Package ‘plyranges’

May 30, 2024

Type Package

Title A fluent interface for manipulating GenomicRanges

Version 1.24.0

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Description A dplyr-like interface for interacting with the common Bioconductor classes Ranges and GenomicRanges. By providing a grammatical and consistent way of manipulating these classes their accessibility for new Bioconductor users is hopefully increased.

Depends R (>= 3.5), BiocGenerics, IRanges (>= 2.12.0), GenomicRanges (>= 1.28.4)

Imports methods, dplyr, rlang (>= 0.2.0), magrittr, tidyselect (>= 1.0.0), rtracklayer, GenomicAlignments, GenomeInfoDb, Rsamtools, S4Vectors (>= 0.23.10), utils

biocViews Infrastructure, DataRepresentation, WorkflowStep, Coverage

BugReports https://github.com/tidyomics/plyranges

License Artistic-2.0

Encoding UTF-8

ByteCompile true

Suggests knitr, BiocStyle, rmarkdown, testthat (>= 2.1.0), HelloRanges, HelloRangesData, BSgenome.Hsapiens.UCSC.hg19, pasillaBamSubset, covr, ggplot2

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Collate 'class-AnchoredRanges.R' 'class-Operator.R'
 'class-DeferredGenomicRanges.R' 'class-GroupedRanges.R'
 'dplyr-arrange.R' 'dplyr-filter.R' 'dplyr-groups.R'
 'dplyr-mutate.R' 'dplyr-select.R' 'dplyr-slice.R'
 'dplyr-summarize.R' 'endo-coverage.R' 'endo-tile.R' 'io-bam.R'
 'io-bed.R' 'io-bigwig.R' 'io-gff.R' 'io-wig.R'
 'methods-DeferredGenomicRanges.R' 'methods-Operator.R'
Contents

'plyranges.R' 'ranges-add-distance.R' 'ranges-anchors.R'
'ranges-arithmetic-flank.R' 'ranges-arithmetic-setters.R'
'ranges-arithmetic-shift.R' 'ranges-arithmetic-stretch.R'
'ranges-bind.R' 'ranges-chop.R' 'ranges-colwise.R'
'ranges-construct.R' 'ranges-disjoin.R' 'ranges-eval-quo.R'
'ranges-eval.R' 'ranges-expand.R' 'ranges-genomeinfo.R'
'ranges-join-follow.R' 'ranges-join-nearest.R'
'ranges-join-precede.R' 'ranges-overlap-count.R'
'ranges-overlap-filter.R' 'ranges-overlap-find.R'
'ranges-overlap-groups.R' 'ranges-overlap-joins-intersect.R'
'ranges-overlap-joins-outer.R' 'ranges-overlap-self-joins.R'
'ranges-pairs.R' 'ranges-rangewise-setops.R' 'ranges-reduce.R'
'ranges-setops.R' 'reexports.R'

git_url https://git.bioconductor.org/packages/plyranges

git_branch RELEASE_3_19

git_last_commit 00d5bec

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-29

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plyranges-package

Description

plyranges is a dplyr like API to the Ranges/GenomicRanges infrastructure in Bioconductor.
plyranges-package

Details

plyranges provides a consistent interface for importing and wrangling genomics data from a variety of sources. The package defines a grammar of genomic data manipulation through a set of verbs. These verbs can be used to construct human readable analysis pipelines based on Ranges objects.

- Modify genomic regions with the `set_width()` and `stretch()` functions.
- Modify genomic regions while fixing the start/end/center coordinates with the `anchors()` family of functions.
- Sort genomic ranges with `arrange()`.
- Modify, subset, and aggregate genomic data with the `mutate()`, `filter()`, and `summarise()` functions.
- Any of the above operations can be performed on partitions of the data with `group_by()`.
- Find nearest neighbour genomic regions with the `join_nearest()` family of functions.
- Find overlaps between ranges with the `join_overlap_inner()` family of functions.
- Merge all overlapping and adjacent genomic regions with `reduce_ranges()`.
- Merge the end points of all genomic regions with `disjoin_ranges()`.
- Import and write common genomic data formats with the `read_/write_` family of functions.

For more details on the features of plyranges, read the vignette: browseVignettes(package = "plyranges")

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See Also

Useful links:

- Report bugs at https://github.com/sa-lee/plyranges
**add_nearest_distance**  
*Add distance to nearest neighbours between two Ranges objects*

**Description**
Appends distance to nearest subject range to query ranges similar to setting distance in join_nearest_. Distance is set to NA for features with no nearest feature by the selected nearest metric.

**Usage**

```r
add_nearest_distance(x, y = x, name = "distance")
add_nearest_distance_left(x, y = x, name = "distance")
add_nearest_distance_right(x, y = x, name = "distance")
add_nearest_distance_upstream(x, y = x, name = "distance")
add_nearest_distance_downstream(x, y = x, name = "distance")
```

**Arguments**

- **x**: The query ranges
- **y**: the subject ranges within which the nearest ranges are found. If missing, query ranges are used as the subject.
- **name**: column name to create containing distance values

**Details**

By default add_nearest_distance will find arbitrary nearest neighbours in either direction and ignore any strand information. The add_nearest_distance_left and add_nearest_distance_right methods will find arbitrary nearest neighbour ranges on x that are left/right of those on y and ignore any strand information.

The add_nearest_distance_upstream method will find arbitrary nearest neighbour ranges on x that are upstream of those on y. This takes into account strandedness of the ranges. On the positive strand nearest upstream will be on the left and on the negative strand nearest upstream will be on the right.

The add_nearest_distance_downstream method will find arbitrary nearest neighbour ranges on x that are upstream of those on y. This takes into account strandedness of the ranges. On the positive strand nearest downstream will be on the right and on the negative strand nearest upstream will be on the left.

**Value**

ranges in x with additional column containing the distance to the nearest range in y.
Anchor Ranges objects

Description
The GRangesAnchored class and the IRangesAnchored class allow components of a GRanges or IRanges (start, end, center) to be held fixed.

Usage
anchor(x)
unanchor(x)
anchor_start(x)
anchor_end(x)
anchor_center(x)
anchor_centre(x)
anchor_3p(x)
anchor_5p(x)

Arguments
x a Ranges object
Details

Anchoring will fix a Ranges start, end, or center positions, so these positions will remain the same when performing arithimetic. For GRanges objects, the function anchor_3p() will fix the start for the negative strand, while anchor_5p() will fix the end for the positive strand. Anchoring modifies how arithmetic is performed, for example modifying the width of a range with set_width() or stretching a range with stretch(). To remove anchoring use unanchor().

Value

a RangesAnchored object which has the same appearance as a regular Ranges object but with an additional slot displaying an anchor.

Constructors

Depending on how you want to fix the components of a Ranges, there are five ways to construct a RangesAnchored class. Here x is either an IRanges or GRanges object.

- anchor_start(x) Fix the start coordinates
- anchor_end(x) Fix the end coordinates
- anchor_center(x) Fix the center coordinates
- anchor_3p(x) On the negative strand fix the start coordinates, and for positive or unstranded ranges fix the end coordinates.
- anchor_5p(x) On the positive or unstranded ranges fix the start coordinates, coordinates and for negative stranded ranges fix the end coordinates.

Accessors

To see what has been anchored use the function anchor. This will return a character vector containing a valid anchor. It will be set to one of c("start", "end", "center") for an IRanges object or one of c("start", "end", "center", "3p", "5p") for a GRanges object.

See Also

mutate, stretch

Examples

def <- data.frame(start = 1:10, width = 5)
rg <- as_iranges(df)
rng_by_start <- anchor_start(rng)
rng_by_start
anchor(rng_by_start)
mutate(rng_by_start, width = 3L)
grng <- as_granges(df,
    seqnames = "chr1",
    strand = c(rep("-", 5), rep("+", 5)))
rng_by_5p <- anchor_5p(grng)
rng_by_5p
mutate(rng_by_5p, width = 3L)
arrange.Ranges  

Sort a Ranges object

Description

Sort a Ranges object

Usage

```r
## S3 method for class 'Ranges'
arrange(.data, ...)
```

Arguments

- `.data` A Ranges object.
- `...` Comma seperated list of variable names.

Value

A sorted Ranges object

Examples

```r
gr <- as_iranges(data.frame(start = 1:10, width = 10:1))
gr <- mutate(rng, score = runif(10))
arrange(rng, score)
# you can also use dplyr::desc to arrange by descending order
```

as_iranges  

Construct a I/GRanges object from a tibble or data.frame

Description

The `as_i(g)ranges` function looks for column names in `.data` called start, end, width, seqnames and strand in order to construct an IRanges or GRanges object. By default other columns in `.data` are placed into the mcols (metadata columns) slot of the returned object.

Usage

```r
as_iranges(.data, ..., keep_mcols = TRUE)
as_granges(.data, ..., keep_mcols = TRUE)
```
**as_ranges**

**Coerce an Rle or RleList object to Ranges**

**Description**

Coerce an Rle or RleList object to Ranges

**Usage**

\[
\text{as_ranges(.data)}
\]
bind_ranges

Arguments

.data a \texttt{Rle()} or an \texttt{RleList()} object.

Details

This function is behind \texttt{compute_coverage()}.

Value

an \texttt{IRanges()} object if the input is an \texttt{Rle()} object or a \texttt{GRanges()} object for an \texttt{RleList()} object.

See Also

\texttt{S4Vectors::Rle()}, \texttt{IRanges::RleList()}

Examples

\begin{verbatim}
x <- S4Vectors::Rle(10:1, 1:10)
as_ranges(x)

# must have names set
y <- IRanges::RleList(chr1 = x)
as_ranges(y)
\end{verbatim}

---

Description

Combine Ranges by concatenating them together

Usage

\texttt{bind_ranges(..., .id = NULL)}

Arguments

\begin{itemize}
  \item \dots Ranges objects to combine. Each argument can be a Ranges object, or a list of Ranges objects.
  \item \texttt{.id} Ranges object identifier. When \texttt{.id} is supplied a new column is created that links each row to the original Range object. The contents of the column correspond to the named arguments or the names of the list supplied.
\end{itemize}

Value

a concatenated Ranges object
chop_by_introns

Note
Currently GRangesList or IRangesList objects are not supported.

Examples
gr <- as_granges(data.frame(start = 10:15,
width = 5,
seqnames = "seq1"))

gr2 <- as_granges(data.frame(start = 11:14,
width = 1:4,
seqnames = "seq2"))

bind_ranges(gr, gr2)

bind_ranges(a = gr, b = gr2, .id = "origin")

bind_ranges(gr, list(gr, gr2), gr2)

bind_ranges(list(a = gr, b = gr2), c = gr, .id = "origin")

chop_by_introns  Group a GRanges object by introns or gaps

Description
Group a GRanges object by introns or gaps

Usage
chop_by_introns(x)

chop_by_gaps(x)

Arguments
x a GenomicRanges object with a cigar string column

Details
Creates a grouped Ranges object from a cigar string column, for chop_by_introns() will check for the presence of "N" in the cigar string and create a new column called intron where TRUE indicates the alignment has a skipped region from the reference. For chop_by_gaps() will check for the presence of "N" or "D" in the cigar string and create a new column called "gaps" where TRUE indicates the alignment has a deletion from the reference or has an intron.

Value
a GRanges object
compute_coverage

Examples
if (require(pasillaBamSubset)) {
  bamfile <- untreated1_chr4()
  # define a region of interest
  roi <- data.frame(seqnames = "chr4", start = 5e5, end = 7e5) %>%
    as_granges()
  # results in a grouped ranges object
  rng <- read_bam(bamfile) %>%
    filter_by_overlaps(roi) %>%
    chop_by_gaps()
  # to find ranges that have gaps use filter with `n()`
  rng %>% filter(n() >= 2)
}

compute_coverage  Compute coverage over a Ranges object

Description
Compute coverage over a Ranges object

Usage
compute_coverage(x, shift, width, weight, ...)

Arguments
x  a Ranges object
shift  shift how much should each range in x be shifted by? (default = 0L)
width  width how long should the returned coverage score be? This must be either a
        positive integer or NULL (default = NULL)
weight  weight how much weight should be assigned to each range? Either an integer or
        numeric vector or a column in x. (default = 1L)
...  other optional parameters to pass to coverage

Value
An expanded Ranges object with a score column corresponding to the coverage value over that
interval. Note that compute_coverage drops metadata associated with the orginal ranges.

See Also
IRanges::coverage(), GenomicRanges::coverage()
count_overlaps

Examples

```r
rng <- as_iranges(data.frame(start = 1:10, width = 5))
compute_coverage(rng)
compute_coverage(rng, shift = 14L)
compute_coverage(rng, width = 10L)
```

---

**Description**

Count the number of overlaps between two Ranges objects

**Usage**

```r
count_overlaps(x, y, maxgap, minoverlap)
# S3 method for class 'IntegerRanges'
count_overlaps(x, y, maxgap = -1L, minoverlap = 0L)

# S3 method for class 'GenomicRanges'
count_overlaps(x, y, maxgap = -1L, minoverlap = 0L)

count_overlaps_within(x, y, maxgap, minoverlap)
# S3 method for class 'IntegerRanges'
count_overlaps_within(x, y, maxgap = 0L, minoverlap = 1L)

# S3 method for class 'GenomicRanges'
count_overlaps_within(x, y, maxgap = 0L, minoverlap = 1L)

count_overlaps_directed(x, y, maxgap, minoverlap)
# S3 method for class 'GenomicRanges'
count_overlaps_directed(x, y, maxgap = -1L, minoverlap = 0L)

count_overlaps_within_directed(x, y, maxgap, minoverlap)
# S3 method for class 'GenomicRanges'
count_overlaps_within_directed(x, y, maxgap = -1L, minoverlap = 0L)
```

**Arguments**

- `x, y` Objects representing ranges
- `maxgap, minoverlap` The maximum gap between intervals as an integer greater than or equal to zero. The minimum amount of overlap between intervals as an integer greater than zero, accounting for the maximum gap.
Value

An integer vector of same length as x.

Examples

```r
query <- data.frame(start = c(5, 10, 15, 20), width = 5, gc = runif(4)) %>%
as_iranges()
subject <- data.frame(start = 2:6, width = 3:7, label = letters[1:5]) %>%
as_iranges()
query %>% mutate(n_olap = count_overlaps(., subject),
n_olap_within = count_overlaps_within(., subject))
```

---

DeferredGenomicRanges-class

**DeferredGenomicRanges objects**

Description

Enables deferred reading of files (currently only BAM files) by caching results after a plyranges verb is called.

Slots

- `delegate` a GenomicRanges object to be cached
- `ops` A FileOperator object

See Also

- `read_bam()`

---

disjoin_ranges

**Disjoin then aggregate a Ranges object**

Description

Disjoin then aggregate a Ranges object

Usage

```r
disjoin_ranges(.data, ...)
disjoin_ranges_directed(.data, ...)
```
**Arguments**

- `.data` a Ranges object to disjoin
- `...` Name-value pairs of summary functions.

**Value**

a Ranges object that is now disjoint (no bases overlap).

**Examples**

```r
df <- data.frame(start = 1:10, width = 5, seqnames = "seq1", strand = sample(c("+", "-", "*"), 10, replace = TRUE), gc = runif(10))
rng <- as_granges(df)
rng %>% disjoin_ranges()
rng %>% disjoin_ranges(gc = mean(gc))
rng %>% disjoin_ranges_directed(gc = mean(gc))
```

---

**Description**

Expand list-columns in a Ranges object

**Usage**

```r
expand_ranges(
  data,
  ..., .drop = FALSE,
  .id = NULL,
  .keep_empty = FALSE,
  .recursive = FALSE
)
```

**Arguments**

- `data` A Ranges object
- `...` list-column names to expand then unlist
- `.drop` Should additional list columns be dropped (default = FALSE)? By default `expand_ranges()` will keep other list columns even if they are nested.
- `.id` A character vector of length equal to number of list columns. If supplied will create new column(s) with name `.id` identifying the index of the list column (default = NULL).
- `.keep_empty` If a list-like column contains empty elements, should those elements be kept? (default = FALSE)
If there are multiple list-columns, should the columns be treated as parallel? If FALSE each column will be unnested recursively, otherwise they are treated as parallel, that is each list column has identical lengths. (default = FALSE)

Value

a GRanges object with expanded list columns

Examples

```r
grng <- as_granges(data.frame(seqnames = "chr1", start = 20:23, width = 1000))
grng <- mutate(grng,
    exon_id = IntegerList(a = 1, b = c(4,5), c = 3, d = c(2,5))
)
expand_ranges(grng)
expand_ranges(grng, .id = "name")

# empty list elements are not preserved by default
grng <- mutate(grng,
    exon_id = IntegerList(a = NULL, b = c(4,5), c = 3, d = c(2,5))
)
expand_ranges(grng)
expand_ranges(grng, .keep_empty = TRUE)
expand_ranges(grng, .id = "name", .keep_empty = TRUE)
```

**FileOperator-class**  
An abstract class to represent operations performed over a file

**Description**

An abstract class to represent operations performed over a file

**Details**

This class is used internally by DeferredGenomicRanges objects. Currently, this class is only implemented for bam files (as a BamFileOperator) but will eventually be extended to the other available readers.
filter-ranges  

Subset a Ranges object

Description

Subset a Ranges object

Usage

```r
## S3 method for class 'Ranges'
filter(.data, ..., .preserve = FALSE)
```

Arguments

- `.data` A Ranges object
- `...` valid logical predictates to subset .data by. These are determined by variables in .data. If more than one condition is supplied, the conditions are combined with &. Only rows where the condition evaluates to TRUE are kept.
- `.preserve` when FALSE (the default) grouping structure is recalculated, TRUE is currently not implemented.

Details

For any Ranges objects filter can act on all core components of the class including start, end, width (for IRanges) or seqnames and strand (for GRanges) in addition to metadata columns. If the Ranges object is grouped, filter will act seperately on each partition of the data.

Value

a Ranges object

See Also

dplyr::filter()

Examples

```r
set.seed(100)
df <- data.frame(start = 1:10,
                 width = 5,
                 seqnames = "seq1",
                 strand = sample(c("+", "+", "x"), 10, replace = TRUE),
                 gc = runif(10))

rng <- as_granges(df)

filter(rng, strand == "+")
filter(rng, gc > 0.5)
```
# multiple criteria
filter(rng, strand == "+" | start > 5)
filter(rng, strand == "+" & start > 5)

# multiple conditions are the same as and
filter(rng, strand == "+", start > 5)

# grouping acts on each subset of the data
rng %>%
  group_by(strand) %>%
  filter(gc > 0.5)

filter_by_overlaps
Filter by overlapping/non-overlapping ranges

Description
Filter by overlapping/non-overlapping ranges

Usage
filter_by_overlaps(x, y, maxgap = -1L, minoverlap = 0L)
filter_by_non_overlaps(x, y, maxgap, minoverlap)
filter_by_overlaps_directed(x, y, maxgap = -1L, minoverlap = 0L)
filter_by_non_overlaps_directed(x, y, maxgap, minoverlap)

Arguments
x, y       Objects representing ranges
maxgap     The maximimum gap between intervals as a single integer greater than or equal to -1. If you modify this argument, minoverlap must be held fixed.
minoverlap The minimum amount of overlap between intervals as a single integer greater than 0. If you modify this argument, maxgap must be held fixed.

Details
By default, filter_by_overlaps and filter_by_non_overlaps ignore strandedness for GRanges() objects. To perform stranded operations use filter_by_overlaps_directed and filter_by_non_overlaps_directed. The argument maxgap is the maximum number of positions between two ranges for them to be considered overlapping. Here the default is set to be -1 as that is the the gap between two ranges that has its start or end strictly inside the other. The argument minoverlap refers to the minimum number of positions overlapping between ranges, to consider there to be overlap.
find_overlaps

Value

a Ranges object

See Also

IRanges::subsetByOverlaps()

Examples

df <- data.frame(seqnames = c("chr1", rep("chr2", 2), rep("chr3", 3), rep("chr4", 4)),
                  start = 1:10,
                  width = 10:1,
                  strand = c("-", "+", "+", "+", "+", "+", "+", "+", "+", "+"),
                  name = letters[1:10])
query <- as_granges(df)

df2 <- data.frame(seqnames = c(rep("chr2", 2), rep("chr1", 3), "chr2"),
                  start = c(4,3,7,13,1,4),
                  width = c(6,6,3,3,9),
                  strand = c(rep("+", 3), rep("-", 3)))
subject <- as_granges(df2)

filter_by_overlaps(query, subject)
filter_by_overlaps_directed(query, subject)
filter_by_non_overlaps(query, subject)
filter_by_non_overlaps_directed(query, subject)
find_overlaps_within(x, y, maxgap, minoverlap, suffix = c(".x", ",.y"))

## S3 method for class 'IntegerRanges'
find_overlaps_within(
  x,
  y,
  maxgap = -1L,
  minoverlap = 0L,
  suffix = c(".x", ",.y")
)

## S3 method for class 'GenomicRanges'
find_overlaps_within(
  x,
  y,
  maxgap = -1L,
  minoverlap = 0L,
  suffix = c(".x", ",.y")
)

find_overlaps_directed(x, y, maxgap, minoverlap, suffix = c(".x", ",.y"))

## S3 method for class 'GenomicRanges'
find_overlaps_directed(
  x,
  y,
  maxgap = -1L,
  minoverlap = 0L,
  suffix = c(".x", ",.y")
)

find_overlaps_within_directed(x, y, maxgap, minoverlap, suffix = c(".x", ",.y"))

## S3 method for class 'GenomicRanges'
find_overlaps_within_directed(x, y, maxgap, minoverlap, suffix = c(".x", ",.y"))

group_by_overlaps(x, y, maxgap, minoverlap)

## S3 method for class 'IntegerRanges'
group_by_overlaps(x, y, maxgap = -1L, minoverlap = 0L)

## S3 method for class 'GenomicRanges'
group_by_overlaps(x, y, maxgap = -1L, minoverlap = 0L)

**Arguments**

- **x, y**  
  Objects representing ranges

- **maxgap, minoverlap**  
  The maximum gap between intervals as an integer greater than or equal to
negative one. The minimum amount of overlap between intervals as an integer greater than zero, accounting for the maximum gap.

**suffix**

A character vector of length two used to identify metadata columns coming from x and y.

**Details**

`find_overlaps()` will search for any overlaps between ranges x and y and return a Ranges object of length equal to the number of times x overlaps y. This Ranges object will have additional metadata columns corresponding to the metadata columns in y. `find_overlaps_within()` is the same but will only search for overlaps within y. For GRanges objects strand is ignored, unless `find_overlaps_directed()` is used. If the Ranges objects have no metadata, one could use `group_by_overlaps()` to be able to identify the index of the input Range x that overlaps a Range in y. Alternatively, `pair_overlaps()` could be used to place the x ranges next to the range in y they overlap.

**Value**

A Ranges object with rows corresponding to the ranges in x that overlap y. In the case of `group_by_overlaps()`, returns a GroupedRanges object, grouped by the number of overlaps of ranges in x that overlap y (stored in a column called query).

**See Also**

IRanges::findOverlaps(), GenomicRanges::findOverlaps()

**Examples**

```r
query <- data.frame(start = c(5,10, 15,20), width = 5, gc = runif(4)) %>%
  as_iranges()
subject <- data.frame(start = 2:6, width = 3:7, label = letters[1:5]) %>%
  as_iranges()

find_overlaps(query, subject)
find_overlaps(query, subject, minoverlap = 5)
find_overlaps_within(query, subject) # same result as minoverlap
find_overlaps(query, subject, maxgap = 1)

# -- GRanges objects, strand is ignored by default
query <- data.frame(seqnames = "chr1",
  start = c(11,101),
  end = c(21, 200),
  name = c("a1", "a2"),
  strand = c("+", "-"),
  score = c(1,2)) %>%
  as_granges()
subject <- data.frame(seqnames = "chr1",
  strand = c("+", "-", "+", "-"),
  start = c(21,91,101,201),
  end = c(30,101,110,210),
  name = paste0("b", 1:4),
```
score = 1:4) %>%
  as_granges()

# ignores strandedness
find_overlaps(query, subject, suffix = c(".query", ".subject"))
find_overlaps(query, subject, suffix = c(".query", ".subject"), minoverlap = 2)
# adding directed prefix includes strand
find_overlaps_directed(query, subject, suffix = c(".query", ".subject"))

---

flank_left  
Generate flanking regions

**Description**

Find flanking regions to the left or right or upstream or downstream of a Ranges object.

**Usage**

flank_left(x, width = 0L)
flank_right(x, width = 0L)
flank_upstream(x, width = 0L)
flank_downstream(x, width = 0L)

**Arguments**

- **x**: a Ranges object.
- **width**: the width of the flanking region relative to the ranges in x. Either an integer vector of length 1 or an integer vector the same length as x. The width can be negative in which case the flanking region is reversed.

**Details**

The function `flank_left` will create the flanking region to the left of starting coordinates in x, while `flank_right` will create the flanking region to the right of the starting coordinates in x. The function `flank_upstream` will `flank_left` if the strand of rows in x is not negative and will `flank_right` if the strand of rows in x is negative. The function `flank_downstream` will `flank_right` if the strand of rows in x is not negative and will `flank_left` if the strand of rows in x is negative.

By default `flank_left` and `flank_right` will ignore strandedness of any ranges, while `flank_upstream` and `flank_downstream` will take into account the strand of x.

**Value**

A Ranges object of same length as x.
See Also

IRanges::flank(), GenomicRanges::flank()

Examples

```r
gr <- as_granges(data.frame(start = 10:15,
    width = 5,
    seqnames = "seq1",
    strand = c("+", "+", "->", "<-", "->", "*")))
flank_left(gr, width = 5L)
flank_right(gr, width = 5L)
flank_upstream(gr, width = 5L)
flank_downstream(gr, width = 5L)
```

Description

The function group_by takes a Ranges object and defines groups by one or more variables. Operations are then performed on the Ranges by their "group". ungroup() removes grouping.

Usage

```r
## S3 method for class 'GenomicRanges'
group_by(.data, ..., add = FALSE)

## S3 method for class 'GroupedGenomicRanges'
ungroup(x, ...)

## S3 method for class 'GroupedGenomicRanges'
groups(x)

## S3 method for class 'GroupedIntegerRanges'
groups(x)
```

Arguments

- `.data` a Ranges object.
- `...` Variable names to group by. These can be either metadata columns or the core variables of a Ranges.
- `add` if `.data` is already a GroupedRanges object, when `add = FALSE` the (default), `group_by()` will override existing groups. If `add = TRUE`, additional groups will be added.
- `x` a GroupedRanges object.
Details

group_by() creates a new object of class GroupedGenomicRanges if the input is a GRanges object or an object of class GroupedIntegerRanges if the input is a IRanges object. Both of these classes contain a slot called groups corresponding to the names of grouping variables. They also inherit from their parent classes, Ranges and GenomicRanges respectively. ungroup() removes the grouping and will return either a GRanges or IRanges object.

Value

The group_by() function will return a GroupedRanges object. These have the same appearance as a regular Ranges object but with an additional groups slot.

Accessors

To return grouping variables on a grouped Ranges use either

- groups(x) Returns a list of symbols
- group_vars(x) Returns a character vector

Examples

set.seed(100)
df <- data.frame(start = 1:10,
                 width = 5,
                 gc = runif(10),
                 cat = sample(letters[1:2], 10, replace = TRUE))
rng <- as_iranges(df)
rng_by_cat <- rng %>% group_by(cat)
# grouping does not change appearance or shape of Ranges
rng_by_cat
# a list of symbols
groups(rng_by_cat)
# ungroup removes any grouping
ungroup(rng_by_cat)
# group_by works best with other verbs
grng <- as_granges(df,
                   seqnames = "chr1",
                   strand = sample(c("+", "-"), size = 10, replace = TRUE))
grng_by_strand <- grng %>% group_by(strand)
grng_by_strand
# grouping with other verbs
grng_by_strand %>% summarise(gc = mean(gc))
grng_by_strand %>% filter(gc == min(gc))
grng_by_strand %>%
    ungroup() %>%
    summarise(gc = mean(gc))
**intersect_ranges**

**Vector-wise Range set-operations**

**Description**
Vector-wise Range set-operations

**Usage**

```
intersect_ranges(x, y)
intersect_ranges_directed(x, y)
union_ranges(x, y)
union_ranges_directed(x, y)
setdiff_ranges(x, y)
setdiff_ranges_directed(x, y)
complement_ranges(x)
complement_ranges_directed(x)
```

**Arguments**

`x, y` Two Ranges objects to compare.

**Details**
These are usual set-operations that act on the sets of the ranges represented in `x` and `y`. By default these operations will ignore any strand information. The directed versions of these functions will take into account strand for GRanges objects.

**Value**
A Ranges object

**Examples**

```
gr1 <- data.frame(seqnames = "chr1",
                  start = c(2,9),
                  end = c(7,9),
                  strand = c("+", "-"))
                %>%
                as_granges()
gr2 <- data.frame(seqnames = "chr1", start = 5, width = 5, strand = "-")
                %>%
                as_granges()
```
union_ranges(gr1, gr2)
union_ranges_directed(gr1, gr2)

intersect_ranges(gr1, gr2)
intersect_ranges_directed(gr1, gr2)

setdiff_ranges(gr1, gr2)
setdiff_ranges_directed(gr1, gr2)

# taking the complement of a ranges requires annotation information
gr1 <- set_genome_info(gr1, seqlengths = 100)
complement_ranges(gr1)

---

### interweave

**Interweave a pair of Ranges objects together**

**Description**

Interweave a pair of Ranges objects together

**Usage**

```r
interweave(left, right, .id = NULL)
```

**Arguments**

- `left, right`: Ranges objects.
- `id`: When supplied a new column that represents the origin column and is linked to each row of the resulting Ranges object.

**Details**

The output of `interweave()` takes pairs of Ranges objects and combines them into a single Ranges object. If an `.id` argument is supplied, an origin column with name `.id` is created indicated which side the resulting Range comes from (e.g.)

**Value**

a Ranges object

**Examples**

```r
gr <- as_granges(data.frame(start = 10:15,
      width = 5,
      seqnames = "seq1",
      strand = c("+", "+", "-", "+", "+", "+", "-", "+", "-", "-", "-", "-", "-", "-")))
interweave(flank_left(gr, width = 5L), flank_right(gr, width = 5L))
interweave(flank_left(gr, width = 5L), flank_right(gr, width = 5L), .id = "origin")
```
join_follow  

Find following Ranges

Description

Find following Ranges

Usage

join_follow(x, y, suffix = c(".x", ".y"))

join_follow_left(x, y, suffix = c(".x", ".y"))

join_follow_upstream(x, y, suffix = c(".x", ".y"))

Arguments

x, y  Ranges objects, which ranges in x follow those in y.
suffix  A character vector of length two used to identify metadata columns coming from x and y.

Details

By default join_follow will find arbitrary ranges in y that are followed by ranges in x and ignore any strand information. On the other hand join_follow_left will find all ranges in y that are on the left-hand side of the ranges in x ignoring any strand information. Finally, join_follow_upstream will find all ranges in x that are that are upstream of the ranges in y. On the positive strand this will result in ranges in y that are left of those in x and on the negative strand it will result in ranges in y that are right of those in x.

Value

A Ranges object corresponding to the ranges in x that are followed by the ranges in y, all metadata is copied over from y.'.

Examples

query <- data.frame(start = c(5,10, 15,20), width = 5, gc = runif(4)) %>%
as_iranges()
subject <- data.frame(start = 2:6, width = 3:7, label = letters[1:5]) %>%
as_iranges()

join_follow(query, subject)

subject <- data.frame(seqnames = "chr1",
                      start = c(11,101),
                      end = c(21, 200),
                      name = c("a1", "a2"),
                      strand = c("+", ";"),
                      width = c(10, 20),
                      gc = runif(2)) %>%
as_iranges()

join_follow_left(subject, query)

join_follow_upstream(subject, query)
```r
score = c(1,2)) %>%
as_granges()
query <- data.frame(seqnames = "chr1",
  strand = c("+", "+", "+", "+"),
  start = c(21,91,101,201),
  end = c(30,101,110,210),
  name = paste0("b", 1:4),
  score = 1:4) %>%
as_granges()

join_follow(query, subject)
join_follow_left(query, subject)
join_follow_upstream(query, subject)
```

---

### join_nearest

Find nearest neighbours between two Ranges objects

#### Description

Find nearest neighbours between two Ranges objects

#### Usage

```r
join_nearest(x, y, suffix = c(".x", ".y"), distance = FALSE)
join_nearest_left(x, y, suffix = c(".x", ".y"), distance = FALSE)
join_nearest_right(x, y, suffix = c(".x", ".y"), distance = FALSE)
join_nearest_upstream(x, y, suffix = c(".x", ".y"), distance = FALSE)
join_nearest_downstream(x, y, suffix = c(".x", ".y"), distance = FALSE)
```

#### Arguments

- **x, y** Ranges objects, add the nearest neighbours of ranges in x to those in y.
- **suffix** A character vector of length two used to identify metadata columns
- **distance** logical vector whether to add a column named "distance" containing the distance to the nearest region. If set to a character vector of length 1, will use that as distance column name.

#### Details

By default `join_nearest` will find arbitrary nearest neighbours in either direction and ignore any strand information. The `join_nearest_left` and `join_nearest_right` methods will find arbitrary nearest neighbour ranges on x that are left/right of those on y and ignore any strand information.
The `join_nearest_upstream` method will find arbitrary nearest neighbour ranges on x that are upstream of those on y. This takes into account strandedness of the ranges. On the positive strand nearest upstream will be on the left and on the negative strand nearest upstream will be on the right.

The `join_nearest_downstream` method will find arbitrary nearest neighbour ranges on x that are upstream of those on y. This takes into account strandedness of the ranges. On the positive strand nearest downstream will be on the right and on the negative strand nearest upstream will be on the left.

**Value**

A Ranges object corresponding to the nearest ranges, all metadata is copied over from the right-hand side ranges y.

**Examples**

```r
query <- data.frame(start = c(5,10, 15,20),
                     width = 5,
                     gc = runif(4)) %>%
               as_iranges()
subject <- data.frame(start = c(2:6, 24),
                      width = 3:8,
                      label = letters[1:6]) %>%
               as_iranges()

join_nearest(query, subject)
join_nearest_left(query, subject)
join_nearest_right(query, subject)

subject <- data.frame(seqnames = "chr1",
                      start = c(11,101),
                      end = c(21, 200),
                      name = c("a1", "a2"),
                      strand = c("+", "+"),
                      score = c(1,2)) %>%
               as_granges()
query <- data.frame(seqnames = "chr1",
                     strand = c("+", "+", "+", "+"),
                     start = c(21,91,101,201),
                     end = c(30,101,110,210),
                     name = paste0("b", 1:4),
                     score = 1:4) %>%
               as_granges()

join_nearest_upstream(query, subject)
join_nearest_downstream(query, subject)
```

---

**join_overlap_intersect**

Join by overlapping Ranges
**Description**

Join by overlapping Ranges

**Usage**

```r
join_overlap_intersect(x, y, maxgap, minoverlap, suffix = c(".x", ".y"))
join_overlap_intersect_within(x, y, maxgap, minoverlap, suffix = c(".x", ".y"))
join_overlap_intersect_directed(
  x,
  y,
  maxgap,
  minoverlap,
  suffix = c(".x", ".y")
)
join_overlap_intersect_within_directed(
  x,
  y,
  maxgap,
  minoverlap,
  suffix = c(".x", ".y")
)
join_overlap_inner(x, y, maxgap = -1L, minoverlap = 0L, suffix = c(".x", ".y"))
join_overlap_inner_within(
  x,
  y,
  maxgap = -1L,
  minoverlap = 0L,
  suffix = c(".x", ".y")
)
join_overlap_inner_directed(
  x,
  y,
  maxgap = -1L,
  minoverlap = 0L,
  suffix = c(".x", ".y")
)
join_overlap_inner_within_directed(
  x,
  y,
  maxgap = -1L,
  minoverlap = 0L,
  suffix = c(".x", ".y")
)
```
join_overlap_intersect

```r
suffix = c(".x", ".y")
}
join_overlap_left(x, y, maxgap, minoverlap, suffix = c(".x", ".y"))
join_overlap_left_within(x, y, maxgap, minoverlap, suffix = c(".x", ".y"))
join_overlap_left_directed(x, y, maxgap, minoverlap, suffix = c(".x", ".y"))
join_overlap_left_within_directed(
  x,
  y,
  maxgap,
  minoverlap,
  suffix = c(".x", ".y")
)
```

Arguments

- `x, y`: Objects representing ranges
- `maxgap, minoverlap`: The maximum gap between intervals as an integer greater than or equal to zero. The minimum amount of overlap between intervals as an integer greater than zero, accounting for the maximum gap.
- `suffix`: Character to vectors to append to common columns in x and y (default = c(".x", ".y").

Details

The function `join_overlap_intersect()` finds the genomic intervals that are the overlapping ranges between x and y and returns a new ranges object with metadata columns from x and y.

The function `join_overlap_inner()` is equivalent to `find_overlaps()`.

The function `join_overlap_left()` performs a left outer join between x and y. It returns all ranges in x that overlap or do not overlap ranges in y plus metadata columns common to both. If there is no overlapping range the metadata column will contain a missing value.

The function `join_overlap_self()` find all overlaps between a ranges object x and itself.

All of these functions have two suffixes that modify their behavior. The within suffix, returns only ranges in x that are completely overlapped within in y. The directed suffix accounts for the strandedness of the ranges when performing overlaps.

Value

- a GRanges object

See Also

- `join_overlap_self()`, `join_overlap_left()`, `find_overlaps()`
Examples

```r
x <- as_iranges(data.frame(start = c(11, 101), end = c(21, 201)))
y <- as_iranges(data.frame(start = c(10, 20, 50, 100, 1),
                           end = c(19, 21, 105, 202, 5)))

# self
join_overlap_self(y)

# intersect takes common interval
join_overlap_intersect(x, y)

# within
join_overlap_intersect_within(x, y)

# left, and inner join, it's often useful having an id column here
y <- y %>% mutate(id = 1:n())
x <- x %>% mutate(id = 1:n())
join_overlap_inner(x, y)
join_overlap_left(y, x, suffix = c(".left", ".right"))
```

---

**join_overlap_self**

*Find overlaps within a Ranges object*

Description

Find overlaps within a Ranges object

Usage

```r
join_overlap_self(x, maxgap, minoverlap)
join_overlap_self_within(x, maxgap, minoverlap)
join_overlap_self_directed(x, maxgap, minoverlap)
join_overlap_self_within_directed(x, maxgap, minoverlap)
```

Arguments

- `x`: A Ranges object
- `maxgap`, `minoverlap`:
  - The maximum gap between intervals as an integer greater than or equal to zero. The minimum amount of overlap between intervals as an integer greater than zero, accounting for the maximum gap.
join_precede

Details
Self overlaps find any overlaps (or overlaps within or overlaps directed) between a ranges object and itself.

Value
a Ranges object

See Also
find_overlaps(), join_overlap_inner()

Examples
query <- data.frame(start = c(5,10, 15,20), width = 5, gc = runif(4)) %>%
  as_iranges()

join_overlap_self(query)

# -- GRanges objects, strand is ignored by default
query <- data.frame(seqnames = "chr1",
  start = c(11,101),
  end = c(21, 200),
  name = c("a1", "a2"),
  strand = c("+", "-"),
  score = c(1,2)) %>%
  as_granges()

# ignores strandedness
join_overlap_self(query)
join_overlap_self_within(query)
# adding directed prefix includes strand
join_overlap_self_directed(query)

join_precede  Find preceding Ranges

Description
Find preceding Ranges

Usage
join_precede(x, y, suffix = c(".x", ".y"))

join_precede_right(x, y, suffix = c(".x", ".y"))

join_precede_downstream(x, y, suffix = c(".x", ".y"))
Arguments

- `x, y`: Ranges objects, which ranges in `x` precede those in `y`.
- `suffix`: A character vector of length two used to identify metadata columns coming from `x` and `y`.

Details

By default `join_precede` will return the ranges in `x` that come before the ranges in `y` and ignore any strand information. The function `join_precede_right` will find all ranges in `y` that are on the right-hand side of the ranges in `x` ignoring any strand information. Finally, `join_precede_downstream` will find all ranges in `y` that are downstream of the ranges in `x`. On the positive strand this will result in ranges in `y` that are right of those in `x` and on the negative strand it will result in ranges in `y` that are left of those in `x`.

Value

A Ranges object corresponding to the ranges in `y` that are preceded by the ranges in `x`, all metadata is copied over from the right-hand side ranges `y`.

Examples

```r
subject <- data.frame(start = c(5,10, 15,20), width = 5, gc = runif(4)) %>%
  as_iranges()
query <- data.frame(start = 2:6, width = 3:7, label = letters[1:5]) %>%
  as_iranges()

join_precede(query, subject)

query <- data.frame(seqnames = "chr1",
  start = c(11,101),
  end = c(21, 200),
  name = c("a1", "a2"),
  strand = c("+", "-"),
  score = c(1,2)) %>%
  as_granges()
subject <- data.frame(seqnames = "chr1",
  strand = c("+", "-"),
  start = c(21,91,101,201),
  end = c(30,101,110,210),
  name = paste0("b", 1:4),
  score = 1:4) %>%
  as_granges()

join_precede(query, subject)
join_precede_right(query, subject)
join_precede_downstream(query, subject)
```
mutate.Ranges

Modify a Ranges object

Description

Modify a Ranges object

Usage

## S3 method for class 'Ranges'
mutate(.data, ...)

Arguments

.data

a Ranges object

... 

Pairs of name-value expressions. The name-value pairs can either create new metadata columns or modify existing ones.

Value

a Ranges object

Examples

df <- data.frame(start = 1:10,
                 width = 5,
                 seqnames = "seq1",
                 strand = sample(c("+", "-", "*"), 10, replace = TRUE),
                 gc = runif(10))
rng <- as_granges(df)

# mutate adds new columns
rng %>%
  mutate(avg_gc = mean(gc), row_id = 1:n())

# can also compute on newly created columns
rng %>%
  mutate(score = gc * width, score2 = score + 1)

# group by partitions the data and computes within each group
rng %>%
  group_by(strand) %>%
  mutate(avg_gc = mean(gc), row_id = 1:n())

# mutate can be used in conjunction with anchoring to resize ranges
rng %>%
  mutate(width = 10)
# by default width modification fixes by start
rng %>%
  anchor_start() %>%
  mutate(width = 10)
# fix by end or midpoint
rng %>%
  anchor_end() %>%
  mutate(width = width + 1)

rng %>%
  anchor_center() %>%
  mutate(width = width + 1)

# anchoring by strand
rng %>%
  anchor_3p() %>%
  mutate(width = width * 2)

rng %>%
  anchor_5p() %>%
  mutate(width = width * 2)

n Compute the number of ranges in each group.

Description
This function should only be used within summarise(), mutate() and filter().

Usage
n()

Value
n() will only be evaluated inside a function call, where it returns an integer.

Examples
ir <- as_iranges(
  data.frame(start = 1:10,
            width = 5,
            name = c(rep("a", 5), rep("b", 3), rep("c", 2))
  )
)
by_names <- group_by(ir, name)
summarise(by_names, n = n())
mutate(by_names, n = n())
filter(by_names, n() >= 3)
**n_distinct**

Compute the number of distinct unique values in a vector or List

*Description*

This is a wrapper to `length(unique(x))` or `lengths(unique(x))` if `x` is a List object.

*Usage*

```
n_distinct(var)
```

*Arguments*

- `var`: a vector of values

*Value*

an integer vector

*Examples*

```r
x <- CharacterList(c("a", "b", "c", "a", "d")
n_distinct(x)
n_distinct(unlist(x))
```

---

**overscope_ranges**

Create an overscoped environment from a Ranges object

*Description*

Create an overscoped environment from a Ranges object.

*Usage*

```
overscope_ranges(x, envir = parent.frame())
```

*Arguments*

- `x`: a Ranges object
- `envir`: the environment to place the Ranges in (default = `parent.frame()`)

*Details*

This is the backend for non-standard evaluation in `plyranges`. 
pair_overlaps

Value
an environment

See Also
rlang::new_data_mask(), rlang::eval_tidy()

Description
Pair together two ranges objects

Usage
pair_overlaps(x, y, maxgap, minoverlap, suffix)

pair_nearest(x, y, suffix)

pair_precede(x, y, suffix)

pair_follow(x, y, suffix)

Arguments
x, y Ranges objects to pair together.

maxgap, minoverlap The maximum gap between intervals as an integer greater than or equal to negative one. The minimum amount of overlap between intervals as an integer greater than zero, accounting for the maximum gap.

suffix A character vector of length two used to identify metadata columns coming from x and y.

Details
These functions return a DataFrame object, and is one way of representing paired alignments with plyranges.

Value
a DataFrame with two ranges columns and the corresponding metadata columns.

See Also
[join_nearest()],[join_overlap_inner()],[join_precede()],[join_follow()]
Examples

```r
query <- data.frame(start = c(5,10, 15,20), width = 5, gc = runif(4)) %>%
       as_iranges()
subject <- data.frame(start = 2:6, width = 3:7, label = letters[1:5]) %>%
       as_iranges()

pair_overlaps(query, subject)
pair_overlaps(query, subject, minoverlap = 5)
pair_nearest(query, subject)

query <- data.frame(seqnames = "chr1",
                     start = c(11,101),
                     end = c(21, 200),
                     name = c("a1", "a2"),
                     strand = c("+", "-"),
                     score = c(1,2)) %>%
       as_granges()

subject <- data.frame(seqnames = "chr1",
                      strand = c("+", "+", "+", "+"),
                      start = c(21,91,101,201),
                      end = c(30,101,110,210),
                      name = paste0("b", 1:4),
                      score = 1:4) %>%
       as_granges()

# ignores strandedness
pair_overlaps(query, subject, suffix = c(".query", ".subject"))
pair_follow(query, subject, suffix = c(".query", ".subject"))
pair_precede(query, subject, suffix = c(".query", ".subject"))
pair_precede(query, subject, suffix = c(".query", ".subject"))
```

Ranges-info

Construct annotation information

Description

To construct annotations by supplying annotation information use genome_info. To add annotations to an existing Ranges object use set_genome_info. To retrieve an annotation as a Ranges object use get_genome_info.

Usage

```r
genome_info(
    genome = NULL,
    seqnames = NULL,
    seqlengths = NULL,
    isCircular = NULL
)
```
set_genome_info(
  .data,
  genome = NULL,
  seqnames = NULL,
  seqlengths = NULL,
  is_circular = NULL
)

get_genome_info(.data)

Arguments

genome A character vector of length one indicating the genome build.
seqnames A character vector containing the name of sequences.
seqlengths An optional integer vector containing the lengths of sequences.
is_circular An optional logical vector indicating whether a sequence is circular.
.data A Ranges object to annotate or retrieve an annotation for.

Value

da GRanges object containing annotations. To retrieve the annotations as a Ranges object use get_genome_info.

See Also

GenomeInfoDb::Seqinfo()

Examples

x <- genome_info(genome = "toy",
  seqnames = letters[1:4],
  seqlengths = c(100, 300, 15, 600),
  is_circular = c(NA, FALSE, FALSE, TRUE))
x

rng <- as_granges(data.frame(seqnames = "a", start = 30:50, width = 10))
rng
rng <- set_genome_info(rng,
  genome = "toy",
  seqnames = letters[1:4],
  seqlengths = c(100, 300, 15, 600),
  is_circular = c(NA, FALSE, FALSE, TRUE))

get_genome_info(rng)

## Not run:
if (interactive()) {
  # requires internet connection
  genome_info(genome = "hg38")
}
## read_bam

Read a BAM file

### Description

Read a BAM file

### Usage

```
read_bam(file, index = file, paired = FALSE)
```

### Arguments

- **file**: A connection or path to a BAM file
- **index**: The path to the BAM index file
- **paired**: Whether to treat alignments as paired end (TRUE) or single end (FALSE). Default is FALSE.

### Details

Reading a BAM file is deferred until an action such as using `summarise()` or `mutate()` occurs. If paired is set to TRUE, when alignments are loaded, the GRanges has two additional columns called read_pair_id and read_pair_group corresponding to paired reads and is grouped by the read_pair_group.

Certain verbs have different behaviour, after using `read_bam()`.

For `select()` valid columns are the fields available in the BAM file. Valid entries are qname (QNAME), flag (FLAG), rname (RNAME), strand, pos (POS), qwidth (width of query), mapq (MAPQ), cigar (CIGAR), mrnm (RNEXT), mpos (PNEXT), isize (TLEN), seq (SEQ), and qual (QUAL). Any two character tags in the BAM file are also valid.

For `filter()` the following fields are valid, to select the FALSE option place ! in front of the field:

- `is_paired` Select either unpaired (FALSE) or paired (TRUE) reads.
- `is_proper_pair` Select either improperly paired (FALSE) or properly paired (TRUE) reads. This is dependent on the alignment software used.
- `is_unmapped_query` Select unmapped (TRUE) or mapped (FALSE) reads.
- `has_unmapped_mate` Select reads with mapped (FALSE) or unmapped (TRUE) mates.
- `is_minus_strand` Select reads aligned to plus (FALSE) or minus (TRUE) strand.
- `is_mate_minus_strand` Select reads where mate is aligned to plus (FALSE) or minus (TRUE) strand.
- `is_first_mate_read` Select reads if they are the first mate (TRUE) or not (FALSE).
• `is_second_mate_read` Select reads if they are the second mate (TRUE) or not (FALSE).
• `is_secondary_alignment` Select reads if their alignment status is secondary (TRUE) or not (FALSE). This might be relevant if there are multimapping reads.
• `is_not_passing_quality_controls` Select reads that either pass quality controls (FALSE) or that do not (TRUE).
• `is_duplicate` Select reads that are unduplicated (FALSE) or duplicated (TRUE). This may represent reads that are PCR or optical duplicates.

Value
A DeferredGenomicRanges object

See Also
Rsamtools::BamFile(), GenomicAlignments::readGAlignments()

Examples
if (require(pasillaBamSubset)) {
  bamfile <- untreated1_chr4()
  # nothing is read until an action has been performed
  print(read_bam(bamfile))
  # define a region of interest
  roi <- data.frame(seqnames = "chr4", start = 5e5, end = 7e5) %>%
    as_granges()
  rng <- read_bam(bamfile) %>%
    select(mapq) %>%
    filter_by_overlaps(roi)
}

---

**read_bed**

*Read a BED or BEDGraph file*

**Description**
This is a lightweight wrapper to the import family of functions defined in *rtracklayer*. Read common interval based formats as GRanges.

**Usage**

```r
read_bed(file, col_names = NULL, genome_info = NULL, overlap_ranges = NULL)
```

```r
read_bed_graph(
  file,
  col_names = NULL,
  genome_info = NULL,
)```
read_bed

```r
overlap_ranges = NULL
)

read_narrowpeaks(
  file,
  col_names = NULL,
  genome_info = NULL,
  overlap_ranges = NULL
)
```

**Arguments**

`file` A path to a file or a connection.

`col_names` An optional character vector for including additional columns in `file` that are not part of the BED/narrowPeaks specification.

`genome_info` An optional character string or a Ranges object that contains information about the genome build. For example the USSC identifier "hg19" will add build information to the returned GRanges.

`overlap_ranges` An optional Ranges object. Only the intervals in the file that overlap the Ranges will be returned.

**Details**

This is a lightweight wrapper to the import family of functions defined in `rtracklayer`. The `read_narrowpeaks` function parses the ENCODE narrowPeak BED format (see https://genome.ucsc.edu/FAQ/FAQformat.html#format12 for details.). As such the parser expects four additional columns called (corresponding to the narrowPeaks spec):

- signalValue
- pValue
- qValue
- peak

**Value**

A GRanges object

**See Also**

`rtracklayer::BEDFile()`

**Examples**

```r
test_path <- system.file("tests", package = "rtracklayer")
bed_file <- file.path(test_path, "test.bed")
gr <- read_bed(bed_file)
gr
gr <- read_bed(bed_file, genome_info = "hg19")
gr
```
read_bigwig

Description

Read a BigWig file

Usage

read_bigwig(file, genome_info = NULL, overlap_ranges = NULL)

Arguments

file A path to a file or URL.
genome_info An optional character string or a Ranges object that contains information about the genome build. For example the identifier "hg19" will add build information to the returned GRanges.
overlap_ranges An optional Ranges object. Only the intervals in the file that overlap the Ranges will be loaded.

Value

a GRanges object

See Also

rtracklayer::BigWigFile()

Examples

if (.Platform$OS.type != "windows") {
  test_path <- system.file("tests", package = "rtracklayer")
  bw_file <- file.path(test_path, "test.bw")
  gr <- read_bigwig(bw_file)
  gr
}
read_gff

Read a GFF/GTF/GVT file

Description

This is a lightweight wrapper to the import family of functions defined in `rtracklayer`.

Usage

```r
read_gff(file, col_names = NULL, genome_info = NULL, overlap_ranges = NULL)
read_gff1(file, col_names = NULL, genome_info = NULL, overlap_ranges = NULL)
read_gff2(file, col_names = NULL, genome_info = NULL, overlap_ranges = NULL)
read_gff3(file, col_names = NULL, genome_info = NULL, overlap_ranges = NULL)
```

Arguments

- **file**: A path to a file or a connection.
- **col_names**: An optional character vector for parsing specific columns in file that are part of the GFF specification. These should name either fixed fields, like source or type, or, for GFF2 and GFF3, any attribute.
- **genome_info**: An optional character string or a Ranges object that contains information about the genome build. For example the UCSC identifier "hg19" will add build information to the returned GRanges.
- **overlap_ranges**: An optional Ranges object. Only the intervals in the file that overlap the Ranges will be returned.

Value

A GRanges object

See Also

`rtracklayer::GFFFile()`

Examples

```r
test_path <- system.file("tests", package = "rtracklayer")
# gff3
test_gff3 <- file.path(test_path, "genes.gff3")
gr <- read_gff3(test_gff3)
gr
# alternatively with read_gff
gr <- read_gff(test_gff3, genome_info = "hg19")
gr
```
Description

This is a lightweight wrapper to the import family of functions defined in \texttt{rtracklayer}.

Usage

\begin{verbatim}
read_wig(file, genome_info = NULL, overlap_ranges = NULL)
\end{verbatim}

Arguments

\begin{description}
\item [file] A path to a file or a connection.
\item [genome_info] An optional character string or a Ranges object that contains information about the genome build. For example the USSC identifier "hg19" will add build information to the returned GRanges.
\item [overlap_ranges] An optional Ranges object. Only the intervals in the file that overlap the Ranges will be returned.
\end{description}

Value

A GRanges object

See Also

\texttt{rtracklayer::WIGFile()}

Examples

\begin{verbatim}
test_path <- system.file("tests", package = "rtracklayer")
test_wig <- file.path(test_path, "step.wig")
gr <- read_wig(test_wig)
gr
gr <- read_wig(test_wig, genome_info = "hg19")
\end{verbatim}
reduce_rangesReduce then aggregate a Ranges object

Description
Reduce then aggregate a Ranges object

Usage
reduce_ranges(.data, min.gapwidth = 1L, ...)
reduce_ranges_directed(.data, min.gapwidth = 1L, ...)

Arguments
.data a Ranges object to reduce
min.gapwidth Ranges separated by a gap of at least min.gapwidth positions are not merged.
... Name-value pairs of summary functions.

Value
a Ranges object with the

Examples
set.seed(10)
df <- data.frame(start = sample(1:10),
width = 5,
seqnames = "seq1",
strand = sample(c("+", "-", "x"), 10, replace = TRUE),
gc = runif(10))
rng <- as_granges(df)
rng %>% reduce_ranges()
rng %>% reduce_ranges(gc = mean(gc))
rng %>% reduce_ranges_directed(gc = mean(gc))
rng %>% reduce_ranges_directed(gc = mean(gc), min.gapwidth = 10)
x <- data.frame(start = c(11:13, 2, 7:6),
width=3,
id=sample(letters[1:3], 6, replace = TRUE),
score= sample(1:6))
x <- as_iranges(x)
x %>% reduce_ranges()
x %>% reduce_ranges(score = sum(score))
x %>% group_by(id) %>% reduce_ranges(score = sum(score))
Objects exported from other packages.

Description

These objects are imported from other packages. Follow the links below to see their documentation.

**dplyr**
arrange, filter, group_by, group_vars, groups, mutate, select, slice, summarise, summarize, ungroup

**magrittr**
%>%

**rlang**
!!, !!!

Tools for working with named Ranges

Description

Tools for working with named Ranges

Usage

remove_names(.data)

names_to_column(.data, var = "name")

id_to_column(.data, var = "id")

Arguments

.data a Ranges object

.var Name of column to use for names

Details

The function names_to_column() and id_to_column() always places var as the first column in mcols(.data), shifting all other columns to the left. The id_to_column() creates a column with sequential row identifiers starting at 1, it will also remove any existing names.

Value

Returns a Ranges object with empty names
Examples

```r
ir <- IRanges::IRanges(start = 1:3, width = 4, names = c("a", "b", "c"))
remove_names(ir)
ir_noname <- names_to_column(ir)
ir_noname
ir_with_id <- id_to_column(ir)
ir_with_id
```

**select.Ranges**

Select metadata columns of the Ranges object by name or position

### Description

Select metadata columns of the Ranges object by name or position

### Usage

```r
## S3 method for class 'Ranges'
select(.data, ..., .drop_ranges = FALSE)
```

### Arguments

- `.data` a Ranges object
- `...` One or more metadata column names.
- `.drop_ranges` If TRUE select will always return a tibble. In this case, you may select columns that form the core part of the Ranges object.

### Details

Note that by default select only acts on the metadata columns (and will therefore return a Ranges object) if a core component of a Ranges is dropped or selected without the other required components (this includes the seqnames, strand, start, end, width names), then select will throw an error unless .drop_ranges is set to TRUE.

### Value

a Ranges object or a tibble

### See Also

`dplyr::select()`
**Examples**

```r
df <- data.frame(start = 1:10, width = 5, seqnames = "seq1", strand = sample(c("+", "-", "*"), 10, replace = TRUE), gc = runif(10), counts = rpois(10, 2))
rng <- as_granges(df)
select(rng, -gc)
select(rng, gc)
select(rng, counts, gc)
select(rng, 2:1)
select(rng, seqnames, strand, .drop_ranges = TRUE)
```

---

**set_width**

*Functional setters for Ranges objects*

**Description**

Functional setters for Ranges objects

**Usage**

```r
set_width(x, width)
set_start(x, start = 0L)
set_end(x, end = 0L)
set_seqnames(x, seqnames)
set_strand(x, strand)
```

**Arguments**

- `x` a Ranges object
- `width` integer amount to modify width by
- `start` integer amount to modify start by
- `end` integer amount to modify end by
- `seqnames` update seqnames column
- `strand` update strand column

**Details**

These methods are used internally in `mutate()` to modify core columns in Ranges objects.

**Value**

a Ranges object
shift_left  

Shift all coordinates in a genomic interval left or right, upstream or downstream

Usage

\[
\begin{align*}
\text{shift_left}(x, \text{shift}) &= 0L \\
\text{shift_right}(x, \text{shift}) &= 0L \\
\text{shift_upstream}(x, \text{shift}) &= 0L \\
\text{shift_downstream}(x, \text{shift}) &= 0L
\end{align*}
\]

Arguments

- **x**: a Ranges object.
- **shift**: the amount to move the genomic interval in the Ranges object by. Either a non-negative integer vector of length 1 or an integer vector the same length as x.

Details

Shifting left or right will ignore any strand information in the Ranges object, while shifting upstream/downstream will shift coordinates on the positive strand left/right and the negative strand right/left. By default, unstranded features are treated as positive. When using \text{shift_upstream()} or \text{shift_downstream()} when the shift argument is indexed by the strandedness of the input ranges.

Value

a Ranges object with start and end coordinates shifted.

See Also

IRanges::\text{shift}(), GenomicRanges::\text{shift}()

Examples

\[
\begin{align*}
\text{ir} &\leftarrow \text{as_iranges(data.frame(start = 10:15, width = 5))} \\
\text{shift_left}(\text{ir}, 5L) \\
\text{shift_right}(\text{ir}, 5L) \\
\text{gr} &\leftarrow \text{as_granges(data.frame(start = 10:15, width = 5, seqnames = "seq1")}
\end{align*}
\]
slice.Ranges

Choose rows by their position

Description

Choose rows by their position

Usage

```r
## S3 method for class 'Ranges'
slice(.data, ..., .preserve = FALSE)

## S3 method for class 'GroupedGenomicRanges'
slice(.data, ..., .preserve = FALSE)

## S3 method for class 'GroupedIntegerRanges'
slice(.data, ..., .preserve = FALSE)
```

Arguments

- `.data` a Ranges object
- `...` Integer row values indicating rows to keep. If `.data` has been grouped via `group_by()`, then the positions are selected within each group.
- `.preserve` when FALSE (the default) the grouping structure is recomputed, otherwise it is kept as is. Currently ignored.

Value

a GRanges object

Examples

```r
df <- data.frame(start = 1:10,
                 width = 5,
                 seqnames = "seq1",
                 strand = sample(c("+", "-", "*"), 10, replace = TRUE),
                 gc = runif(10))
rng <- as_granges(df)
dplyr::slice(rng, 1:2)
dplyr::slice(rng, -n())
dplyr::slice(rng, -5:-n())

by_strand <- group_by(rng, strand)
```
# slice with group by finds positions within each group
dplyr::slice(by_strand, n())
dplyr::slice(by_strand, which.max(gc))

# if the index is beyond the number of groups slice are ignored
dplyr::slice(by_strand, 1:3)

---

### stretch

**Stretch a genomic interval**

**Description**

By default, `stretch(x)` will anchor by the center of a `Ranges` object. This means that half of the value of `extend` will be added to the end of the range and the remaining half subtracted from the start of the Range. The other anchors will leave the start/end fixed and stretch the end/start respectively.

**Usage**

`stretch(x, extend)`

**Arguments**

- **x**
  
a Ranges object, to fix by either the start, end or center of an interval use `anchor_start(x)`, `anchor_end(x)`, `anchor_center(x)`. To fix by strand use `anchor_3p(x)` or `anchor_5p(x)`.

- **extend**
  
the amount to alter the width of a Ranges object by. Either an integer vector of length 1 or an integer vector the same length as `x`.

**Value**

a Ranges object with modified start or end (or both) coordinates

**See Also**

`anchor()`, `mutate()`

**Examples**

```r
rng <- as_iranges(data.frame(start=c(2:-1, 13:15), width=c(0:3, 2:0)))
rng2 <- stretch(anchor_center(rng), 10)
stretch(anchor_start(rng2), 10)
stretch(anchor_end(rng2), 10)

grng <- as_granges(data.frame(seqnames = "chr1",
                               strand = c("+", "-", "-", "+", "+", "+", "+", "+", "+", "+"),
                               start=c(2:-1, 13:15),
                               width=c(0:3, 2:0)))
```
summarise.Ranges

Reduce multiple values in a Ranges down to a single value

Description

Reduce multiple values in a Ranges down to a single value

Usage

## S3 method for class 'Ranges'
summarise(.data, ...)

Arguments

.data a Ranges object

... Name-value pairs of summary functions. The name will be the name of the
variable in the result. The value should be an expression that will return a value
that has length one or length equal to the number of groups.

Details

Creates one or more variables as a S4Vectors::DataFrame() from the input Ranges object. If
the ranges object is grouped, there will be a row for each group. Because grouping may remove
whether a Ranges object is valid, a DataFrame is always returned.

Value

A S4Vectors::DataFrame()

Examples

df <- data.frame(start = 1:10, width = 5, seqnames = "seq1", strand = sample(c("+", "-", "*")), 10, replace = TRUE), gc = runif(10))
rng <- as_granges(df)
rng %>% summarise(gc = mean(gc))
rng %>% group_by(strand) %>% summarise(gc = mean(gc))
tile_ranges

Slide or tile over a Ranges object

Description

Slide or tile over a Ranges object

Usage

```
tile_ranges(x, width)
slide_ranges(x, width, step)
```

Arguments

- `x` a Ranges object
- `width` the maximum width of each window/tile (integer vector of length 1)
- `step` the distance between start position of each sliding window (integer vector of length 1)

Details

The `tile_ranges()` function partitions a Ranges object `x` by the given the `width` over all ranges in `x`, truncated by the sequence end. The `slide_ranges()` function makes sliding windows within each range of `x` of size `width` and sliding by `step`. Both `slide_ranges()` and `tile_ranges()` return a new Ranges object with a metadata column called "partition" which contains the index of the input range `x` that a partition belongs to.

Value

- a Ranges object

See Also

- GenomicRanges::tile()

Examples

```
gr <- data.frame(seqnames = c("chr1", rep("chr2", 3), rep("chr1", 2), rep("chr3", 4)),
                 start = 1:10,
                 end = 11,
                 strand = c("-", rep("+", 2), rep("x", 2), rep("+", 3), rep("-", 2)))
as_granges() %>%
set_genome_info(seqlengths = c(11,12,13))
```

# partition ranges into subranges of width 2, odd width ranges
# will have one subrange of width 1
tile_ranges(gr, width = 2)
# make sliding windows of width 3, moving window with step size of 2
slide_ranges(gr, width = 3, step = 2)

write_bed

Write a BED or BEDGraph file

Description
This is a lightweight wrapper to the export family of functions defined in rtracklayer.

Usage
write_bed(x, file, index = FALSE)
write_bed_graph(x, file, index = FALSE)
write_narrowpeaks(x, file)

Arguments
x   A GRanges object
file File name, URL or connection specifying a file to write x to. Compressed files
      with extensions such as `.gz' are handled automatically. If you want to index the
      file with tabix use the index argument.
index Compress and index the output file with bgzf and tabix (default = FALSE). Note
       that tabix indexing will sort the data by chromosome and start.

Value
The write functions return a BED(Graph)File invisibly

See Also
rtracklayer::BEDFile()

Examples
## Not run:
test_path <- system.file("tests", package = "rtracklayer")
bed_file <- file.path(test_path, "test.bed")
gr <- read_bed(bed_file)
bed_file_out <- file.path(tempdir(), "new.bed")
write_bed(gr, bed_file_out)
read_bed(bed_file_out)
'bedgraph'
bg_file <- file.path(test_path, "test.bedGraph")
write_bigwig

Write a BigWig file

Description

This is a lightweight wrapper to the export family of functions defined in rtracklayer.

Usage

write_bigwig(x, file)

Arguments

  x       A GRanges object
  file    File name, URL or connection specifying a file to write x to. Compressed files
          with extensions such as '.gz' are handled automatically.

Value

The write functions return a BigWigFile invisibly

See Also

rtracklayer::BigWigFile()

Examples

## Not run:
if (.Platform$OS.type != "windows") {
  test_path <- system.file("tests", package = "rtracklayer")
  bw_file <- file.path(test_path, "test.bw")
  gr <- read_bigwig(bw_file)
  gr
  bw_out <- file.path(tempdir(), "test_out.bw")
  write_bigwig(gr, bw_out)
  read_bigwig(bw_out)
write_gff

Write a GFF(123) file

Description

This is a lightweight wrapper to the export family of functions defined in rtracklayer.

Usage

`write_gff(x, file, index = FALSE)`

`write_gff1(x, file, index = FALSE)`

`write_gff2(x, file, index = FALSE)`

`write_gff3(x, file, index = FALSE)`

Arguments

`x`          A GRanges object

`file`       Path or connection to write to

`index`      If TRUE the output file will be compressed and indexed using bgzf and tabix.

Value

The write function returns a GFFFile object invisibly

See Also

rtracklayer::GFFFile()

Examples

```r
## Not run:
test_path <- system.file("tests", package = "rtracklayer")
test_gff3 <- file.path(test_path, "genes.gff3")
gr <- read_gff3(test_gff3)
out_gff3 <- file.path(tempdir(), "test.gff3")
write_gff3(gr, out_gff3)
read_gff3(out_gff3)
```

## End(Not run)
### write_wig

**Description**

Write a WIG file

**Usage**

```r
write_wig(x, file)
```

**Arguments**

- `x` A GRanges object
- `file` File name, URL or connection specifying a file to write `x` to. Compressed files with extensions such as `.gz` are handled automatically.

**Value**

The write function returns a WIGFile invisibly.

**See Also**

- `rtracklayer::WIGFile()`

### %union%

**Description**

Row-wise set operations on Ranges objects

**Usage**

```r
x %union% y
x %intersect% y
x %setdiff% y
between(x, y)
span(x, y)
```
Arguments

x, y  Ranges objects

Details

Each of these functions acts on the rows between pairs of Ranges object. The function `%union%()` will return the entire range between two ranges objects assuming there are no gaps, if you would like to force gaps use `span()` instead. The function `%intersect%()` will create a new ranges object with a hit column indicating whether or not the two ranges intersect. The function `%setdiff%()` will return the ranges for each row in x that are not in the corresponding row of y. The function `between()` will return the gaps between two ranges.

Value

A Ranges object

See Also

[IRanges::punion()][IRanges::pintersect()][IRanges::pgap()][IRanges::psetdiff()]

Examples

```r
x <- as_iranges(data.frame(start = 1:10, width = 5))  # stretch x by 3 on the right
y <- stretch(anchor_start(x), 3)  # take the rowwise union
x %union% y  # take the rowwise intersection
x %intersect% y  # asymmetric difference
y %setdiff% x
x %setdiff% y

# if there are gaps between the rows of each range use span
y <- as_iranges(data.frame(start = c(20:15, 2:5),
                       width = c(10:15, 1:4)))  # fill in the gaps and take the rowwise union
span(x,y)
# find the gaps
between(x,y)
```
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