use where queried regions are empty. Default is 0 and appropriate for both calculated coverage and bedgraph/bigwig like files. Will automatically switch to "MISSING" if data is guessed to be qualitative.
anchor	character, one of c("center", "center_unstranded", "left", "left_unstranded")
return_data.table	logical. If TRUE the internal data.table is returned instead of GRanges. Default is FALSE.
n_cores	integer number of cores to use. Uses mc.cores option if not supplied.
force_skip_centerFix	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if win_method == "summary" but may have applications where win_method == "sample".

### Value

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

### Examples

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

---

ssvFetchSignal	<i>signal loading framework</i>
----------------	---------------------------------

---

### Description

Does nothing unless load\_signal is overridden to carry out reading data from file\_paths (likely via the appropriate ssvFetch\* function, ie. [ssvFetchBigwig](#) or [ssvFetchBam](#))

### Usage

```
ssvFetchSignal(
  file_paths,
  qgr,
  unique_names = NULL,
  names_variable = "sample",
  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),
  force_skip_centerFix = FALSE
)
```

**Arguments**

<code>file_paths</code>	character vector of <code>file_paths</code> to load from. Alternatively, <code>file_paths</code> can be a <code>data.frame</code> or <code>data.table</code> whose first column is a character vector of paths and additional columns will be used as metadata.
<code>qgr</code>	<code>GRanges</code> of intervals to return from each file
<code>unique_names</code>	unique file ids for each file in <code>file_paths</code> . Default is names of <code>file_paths</code> vector
<code>names_variable</code>	character, variable name for column containing <code>unique_names</code> entries. Default is "sample"
<code>win_size</code>	numeric/integer window size resolution to load signal at. Default is 50.
<code>win_method</code>	character. one of <code>c("sample", "summary")</code> . Determines if <code>viewGRangesWinSample_dt</code> or <code>viewGRangesWinSummary_dt</code> is used to represent each region in <code>qgr</code> .
<code>return_data.table</code>	logical. If TRUE <code>data.table</code> is returned instead of <code>GRanges</code> , the default.
<code>load_signal</code>	function taking <code>f</code> , <code>nam</code> , and <code>qgr</code> arguments. <code>f</code> is from <code>file_paths</code> , <code>nam</code> is from <code>unique_names</code> , and <code>qgr</code> is <code>qgr</code> . See details.
<code>n_cores</code>	integer number of cores to use. Uses <code>mc.cores</code> option if not supplied.
<code>force_skip_centerFix</code>	boolean, if TRUE all query ranges will be used "as is". This is already the case by default if <code>win_method == "summary"</code> but may have applications where <code>win_method == "sample"</code> .

**Details**

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

**Value**

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

**Examples**

```
library(GenomicRanges)
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)
  dt[["sample"]] = nam
  message("finished loading ", nam, ".")
  dt
}
ssvFetchSignal(bam_files, qgr, load_signal = load_bam)
```



---

ssvMakeMembTable	<i>generic for methods to convert various objects to a logical matrix indicating membership of items (rows) in sets (columns)</i>
------------------	---

---

### Description

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

list of character vectors input

GRangesList input

GRanges with mcols input

DataFrame input

matrix of logicals, membership table

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

### Usage

```
ssvMakeMembTable(object)

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

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

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

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

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

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

### Arguments

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

### Value

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

**Examples**

```

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

```

---

ssvOverlapIntervalSets

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

---

**Description**

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

**Usage**

```
ssvOverlapIntervalSets(gr, ext = 0, use_first = FALSE)
```

**Arguments**

gr	A list of GRanges
ext	An integer specifying how far to extend ranges before merging. In effect, ranges within $2 \times \text{ext}$ of one another will be joined during the merge
use_first	A logical. If True, instead of merging all grs, only use first and add metadata logicals for others.

**Value**

GRanges with metadata columns describing overlap of input grs

**Examples**

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

---

ssvSignalBandedQuantiles

*plot profiles from bigwigs*


---

**Description**

plot profiles from bigwigs

**Usage**

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

**Arguments**

bw_data	a GRanges or data.table of bigwig signal. As returned from <a href="#">ssvFetchBam</a> and <a href="#">ssvFetchBigwig</a>
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**

```
#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*

---

**Description**

clustering as for a heatmap

**Usage**

```
ssvSignalClustering(
  bw_data,
  nclust = 6,
  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 = c("hclust", "sort")[2],
  dcast_fill = NA
)
```

**Arguments**

bw_data	a GRanges or data.table of bigwig signal. As returned from <code>ssvFetchBam</code> and <code>ssvFetchBigwig</code>
nclust	number of clusters
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
cluster_	variable name to use for cluster info
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" 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.

**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 targetted to a specific part of the region
clust_dt3 = ssvSignalClustering(CTCF_in_10a_profiles_gr, nclust = 2,
  clustering_col_min = -250, clustering_col_max = -150)
ssvSignalHeatmap(clust_dt3)
clust_dt4 = ssvSignalClustering(CTCF_in_10a_profiles_gr, nclust = 2,
  clustering_col_min = 150, clustering_col_max = 250)
ssvSignalHeatmap(clust_dt4)

```

---

ssvSignalHeatmap	<i>heatmap style representation of membership table. instead of clustering, each column is sorted starting from the left.</i>
------------------	---

---

**Description**

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

**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,
  clustering_col_min = -Inf,
  clustering_col_max = Inf,
  within_order_strategy = c("hclust", "sort")[2],
  dcast_fill = NA,
  return_data = FALSE,
  show_clusterBars = TRUE
)
```

**Arguments**

<code>bw_data</code>	a GRanges or data.table of bigwig signal. As returned from <a href="#">ssvFetchBam</a> and <a href="#">ssvFetchBigwig</a>
<code>nclust</code>	number of clusters
<code>perform_clustering</code>	should clustering be done? default is auto. auto considers if <code>row_</code> has been ordered by being a factor and if <code>cluster_</code> is a numeric.
<code>row_</code>	variable name mapped to row, likely peak id or gene name for ngs data
<code>column_</code>	variable mapped to column, likely bp position for ngs data
<code>fill_</code>	numeric variable to map to fill
<code>facet_</code>	variable name to facet horizontally by
<code>cluster_</code>	variable name to use for cluster info
<code>max_rows</code>	for speed rows are sampled to 500 by default, use Inf to plot full data
<code>max_cols</code>	for speed columns are sampled to 100 by default, use Inf to plot full data
<code>clustering_col_min</code>	numeric minimum for col range considered when clustering, default in -Inf
<code>clustering_col_max</code>	numeric maximum for col range considered when clustering, default in Inf
<code>within_order_strategy</code>	one of "hclust" or "sort". if hclust, hierarchical clustering will be used. if sort, a simple decreasing sort of rosSums.
<code>dcast_fill</code>	value to supply to dcast fill argument. default is NA.
<code>return_data</code>	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.
<code>show_clusterBars</code>	if TRUE, show bars indicating cluster membership.

**Value**

ggplot heatmap of signal profiles, faceted by sample

**Examples**

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

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

---

ssvSignalLineplot	<i>construct line type plots where each region in each sample is represented</i>
-------------------	--

---

**Description**

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

**Usage**

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

**Arguments**

bw_data	a GRanges or data.table of bigwig signal. As returned from <a href="#">ssvFetchBam</a> and <a href="#">ssvFetchBigwig</a>
x_	variable name mapped to x aesthetic, x by default.
y_	variable name mapped to y aesthetic, y by default.
color_	variable name mapped to color aesthetic, sample by default.
sample_	variable name, along with region_ used to group and facet by default, change group_ or facet_ to override.
region_	variable name, along with sample_ used to group and facet by default, change group_ or facet_ to override.

group_	group aesthetic keeps lines of geom_path from mis-connecting. auto_grp by default which combines sample_ and region_. probably shouldn't change.
line_alpha	alpha value for lines. default is 1.
facet_	facetting divides up plots. auto_facet by default which combines sample_ and region_. if overriding facet_method with facet_grid, make sure to include ~ between two variables, ie. "a~b", ".~b", "a~."
facet_method	ggplot2 facetting method or wrapper for same, facet_wrap by default.
spline_n	if not NULL, applySpline will be called with n = spline_n. default is NULL.
return_data	logical. If TRUE, return value is no longer ggplot and is instead the data used to generate that plot. Default is FALSE.

### Value

ggplot of signal potentially faceted 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**

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

**Value**

ggplot of signal aggregated with `agg_fun()` by sample.

**Examples**

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

---

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

---

**Description**

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

**Usage**

```
ssvSignalScatterplot(
  bw_data,
  x_name,
  y_name,
  color_table = NULL,
```

```

value_variable = "y",
xy_variable = "sample",
value_function = max,
by_ = "id",
plot_type = c("standard", "volcano")[1],
show_help = FALSE,
fixed_coords = TRUE,
return_data = FALSE
)

```

### Arguments

<code>bw_data</code>	a GRanges or data.table of bigwig signal. As returned from <code>ssvFetchBam</code> and <code>ssvFetchBigwig</code>
<code>x_name</code>	sample name to map to x-axis, must be stored in variable specified in <code>xy_variable</code>
<code>y_name</code>	sample name to map to y-axis, must be stored in variable specified in <code>xy_variable</code>
<code>color_table</code>	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 <code>by_</code> parameter and is used for merging.
<code>value_variable</code>	variable name that stores numeric values for plotting, default is "y"
<code>xy_variable</code>	variable name that stores sample, must contain entire for <code>x_name</code> and <code>y_name</code>
<code>value_function</code>	a function to apply to <code>value_variable</code> in all combinations of <code>by_</code> per <code>x_name</code> and <code>y_name</code>
<code>by_</code>	variables that store individual measurement ids
<code>plot_type</code>	standard or volcano, default is "standard"
<code>show_help</code>	if TRUE overlay labels to aid plot interpretation, default is FALSE
<code>fixed_coords</code>	if TRUE coordinate system is 1:1 ratio, default is TRUE
<code>return_data</code>	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

```

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)

```

---

test_peaks	<i>4 random peaks for single-end data and 4 control regions 30kb downstream from each peak.</i>
------------	---

---

**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	<i>get a windowed sampling of score_gr</i>
-------------------------	--

---

**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.

**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 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[1:5]
qgr = GenomicRanges::resize(qgr, width = 500, fix = "center")
bam_gr = seqsetvis::fetchBam(bam_file, qgr)
bam_dt = viewGRangesWinSample_dt(bam_gr, qgr, 50)

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

---

viewGRangesWinSummary\_dt

*Summarizes signal in bins. The same number of bins per region in qgr is used and widths can vary in qgr; in contrast to [viewGRangesWinSample\\_dt](#) where width must be constant across regions.*

---

### Description

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

### Usage

```
viewGRangesWinSummary_dt(
  score_gr,
  qgr,
  n_tiles = 100,
  attrib_var = "score",
  attrib_type = NULL,
  fill_value = 0,
```

```

    anchor = c("center", "center_unstranded", "left", "left_unstranded")[1],
    summary_FUN = stats::weighted.mean
  )

```

### Arguments

score_gr	GRanges with a "score" metadata column.
qgr	regions to view by window.
n_tiles	numeric >= 1, the number of tiles to use for every region in qgr.
attrib_var	character name of attribute to pull data from. Default is "score", compatible with 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 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[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)
}

```

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