

# Package ‘plyranges’

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**Type** Package

**Title** A fluent interface for manipulating GenomicRanges

**Version** 1.33.0

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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.

**URL** <https://tidyomics.github.io/plyranges>

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**BugReports** <https://github.com/tidyomics/plyranges>

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'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' '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-mcols.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'  
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## Contents

plyranges-package . . . . .	3
add_nearest_distance . . . . .	4
anchor . . . . .	5
arrange.Ranges . . . . .	7
as_iranges . . . . .	8
as_ranges . . . . .	9
bind_ranges . . . . .	9
chop_by_introns . . . . .	10
compute_coverage . . . . .	11
count_overlaps . . . . .	12
DeferredGenomicRanges-class . . . . .	13
disjoin_ranges . . . . .	14
expand_ranges . . . . .	14
FileOperator-class . . . . .	15
filter-ranges . . . . .	16
filter_by_overlaps . . . . .	17
find_overlaps . . . . .	18
flank_left . . . . .	20
GroupedGenomicRanges-class . . . . .	22
intersect_ranges . . . . .	23
interweave . . . . .	24
join_follow . . . . .	25
join_mcols_inner . . . . .	26

join_nearest . . . . .	27
join_overlap_intersect . . . . .	29
join_overlap_self . . . . .	31
join_precede . . . . .	32
mutate.Ranges . . . . .	33
n . . . . .	35
n_distinct . . . . .	35
overscope_ranges . . . . .	36
pair_overlaps . . . . .	36
pull-ranges . . . . .	38
ranges-info . . . . .	39
read_bam . . . . .	40
read_bed . . . . .	42
read_bigwig . . . . .	43
read_gff . . . . .	44
read_wig . . . . .	45
reduce_ranges . . . . .	46
remove_names . . . . .	47
select.Ranges . . . . .	47
set_width . . . . .	48
shift_left . . . . .	49
slice.Ranges . . . . .	50
stretch . . . . .	54
summarise.Ranges . . . . .	55
tile_ranges . . . . .	55
write_bed . . . . .	56
write_bigwig . . . . .	57
write_gff . . . . .	58
write_wig . . . . .	59
%union% . . . . .	60
%>% . . . . .	61
<b>Index</b>	<b>62</b>

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plyranges-package      *plyranges: a grammar of genomic data manipulation*

---

## Description

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

## 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")`

### Author(s)

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### See Also

Useful links:

- <https://tidyomics.github.io/plyranges>
- Report bugs at <https://github.com/tidyomics/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

```
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 downstream 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.

**See Also**

[join\\_nearest](#)

**Examples**

```
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()

add_nearest_distance(query, subject)
add_nearest_distance_left(query, subject)
add_nearest_distance_right(query, subject)
```

---

anchor

*Anchored 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 arithmetic. 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.Ranges](#), [stretch](#)

**Examples**

```
df <- data.frame(start = 1:10, width = 5)
rng <- 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	<i>Sort a Ranges object</i>
----------------	-----------------------------

---

**Description**

Sort a Ranges object

**Usage**

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

**Arguments**

<code>.data</code>	A Ranges object.
<code>...</code>	Comma separated list of variable names.

**Value**

A sorted Ranges object

**Examples**

```
rng <- as_iranges(data.frame(start = 1:10, width = 10:1))
rng <- 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**

```
as_iranges(.data, ..., keep_mcols = TRUE)
```

```
as_granges(.data, ..., keep_mcols = TRUE)
```

**Arguments**

`.data` a `data.frame()` or `dplyr::tibble()` to construct a Ranges object from  
`...` optional named arguments specifying which the columns in `.data` contain the core components a Ranges object.  
`keep_mcols` place the remaining columns into the metadata columns slot (default=TRUE)

**Value**

a Ranges object.

**See Also**

`IRanges::IRanges()`, `GenomicRanges::GRanges()`

**Examples**

```
df <- data.frame(start=c(2:-1, 13:15), width=c(0:3, 2:0))
as_iranges(df)

df <- data.frame(start=c(2:-1, 13:15), width=c(0:3, 2:0), strand = "+")
# will return an IRanges object
as_iranges(df)

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

# as_g/iranges understand alternate name specification
df <- data.frame(start=c(2:-1, 13:15), width=c(0:3, 2:0),
strand = "+", chr = "chr1")
as_granges(df, seqnames = chr)

# can also handle DFrame input
df <- methods::as(df, "DFrame")
df$y <- IRanges::IntegerList(c(1,2,3), NA, 5, 6, 8, 9, 10:12)
as_iranges(df)
as_granges(df, seqnames = chr)
```

---

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

---

**Description**

Coerce an Rle or RleList object to Ranges

**Usage**

```
as_ranges(.data)
```

**Arguments**

`.data` a `S4Vectors::Rle()` or an `IRanges::RleList()` object.

**Details**

This function is behind `compute_coverage()`.

**Value**

an `IRanges::IRanges()` object if the input is an `S4Vectors::Rle()` object or a `GenomicRanges::GRanges()` object for an `IRanges::RleList()` object.

**See Also**

`S4Vectors::Rle()`, `IRanges::RleList()`

**Examples**

```
x <- S4Vectors::Rle(10:1, 1:10)
as_ranges(x)

# must have names set
y <- IRanges::RleList(chr1 = x)
as_ranges(y)
```

---

`bind_ranges`*Combine Ranges by concatenating them together*

---

**Description**

Combine Ranges by concatenating them together

**Usage**

```
bind_ranges(..., .id = NULL)
```

**Arguments**

...	Ranges objects to combine. Each argument can be a Ranges object, or a list of Ranges objects.
.id	Ranges object identifier. When .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.

**Value**

a concatenated Ranges object

**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

**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 original ranges.

**See Also**

`IRanges::coverage()`, `GenomicRanges::coverage()`

**Examples**

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

---

count\_overlaps

*Count the number of overlaps between two Ranges objects*

---

**Description**

Count the number of overlaps between two Ranges objects

**Usage**

```
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**

```
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

*DeferredGenomiRanges 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**

```
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**

```
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))
```

---

expand\_ranges                    *Expand list-columns in a Ranges object*

---

**Description**

Expand list-columns in a Ranges object

**Usage**

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

**Arguments**

<code>data</code>	A Ranges object
<code>...</code>	list-column names to expand then unlist
<code>.drop</code>	Should additional list columns be dropped (default = FALSE)? By default <code>expand_ranges()</code> will keep other list columns even if they are nested.
<code>.id</code>	A character vector of length equal to number of list columns. If supplied will create new column(s) with name <code>.id</code> identifying the index of the list column (default = NULL).
<code>.keep_empty</code>	If a list-like column contains empty elements, should those elements be kept? (default = FALSE)
<code>.recursive</code>	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**

```
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	<i>Subset a Ranges object</i>
---------------	-------------------------------

---

**Description**

Subset a Ranges object

**Usage**

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

**Arguments**

.data	A Ranges object
...	valid logical predicates 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 separately on each partition of the data.

**Value**

a Ranges object

**See Also**

[dplyr::filter\(\)](#)

**Examples**

```
set.seed(100)
df <- data.frame(start = 1:10,
                 width = 5,
                 seqnames = "seq1",
                 strand = sample(c("+", "-", "*"), 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

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

## Details

By default, `filter_by_overlaps` and `filter_by_non_overlaps` ignore strandedness for `GenomicRanges::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.

## 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(6,6,3,3,3,9),
                 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

*Find overlap between two Ranges*


---

**Description**

Find overlap between two Ranges

**Usage**

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

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

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

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**

```
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

```
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)
```

---

GroupedGenomicRanges-class

*Group a Ranges by one or more variables*

---

### 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

```
## 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

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

```
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 (eit)

**Value**

a Ranges object

**Examples**

```
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**

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

**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 copi

**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("+", "-"),
  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_mcols_inner	<i>Join data by metadata columns</i>
------------------	--------------------------------------

---

**Description**

These functions enable joins based on metadata of *x* and data in *y*, utilizing `S4Vectors::merge()`.

**Usage**

```
join_mcols_inner(x, y, by = NULL, ...)
```

```
join_mcols_left(x, y, by = NULL, ...)
```

**Arguments**

<i>x</i>	Object representing ranges, with metadata columns containing variables for matching
<i>y</i>	A table of data, <code>DataFrame</code> , <code>data.frame</code> or <code>tibble</code>
<i>by</i>	Specifications of the columns used for merging. Passed to <code>S4Vectors::merge()</code>
<i>...</i>	Additional arguments passed to <code>S4Vectors::merge()</code>

**Details**

The function `join_mcols_inner()` returns ranges in `x` only when a match is found in the columns specified with `by` in the table `y`.

The function `join_mcols_left()` returns all ranges in `x` regardless of a match in `y`, with duplications possible from multiple matches.

**Value**

Object representing ranges, with new metadata columns

**Examples**

```
x <- as_granges(data.frame(
  seqnames = "chr1", start = 1:5, width=10,
  id=c(1:4,4), foo=letters[1:5]
))
y <- DataFrame(id=c(1:2,2,4), bar=letters[6:9])

# metadata joins:
join_mcols_inner(x, y, by="id")
join_mcols_left(x, y, by="id")
```

---

 join\_nearest

*Find nearest neighbours between two Ranges objects*


---

**Description**

Find nearest neighbours between two Ranges objects

**Usage**

```
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**

<code>x, y</code>	Ranges objects, add the nearest neighbours of ranges in <code>x</code> to those in <code>y</code> .
<code>suffix</code>	A character vector of length two used to identify metadata columns
<code>distance</code>	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 downstream 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

```
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**`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_left(x, y, maxgap, minoverlap, suffix = c(".x", ".y"), distance)

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

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

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

```

### Arguments

<code>x, y</code>	Objects representing ranges
<code>maxgap, minoverlap</code>	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.
<code>suffix</code>	Character to vectors to append to common columns in <code>x</code> and <code>y</code> (default = <code>c(".x", ".y")</code> ).
<code>distance</code>	logical, whether to add a column named "distance" containing the distance between the ranges, relevant with non-zero <code>maxgap</code> values. Available for <code>join_overlap_left()</code> and the <code>_directed()</code> version.

### 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**

```
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**

```
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.

**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**

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

**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 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**

```
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	<i>Compute the number of ranges in each group.</i>
---	--

---

**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	<i>Compute the number of distinct unique values in a vector or List</i>
------------	---

---

**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**

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

---

overscope_ranges	<i>Create an overscoped environment from a Ranges object</i>
------------------	--

---

**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.

**Value**

an environment

**See Also**

[rlang::new\\_data\\_mask\(\)](#), [rlang::eval\\_tidy\(\)](#)

---

pair_overlaps	<i>Pair together two ranges objects</i>
---------------	---

---

**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**

```
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"))
```

---

 pull-ranges

---

*Extract a single column from a Ranges object as a vector*


---

### Description

Extract a single column from a Ranges object as a vector

### Usage

```
## S3 method for class 'Ranges'
pull(.data, var = -1, name = NULL, ...)
```

### Arguments

.data	a Ranges object
var	A variable specified as: <ul style="list-style-type: none"> <li>• a literal variable name</li> <li>• a positive integer, giving the position counting from the left. In this case order is start, end, width, (strand, seqnames), gc and score.</li> <li>• a negative integer, giving the position counting from the right. The default returns the last column (on the assumption that's the column you've created most recently). This argument is taken by expression and supports quasiquotation (you can unquote column names and column locations).</li> </ul>
name	An optional parameter that specifies the column to be used as names for a named vector. Specified in a similar manner as var.
...	For use by methods.

### See Also

[dplyr::pull\(\)](#)

### Examples

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

# Pull parts of the range
pull(rng, start)
# equivalent to start(rng)

# Pull by column name
pull(rng, gc)
pull(rng, score)

# Pull by position (positive from left, negative from right)
pull(rng, 1) # First metadata column
```

```

pull(rng, -1) # Last metadata column (default)
pull(rng, -2) # Second to last metadata column

# Pull with names
pull(rng, score, name = gc)

```

---

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

```

genome_info(
  genome = NULL,
  seqnames = NULL,
  seqlengths = NULL,
  is_circular = NULL
)

set_genome_info(
  .data,
  genome = NULL,
  seqnames = NULL,
  seqlengths = NULL,
  is_circular = NULL
)

get_genome_info(.data)

```

## Arguments

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

## Value

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

## See Also

[Seqinfo::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")
}

## End(Not run)
```

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), mrrm (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

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

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

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

### Arguments

<code>file</code>	A path to a file or a connection.
<code>col_names</code>	An optional character vector for including additional columns in file that are not part of the BED/narrowPeaks specification.
<code>genome_info</code>	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.
<code>overlap_ranges</code>	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**

```
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
olap <- as_granges(data.frame(seqnames = "chr7", start = 1, end = 127473000))
gr <- read_bed(bed_file,
               overlap_ranges = olap)
# bedGraph
bg_file <- file.path(test_path, "test.bedGraph")
gr <- read_bed_graph(bg_file)
gr
# narrowpeaks
np_file <- system.file("extdata", "demo.narrowPeak.gz", package="rtracklayer")
gr <- read_narrowpeaks(np_file, genome_info = "hg19")
gr
```

---

read\_bigwig

*Read a BigWig file*

---

**Description**

Read a BigWig file

**Usage**

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

**Arguments**

<code>file</code>	A path to a file or URL.
<code>genome_info</code>	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.
<code>overlap_ranges</code>	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**

```
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**

<code>file</code>	A path to a file or a connection.
<code>col_names</code>	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.
<code>genome_info</code>	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.
<code>overlap_ranges</code>	An optional Ranges object. Only the intervals in the file that overlap the Ranges will be returned.

**Value**

A GRanges object  
 a GRanges object

**See Also**

`rtracklayer::GFFFile()`

## Examples

```
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
```

---

read\_wig

*Read a WIG file*

---

## Description

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

## Usage

```
read_wig(file, genome_info = NULL, overlap_ranges = NULL)
```

## Arguments

file	A path to a file or a connection.
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.

## Value

A GRanges object  
A GRanges object

## See Also

`rtracklayer::WIGFile()`

## Examples

```
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")
```

---

reduce_ranges	<i>Reduce then aggregate a Ranges object</i>
---------------	--

---

### 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("+", "-", "*"), 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))
```

---

remove_names	<i>Tools for working with named Ranges</i>
--------------	--

---

**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**

```
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	<i>Select metadata columns of the Ranges object by name or position</i>
---------------	---

---

**Description**

Select metadata columns of the Ranges object by name or position

**Usage**

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

**Arguments**

<code>.data</code>	a Ranges object
<code>...</code>	One or more metadata column names.
<code>.drop_ranges</code>	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**

```
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**

```
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	<i>Shift all coordinates in a genomic interval left or right, upstream or downstream</i>
------------	--

---

**Description**

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

**Usage**

```
shift_left(x, shift = 0L)
```

```
shift_right(x, shift = 0L)
```

```
shift_upstream(x, shift = 0L)
```

```
shift_downstream(x, shift = 0L)
```

**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 `shift_upstream()` or `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::shift(), GenomicRanges::shift()

**Examples**

```
ir <- as_iranges(data.frame(start = 10:15, width = 5))
shift_left(ir, 5L)
shift_right(ir, 5L)
gr <- as_granges(data.frame(start = 10:15,
                           width = 5,
                           seqnames = "seq1",
                           strand = c("+", "+", "-", "-", "+", "*")))
shift_upstream(gr, 5L)
shift_downstream(gr, 5L)
```

---

slice.Ranges

*Choose ranges by their position*

---

**Description**

The slice family of functions let you select ranges by position. They follow the same conventions as their dplyr counterparts for data frames:

- slice() selects ranges by explicit integer position.
- slice\_head() / slice\_tail() select the first or last ranges.
- slice\_sample() randomly selects ranges.
- slice\_min() / slice\_max() select ranges with the smallest or largest values of a metadata column.

All functions preserve grouping: when .data has been grouped with dplyr::group\_by(), selection is performed within each group.

**Usage**

```
## 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)

## S3 method for class 'Ranges'
slice_head(.data, ..., n = NULL, prop = NULL, .preserve = FALSE)

## S3 method for class 'GroupedGenomicRanges'
```

```
slice_head(.data, ..., n = NULL, prop = NULL, .preserve = FALSE)

## S3 method for class 'GroupedIntegerRanges'
slice_head(.data, ..., n = NULL, prop = NULL, .preserve = FALSE)

## S3 method for class 'Ranges'
slice_tail(.data, ..., n = NULL, prop = NULL, .preserve = FALSE)

## S3 method for class 'GroupedGenomicRanges'
slice_tail(.data, ..., n = NULL, prop = NULL, .preserve = FALSE)

## S3 method for class 'GroupedIntegerRanges'
slice_tail(.data, ..., n = NULL, prop = NULL, .preserve = FALSE)

## S3 method for class 'Ranges'
slice_sample(
  .data,
  ...,
  n = NULL,
  prop = NULL,
  weight_by = NULL,
  replace = FALSE,
  .preserve = FALSE
)

## S3 method for class 'GroupedGenomicRanges'
slice_sample(
  .data,
  ...,
  n = NULL,
  prop = NULL,
  weight_by = NULL,
  replace = FALSE,
  .preserve = FALSE
)

## S3 method for class 'GroupedIntegerRanges'
slice_sample(
  .data,
  ...,
  n = NULL,
  prop = NULL,
  weight_by = NULL,
  replace = FALSE,
  .preserve = FALSE
)

## S3 method for class 'Ranges'
slice_min(
  .data,
  order_by,
  ...,
```

```
n = NULL,
prop = NULL,
with_ties = TRUE,
.preserve = FALSE
)

## S3 method for class 'GroupedGenomicRanges'
slice_min(
  .data,
  order_by,
  ...,
  n = NULL,
  prop = NULL,
  with_ties = TRUE,
  .preserve = FALSE
)

## S3 method for class 'GroupedIntegerRanges'
slice_min(
  .data,
  order_by,
  ...,
  n = NULL,
  prop = NULL,
  with_ties = TRUE,
  .preserve = FALSE
)

## S3 method for class 'Ranges'
slice_max(
  .data,
  order_by,
  ...,
  n = NULL,
  prop = NULL,
  with_ties = TRUE,
  .preserve = FALSE
)

## S3 method for class 'GroupedGenomicRanges'
slice_max(
  .data,
  order_by,
  ...,
  n = NULL,
  prop = NULL,
  with_ties = TRUE,
  .preserve = FALSE
)

## S3 method for class 'GroupedIntegerRanges'
slice_max(
```

```

    .data,
    order_by,
    ...,
    n = NULL,
    prop = NULL,
    with_ties = TRUE,
    .preserve = FALSE
  )

```

### Arguments

<code>.data</code>	a Ranges object.
<code>...</code>	<data-masking> Integer row values indicating positions to keep. Only used by <code>slice()</code> ; ignored elsewhere.
<code>.preserve</code>	Ignored; retained for compatibility with the dplyr generic.
<code>n</code>	Number of ranges to select. Mutually exclusive with <code>prop</code> . For <code>slice_min()</code> and <code>slice_max()</code> , negative values are not supported.
<code>prop</code>	Fraction of ranges to select, in $(0, 1]$ . Mutually exclusive with <code>n</code> .
<code>weight_by</code>	<data-masking> Unquoted name of a non-negative numeric metadata column used as sampling weights. Used by <code>slice_sample()</code> .
<code>replace</code>	Should sampling be with replacement? Default FALSE. Used by <code>slice_sample()</code> .
<code>order_by</code>	<data-masking> Unquoted name of a numeric metadata column to order by. Used by <code>slice_min()</code> and <code>slice_max()</code> .
<code>with_ties</code>	If TRUE (the default), all ranges tied at the boundary rank are kept, which may return more than <code>n</code> ranges. Set to FALSE to return exactly <code>n</code> . Used by <code>slice_min()</code> and <code>slice_max()</code> .

### Value

A GRanges (or IRanges) object of the same class as `.data`, with grouping structure re-applied when `.data` was grouped.

### Examples

```

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	<i>Stretch a genomic interval</i>
---------	-----------------------------------

---

### 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 <code>anchor_start(x)</code> , <code>anchor_end(x)</code> , <code>anchor_center(x)</code> . To fix by strand use <code>anchor_3p(x)</code> or <code>anchor_5p(x)</code> .
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

```
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)))
stretch(anchor_3p(grng), 10)
stretch(anchor_5p(grng), 10)
```

---

summarise.Ranges	<i>Reduce multiple values in a Ranges down to a single value</i>
------------------	--

---

**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	<i>Slide or tile over a Ranges object</i>
-------------	---

---

**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("*", 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")
gr <- read_bed_graph(bg_file)
bg_file_out <- file.path(tempdir(), "new.bg")
write_bed(gr, bg_file_out)
read_bed(bg_file_out)
# narrowpeaks
np_file <- system.file("extdata", "demo.narrowPeak.gz", package="rtracklayer")
gr <- read_narrowpeaks(np_file, genome_info = "hg19")
np_file_out <- file.path(tempdir(), "new.bg")
write_narrowpeaks(gr, np_file_out)
read_narrowpeaks(np_file_out)

## End(Not run)
```

---

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)
}

## End(Not run)
```

---

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**

```
## 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

*Write a WIG file*

---

**Description**

Write a WIG file

**Usage**

```
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%`*Row-wise set operations on Ranges objects*

---

**Description**

Row-wise set operations on Ranges objects

**Usage**`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**

```
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)
```

---

`%>%`*Pipe operator*

---

**Description**

See *magrittr* documentation for ‘`%>%`’ for details.

**Usage**

```
lhs %>% rhs
```

**Arguments**

lhs	A value or the magrittr placeholder.
rhs	A function call using the magrittr semantics.

**Value**

The result of calling `rhs(lhs)`.

# Index

- \* **internal**
  - %>%, 61
- %intersect% (%union%), 60
- %setdiff% (%union%), 60
- %>%, 61
- %union%, 60
  
- add\_nearest\_distance, 4
- add\_nearest\_distance\_downstream
  - (add\_nearest\_distance), 4
- add\_nearest\_distance\_left
  - (add\_nearest\_distance), 4
- add\_nearest\_distance\_right
  - (add\_nearest\_distance), 4
- add\_nearest\_distance\_upstream
  - (add\_nearest\_distance), 4
- anchor, 5
- anchor\_3p (anchor), 5
- anchor\_5p (anchor), 5
- anchor\_center (anchor), 5
- anchor\_centre (anchor), 5
- anchor\_end (anchor), 5
- anchor\_start (anchor), 5
- arrange.Ranges, 7
- as\_granges (as\_iranges), 8
- as\_iranges, 8
- as\_ranges, 9
  
- BamFile(), 41
- BamFileOperator-class
  - (FileOperator-class), 15
- BEDFile(), 43, 57
- between (%union%), 60
- between(), 60
- BigWigFile(), 44, 58
- bind\_ranges, 9
  
- chop\_by\_gaps (chop\_by\_introns), 10
- chop\_by\_introns, 10
- complement\_ranges (intersect\_ranges), 23
- complement\_ranges\_directed
  - (intersect\_ranges), 23
- compute\_coverage, 11
- compute\_coverage(), 9
  
- count\_overlaps, 12
- count\_overlaps\_directed
  - (count\_overlaps), 12
- count\_overlaps\_within (count\_overlaps), 12
- count\_overlaps\_within\_directed
  - (count\_overlaps), 12
- coverage(), 12
  
- data.frame(), 8
- DataFrame(), 55
- DeferredGenomicRanges-class, 13
- disjoin\_ranges, 14
- disjoin\_ranges\_directed
  - (disjoin\_ranges), 14
- dplyr::filter(), 16
- dplyr::group\_by(), 50
- dplyr::pull(), 38
- dplyr::select(), 48
- dplyr::tibble(), 8
  
- expand\_ranges, 14
  
- FileOperator-class, 15
- filter-ranges, 16
- filter.Ranges (filter-ranges), 16
- filter\_by\_non\_overlaps
  - (filter\_by\_overlaps), 17
- filter\_by\_non\_overlaps\_directed
  - (filter\_by\_overlaps), 17
- filter\_by\_overlaps, 17
- filter\_by\_overlaps\_directed
  - (filter\_by\_overlaps), 17
- find\_overlaps, 18
- find\_overlaps(), 30–32
- find\_overlaps\_directed (find\_overlaps), 18
- find\_overlaps\_within (find\_overlaps), 18
- find\_overlaps\_within\_directed
  - (find\_overlaps), 18
- findOverlaps(), 20
- flank(), 21
- flank\_downstream (flank\_left), 20
- flank\_left, 20

- flank\_right (flank\_left), 20
- flank\_upstream (flank\_left), 20
- genome\_info (ranges-info), 39
- GenomicAlignments::readGAlignments(), 41
- GenomicRanges::GRanges(), 9, 17
- get\_genome\_info (ranges-info), 39
- GFFFile(), 44, 59
- GRanges(), 8
- group\_by-ranges
  - (GroupedGenomicRanges-class), 22
- group\_by.GenomicRanges
  - (GroupedGenomicRanges-class), 22
- group\_by\_overlaps (find\_overlaps), 18
- GroupedGenomicRanges-class, 22
- GroupedIntegerRanges-class
  - (GroupedGenomicRanges-class), 22
- groups.GroupedGenomicRanges
  - (GroupedGenomicRanges-class), 22
- groups.GroupedIntegerRanges
  - (GroupedGenomicRanges-class), 22
- id\_to\_column (remove\_names), 47
- intersect\_ranges, 23
- intersect\_ranges\_directed
  - (intersect\_ranges), 23
- interweave, 24
- IRanges(), 8
- IRanges::IRanges(), 9
- IRanges::RleList(), 9
- join\_follow, 25
- join\_follow\_left (join\_follow), 25
- join\_follow\_upstream (join\_follow), 25
- join\_mcols\_inner, 26
- join\_mcols\_inner(), 27
- join\_mcols\_left (join\_mcols\_inner), 26
- join\_mcols\_left(), 27
- join\_nearest, 5, 27
- join\_nearest\_downstream (join\_nearest), 27
- join\_nearest\_left (join\_nearest), 27
- join\_nearest\_right (join\_nearest), 27
- join\_nearest\_upstream (join\_nearest), 27
- join\_overlap\_inner
  - (join\_overlap\_intersect), 29
- join\_overlap\_inner(), 30, 32
- join\_overlap\_inner\_directed
  - (join\_overlap\_intersect), 29
- join\_overlap\_inner\_within
  - (join\_overlap\_intersect), 29
- join\_overlap\_inner\_within\_directed
  - (join\_overlap\_intersect), 29
- join\_overlap\_intersect, 29
- join\_overlap\_intersect(), 30
- join\_overlap\_intersect\_directed
  - (join\_overlap\_intersect), 29
- join\_overlap\_intersect\_within
  - (join\_overlap\_intersect), 29
- join\_overlap\_intersect\_within\_directed
  - (join\_overlap\_intersect), 29
- join\_overlap\_left
  - (join\_overlap\_intersect), 29
- join\_overlap\_left(), 30, 31
- join\_overlap\_left\_directed
  - (join\_overlap\_intersect), 29
- join\_overlap\_left\_within
  - (join\_overlap\_intersect), 29
- join\_overlap\_left\_within\_directed
  - (join\_overlap\_intersect), 29
- join\_overlap\_self, 31
- join\_overlap\_self(), 30, 31
- join\_overlap\_self\_directed
  - (join\_overlap\_self), 31
- join\_overlap\_self\_within
  - (join\_overlap\_self), 31
- join\_overlap\_self\_within\_directed
  - (join\_overlap\_self), 31
- join\_precede, 32
- join\_precede\_downstream (join\_precede), 32
- join\_precede\_right (join\_precede), 32
- mutate.Ranges, 7, 33
- n, 35
- n\_distinct, 35
- names\_to\_column (remove\_names), 47
- overscope\_ranges, 36
- pair\_follow (pair\_overlaps), 36
- pair\_nearest (pair\_overlaps), 36
- pair\_overlaps, 36
- pair\_precede (pair\_overlaps), 36
- plyranges (plyranges-package), 3
- plyranges-package, 3
- pull-ranges, 38
- pull.Ranges (pull-ranges), 38
- ranges-info, 39

- read\_bam, 40
- read\_bed, 42
- read\_bed\_graph (read\_bed), 42
- read\_bigwig, 43
- read\_gff, 44
- read\_gff1 (read\_gff), 44
- read\_gff2 (read\_gff), 44
- read\_gff3 (read\_gff), 44
- read\_narrowpeaks (read\_bed), 42
- read\_wig, 45
- reduce\_ranges, 46
- reduce\_ranges\_directed (reduce\_ranges), 46
- remove\_names, 47
- rlang::eval\_tidy(), 36
- rlang::new\_data\_mask(), 36
- Rle(), 9
- RleList(), 9
- S4Vectors::merge(), 26
- S4Vectors::Rle(), 9
- select.Ranges, 47
- Seqinfo::Seqinfo(), 39
- set\_end (set\_width), 48
- set\_genome\_info (ranges-info), 39
- set\_seqnames (set\_width), 48
- set\_start (set\_width), 48
- set\_strand (set\_width), 48
- set\_width, 48
- setdiff\_ranges (intersect\_ranges), 23
- setdiff\_ranges\_directed (intersect\_ranges), 23
- shift(), 50
- shift\_downstream (shift\_left), 49
- shift\_downstream(), 49
- shift\_left, 49
- shift\_right (shift\_left), 49
- shift\_upstream (shift\_left), 49
- shift\_upstream(), 49
- slice.GroupedGenomicRanges (slice.Ranges), 50
- slice.GroupedIntegerRanges (slice.Ranges), 50
- slice.Ranges, 50
- slice\_head.GroupedGenomicRanges (slice.Ranges), 50
- slice\_head.GroupedIntegerRanges (slice.Ranges), 50
- slice\_head.Ranges (slice.Ranges), 50
- slice\_max.GroupedGenomicRanges (slice.Ranges), 50
- slice\_max.GroupedIntegerRanges (slice.Ranges), 50
- slice\_max.Ranges (slice.Ranges), 50
- slice\_min.GroupedGenomicRanges (slice.Ranges), 50
- slice\_min.GroupedIntegerRanges (slice.Ranges), 50
- slice\_min.Ranges (slice.Ranges), 50
- slice\_sample.GroupedGenomicRanges (slice.Ranges), 50
- slice\_sample.GroupedIntegerRanges (slice.Ranges), 50
- slice\_sample.Ranges (slice.Ranges), 50
- slice\_tail.GroupedGenomicRanges (slice.Ranges), 50
- slice\_tail.GroupedIntegerRanges (slice.Ranges), 50
- slice\_tail.Ranges (slice.Ranges), 50
- slide\_ranges (tile\_ranges), 55
- span (%union%), 60
- span(), 60
- stretch, 7, 54
- subsetByOverlaps(), 17
- summarise.Ranges, 55
- tile(), 56
- tile\_ranges, 55
- unanchor (anchor), 5
- ungroup.GroupedGenomicRanges (GroupedGenomicRanges-class), 22
- union\_ranges (intersect\_ranges), 23
- union\_ranges\_directed (intersect\_ranges), 23
- WIGFile(), 45, 59
- write\_bed, 56
- write\_bed\_graph (write\_bed), 56
- write\_bigwig, 57
- write\_gff, 58
- write\_gff1 (write\_gff), 58
- write\_gff2 (write\_gff), 58
- write\_gff3 (write\_gff), 58
- write\_narrowpeaks (write\_bed), 56
- write\_wig, 59