Package 'valr'

July 9, 2026

Type Package

Title Genome Interval Arithmetic

Version 0.10.0

Description Read and manipulate genome intervals and signals. Provides functionality similar to command-line tool suites within R, enabling interactive analysis and visualization of genome-scale data. Riemondy et al. (2017) <doi:10.12688/f1000research.11997.1>.

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URL https://github.com/rnabioco/valr, https://rnabioco.github.io/valr/

BugReports https://github.com/rnabioco/valr/issues

Depends R (>= 4.1)

Imports broom, cli, cpp11bigwig (>= 0.3.1), dplyr (>= 1.0.0), ggplot2 (>= 3.3.0), lifecycle, readr, rlang, stringr, tibble (>= 1.4.2)

Suggests bench, covr, cowplot, curl, DBI, dbplyr, devtools, DT, GenomicRanges, IRanges, knitr, purrr, RMariaDB, rmarkdown, S4Vectors, testthat (>= 3.0.0), tidyr, vdiffr (>= 1.0.0)

LinkingTo cpp11

VignetteBuilder knitr

Config/Needs/website rnabioco/rbitemplate

Config/testthat/edition 3

Config/testthat/parallel true

Config/usethis/last-upkeep 2025-12-10

Encoding UTF-8

Config/roxygen2/version 8.0.0

NeedsCompilation yes

Author Jay Hesselberth [aut, cre] (ORCID: <https://orcid.org/0000-0002-6299-179X>), Kent Riemondy [aut] (ORCID: <https://orcid.org/0000-0003-0750-1273>), RNA Bioscience Initiative [fnd, cph] (ROR: <https://ror.org/03wmf1y16>)

Maintainer Jay Hesselberth <jay.hesselberth@gmail.com>

Repository CRAN

Date/Publication 2026-07-09 08:20:02 UTC

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bed12_to_exons *Convert BED12 to individual exons in BED6.*

Description

After conversion to BED6 format, the `score` column contains the exon number, with respect to strand (i.e., the first exon for `-` strand genes will have larger start and end coordinates).

Usage

```
bed12_to_exons(x)
```

Arguments

x	ivl_df, or a path or URL to a BED12 bigBed (`.bb`) file, in which case the whole file is read and validated as BED12 (via its header's declared field count) before conversion.

See Also

Other utilities: `bed_makewindows()`, `bound_intervals()`, `flip_strands()`, `interval_spacing()`

Examples

```
x <- read_bed12(valr_example("mm9.refGene.bed.gz"))

bed12_to_exons(x)

# BED12 from any source with the standard column order is accepted,
# including `cpp11bigwig::read_bigbed()`, which uses UCSC column names.
bb <- system.file("extdata", "test.bb", package = "cpp11bigwig")
bed12_to_exons(cpp11bigwig::read_bigbed(bb))

# a .bb path can also be passed directly; it is read and validated as BED12
bed12_to_exons(bb)
```

bed_absdist *Compute absolute distances between intervals.*

Description

Computes the absolute distance between the midpoint of each x interval and the midpoints of each closest y interval.

Usage

```
bed_absdist(x, y, genome)
```

Arguments

x	ivl_df
y	ivl_df
genome	genome_df

Details

Absolute distances are scaled by the inter-reference gap for the chromosome as follows. For Q query points and R reference points on a chromosome, scale the distance for each query point i to the closest reference point by the inter-reference gap for each chromosome. If an x interval has no matching y chromosome, .absdist is NA.

$$d_i(x, y) = min_k(|q_i - r_k|)\frac{R}{Length\ of\ chromosome}$$

Both absolute and scaled distances are reported as .absdist and .absdist_scaled.

Interval statistics can be used in combination with dplyr::group_by() and dplyr::reframe() to calculate statistics for subsets of data. See vignette('interval-stats') for examples.

Value

ivl_df with .absdist and .absdist_scaled columns.

See Also

https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1002529

Other interval statistics: bed_fisher(), bed_jaccard(), bed_projection(), bed_reldist()

Examples

```
genome <- read_genome(valr_example("hg19.chrom.sizes.gz"))

x <- bed_random(genome, seed = 1010486)
y <- bed_random(genome, seed = 9203911)

bed_absdist(x, y, genome)
```

`bed_closest` *Identify closest intervals.*

Description

Identify closest intervals.

Usage

```
bed_closest(x, y, overlap = TRUE, suffix = c(".x", ".y"))
```

Arguments

`x`	ivl_df
`y`	ivl_df
`overlap`	report overlapping intervals
`suffix`	colname suffixes in output

Details

input tbls are grouped by `chrom` by default, and additional groups can be added using `dplyr::group_by()`. For example, grouping by `strand` will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the y tbl can first be inverted using `flip_strands()`.

Value

ivl_df with additional columns:

- `.overlap` amount of overlap with overlapping interval. Non-overlapping or adjacent intervals have an overlap of 0. `.overlap` will not be included in the output if `overlap = FALSE`.
- `.dist` distance to closest interval. Negative distances denote upstream intervals. Book-ended intervals have a distance of 1.

Note

For each interval in x `bed_closest()` returns overlapping intervals from y and the closest non-intersecting y interval. Setting `overlap = FALSE` will report the closest non-intersecting y intervals, ignoring any overlapping y intervals.

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/closest.html

Other multiple set operations: bed_coverage(), bed_intersect(), bed_map(), bed_subtract(), bed_window()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 100,    125
)

y <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 25,     50,
  "chr1", 140,    175
)

bed_glyph(bed_closest(x, y))

x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 500,    600,
  "chr2", 5000,   6000
)

y <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 100,    200,
  "chr1", 150,    200,
  "chr1", 550,    580,
  "chr2", 7000,   8500
)

bed_closest(x, y)

bed_closest(x, y, overlap = FALSE)

# Report distance based on strand
x <- tibble::tribble(
  ~chrom, ~start, ~end, ~name, ~score, ~strand,
  "chr1", 10, 20, "a", 1, "-"
)

y <- tibble::tribble(
  ~chrom, ~start, ~end, ~name, ~score, ~strand,
  "chr1", 8, 9, "b", 1, "+",
  "chr1", 21, 22, "b", 1, "-"
)

res <- bed_closest(x, y)
```

```
# convert distance based on strand
res$.dist_strand <- ifelse(res$strand.x == "+", res$.dist, -(res$.dist))
res

# report absolute distances
res$.abs_dist <- abs(res$.dist)
res
```

`bed_cluster` *Cluster neighboring intervals.*

Description

The output `.id` column can be used in downstream grouping operations. Default `max_dist = 0` means that both overlapping and book-ended intervals will be clustered.

Usage

```
bed_cluster(x, max_dist = 0)
```

Arguments

`x`	ivl_df
`max_dist`	maximum distance between clustered intervals.

Details

input tbls are grouped by `chrom` by default, and additional groups can be added using `dplyr::group_by()`. For example, grouping by `strand` will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the y tbl can first be inverted using `flip_strands()`.

Value

ivl_df with `.id` column specifying sets of clustered intervals.

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/cluster.html

Other single set operations: `bed_complement()`, `bed_flank()`, `bed_genomecov()`, `bed_merge()`, `bed_partition()`, `bed_shift()`, `bed_slop()`

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 100,    200,
  "chr1", 180,    250,
  "chr1", 250,    500,
  "chr1", 501,    1000,
  "chr2", 1,      100,
  "chr2", 150,    200
)

bed_cluster(x)

# glyph illustrating clustering of overlapping and book-ended intervals
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 1,      10,
  "chr1", 5,      20,
  "chr1", 30,     40,
  "chr1", 40,     50,
  "chr1", 80,     90
)

bed_glyph(bed_cluster(x), label = ".id")
```

---

bed_complement *Identify intervals in a genome not covered by a query.*

Description

Identify intervals in a genome not covered by a query.

Usage

```
bed_complement(x, genome)
```

Arguments

x	ivl_df
genome	ivl_df

Value

ivl_df

See Also

Other single set operations: bed_cluster(), bed_flank(), bed_genomecov(), bed_merge(), bed_partition(), bed_shift(), bed_slop()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 0,      10,
  "chr1", 75,     100
)

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 200
)

bed_glyph(bed_complement(x, genome))

genome <- tibble::tribble(
  ~chrom,  ~size,
  "chr1",  500,
  "chr2",  600,
  "chr3",  800
)

x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 100,    300,
  "chr1", 200,    400,
  "chr2", 0,      100,
  "chr2", 200,    400,
  "chr3", 500,    600
)

# intervals not covered by x
bed_complement(x, genome)
```

---

bed_coverage *Compute coverage of intervals.*

Description

Compute coverage of intervals.

Usage

```
bed_coverage(x, y, ..., min_overlap = 1L)
```

Arguments

x	ivl_df

y	ivl_df, or a path or URL to a bigWig (.bw) or bigBed (.bb) file. When a file is supplied, only the regions spanned by x are read from it (local files and http(s):// URLs are both supported), avoiding the cost of loading the entire file.
...	extra arguments (not used)
min_overlap	minimum overlap in base pairs required for the operation. Defaults to 1, which excludes book-ended intervals (those that touch but do not overlap), matching bedtools behavior. Set to 0 to include book-ended intervals (the legacy valr behavior).

Details

input tbls are grouped by chrom by default, and additional groups can be added using dplyr::group_by(). For example, grouping by strand will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the y tbl can first be inverted using flip_strands().

Value

ivl_df with the following additional columns:

- .ints number of x intersections
- .cov per-base coverage of x intervals
- .len total length of y intervals covered by x intervals
- .frac .len scaled by the number of y intervals

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/coverage.html

Other multiple set operations: bed_closest(), bed_intersect(), bed_map(), bed_subtract(), bed_window()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end, ~strand,
  "chr1", 100,    500,  "+",
  "chr2", 200,    400,  "+",
  "chr2", 300,    500,  "-",
  "chr2", 800,    900,  "-"
)

y <- tibble::tribble(
  ~chrom, ~start, ~end, ~value, ~strand,
  "chr1", 150,    400,  100,    "+",
  "chr1", 500,    550,  100,    "+",
  "chr2", 230,    430,  200,    "-",
  "chr2", 350,    430,  300,    "-"
)
```

```
bed_coverage(x, y)

# `y` can also be a bigWig/bigBed file path or `http(s)://` URL; only the
# regions spanned by `x` are read from the file
x <- tibble::tribble(
  ~chrom,  ~start,   ~end,
  "chr1",  4800000, 4830000,
  "chr10", 4850000, 4860000
)

bed_coverage(x, valr_example("test.bb"), min_overlap = 1L)
```

`bed_fisher` *Fisher's test to measure overlap between two sets of intervals.*

Description

Calculate Fisher's test on number of intervals that are shared and unique between two sets of `x` and `y` intervals.

Usage

```
bed_fisher(x, y, genome)
```

Arguments

`x`	ivl_df
`y`	ivl_df
`genome`	genome_df

Details

Interval statistics can be used in combination with `dplyr::group_by()` and `dplyr::reframe()` to calculate statistics for subsets of data. See `vignette('interval-stats')` for examples.

Value

ivl_df

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/fisher.html

Other interval statistics: `bed_absdist()`, `bed_jaccard()`, `bed_projection()`, `bed_reldist()`

Examples

```
genome <- read_genome(valr_example("hg19.chrom.sizes.gz"))

x <- bed_random(genome, n = 1e4, seed = 1010486)
y <- bed_random(genome, n = 1e4, seed = 9203911)

bed_fisher(x, y, genome)
```

`bed_flank` *Create flanking intervals from input intervals.*

Description

Create flanking intervals from input intervals.

Usage

```
bed_flank(
  x,
  genome,
  both = 0,
  left = 0,
  right = 0,
  fraction = FALSE,
  strand = FALSE,
  trim = FALSE,
  ...
)
```

Arguments

`x`	ivl_df
`genome`	genome_df
`both`	number of bases on both sizes
`left`	number of bases on left side
`right`	number of bases on right side
`fraction`	define flanks based on fraction of interval length
`strand`	define `left` and `right` based on strand
`trim`	adjust coordinates for out-of-bounds intervals
`...`	extra arguments (not used)

Value

ivl_df

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/flank.html

Other single set operations: bed_cluster(), bed_complement(), bed_genomecov(), bed_merge(), bed_partition(), bed_shift(), bed_slop()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 25, 50,
  "chr1", 100, 125
)

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 130
)

bed_glyph(bed_flank(x, genome, both = 20))

x <- tibble::tribble(
  ~chrom, ~start, ~end, ~name, ~score, ~strand,
  "chr1", 500,    1000, ".",   ".",    "+",
  "chr1", 1000,   1500, ".",   ".",    "-"
)

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 5000
)

bed_flank(x, genome, left = 100)

bed_flank(x, genome, right = 100)

bed_flank(x, genome, both = 100)

bed_flank(x, genome, both = 0.5, fraction = TRUE)
```

---

bed_genomecov *Calculate coverage across a genome*

Description

This function is useful for calculating interval coverage across an entire genome.

Usage

```
bed_genomecov(x, genome, zero_depth = FALSE)
```

Arguments

x	ivl_df
genome	genome_df
zero_depth	If TRUE, report intervals with zero depth. Zero depth intervals will be reported with respect to groups.

Details

input tbls are grouped by `chrom` by default, and additional groups can be added using `dplyr::group_by()`. For example, grouping by `strand` will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the y tbl can first be inverted using `flip_strands()`.

Value

ivl_df with the an additional column:

- `.depth` depth of interval coverage

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/genomecov.html

Other single set operations: `bed_cluster()`, `bed_complement()`, `bed_flank()`, `bed_merge()`, `bed_partition()`, `bed_shift()`, `bed_slop()`

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end, ~strand,
  "chr1", 20, 70, "+",
  "chr1", 50, 100, "-",
  "chr1", 200, 250, "+",
  "chr1", 220, 250, "+"
)

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 500,
  "chr2", 1000
)

bed_genomecov(x, genome)

bed_genomecov(dplyr::group_by(x, strand), genome)

bed_genomecov(dplyr::group_by(x, strand), genome, zero_depth = TRUE)
```

bed_glyph *Create example glyphs for valr functions.*

Description

Used to illustrate the output of valr functions with small examples.

Usage

```
bed_glyph(expr, label = NULL, max_rows = 100L)
```

Arguments

expr	expression to evaluate
label	column name to use for label values. should be present in the result of the call.
max_rows	maximum number of rows in the evaluated result that can be plotted. Calls producing more rows than this raise an error.

Value

ggplot2::ggplot()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 25,     50,
  "chr1", 100,    125
)

y <- tibble::tribble(
  ~chrom, ~start, ~end, ~value,
  "chr1", 30, 75, 50
)

bed_glyph(bed_intersect(x, y))

x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 30,     75,
  "chr1", 50,     90,
  "chr1", 91,     120
)

bed_glyph(bed_merge(x))

bed_glyph(bed_cluster(x), label = ".id")
```

bed_intersect *Identify intersecting intervals.*

Description

Report intersecting intervals from x and y tbls.

Usage

```
bed_intersect(x, ..., invert = FALSE, suffix = c(".x", ".y"), min_overlap = 1L)
```

Arguments

x	ivl_df
...	one or more (e.g. a list of) y ivl_df()s. Each y may also be a path or URL to a bigWig (.bw) or bigBed (.bb) file, in which case only the regions spanned by x are read from it (local files and http(s):// URLs are both supported), avoiding the cost of loading the entire file.
invert	report x intervals not in y
suffix	colname suffixes in output
min_overlap	minimum overlap in base pairs required for the operation. Defaults to 1, which excludes book-ended intervals (those that touch but do not overlap), matching bedtools behavior. Set to 0 to include book-ended intervals (the legacy valr behavior).

Details

input tbls are grouped by chrom by default, and additional groups can be added using dplyr::group_by(). For example, grouping by strand will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the y tbl can first be inverted using flip_strands().

Value

ivl_df with original columns from x and y suffixed with .x and .y, and a new .overlap column with the extent of overlap for the intersecting intervals.

If multiple y tbls are supplied, the .source contains variable names associated with each interval. All original columns from the y are suffixed with .y in the output.

If ... contains named inputs (i.e a = y, b = z or list(a = y, b = z)), then .source will contain supplied names (see examples).

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/intersect.html

Other multiple set operations: bed_closest(), bed_coverage(), bed_map(), bed_subtract(), bed_window()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 25, 50,
  "chr1", 100, 125
)

y <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 30,     75
)

bed_glyph(bed_intersect(x, y))

bed_glyph(bed_intersect(x, y, invert = TRUE))

x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 100,    500,
  "chr2", 200,    400,
  "chr2", 300,    500,
  "chr2", 800,    900
)

y <- tibble::tribble(
  ~chrom, ~start, ~end, ~value,
  "chr1", 150,    400,  100,
  "chr1", 500,    550,  100,
  "chr2", 230,    430,  200,
  "chr2", 350,    430,  300
)

bed_intersect(x, y)

bed_intersect(x, y, invert = TRUE)

# start and end of each overlapping interval
res <- bed_intersect(x, y)
dplyr::mutate(res,
  start = pmax(start.x, start.y),
  end = pmin(end.x, end.y)
)

z <- tibble::tribble(
  ~chrom, ~start, ~end, ~value,
  "chr1", 150,    400,  100,
  "chr1", 500,    550,  100,
  "chr2", 230,    430,  200,
  "chr2", 750,    900,  400
)

bed_intersect(x, y, z)
```

```
bed_intersect(x, exons = y, introns = z)

# a list of tbl_intervals can also be passed
bed_intersect(x, list(exons = y, introns = z))

# a bigWig/bigBed file path or `http(s)://` URL can be used in place of a
# `y` tbl; only the regions spanned by `x` are read from the file
x <- tibble::tribble(
  ~chrom,  ~start,   ~end,
  "chr1",  4800000, 4830000,
  "chr10", 4850000, 4860000
)

bed_intersect(x, valr_example("test.bb"), min_overlap = 1L)
```

`bed_jaccard` *Calculate the Jaccard statistic for two sets of intervals.*

Description

Quantifies the extent of overlap between to sets of intervals in terms of base-pairs. Groups that are shared between input are used to calculate the statistic for subsets of data.

Usage

```
bed_jaccard(x, y)
```

Arguments

x	ivl_df
y	ivl_df

Details

The Jaccard statistic takes values of `[0,1]` and is measured as:

$$J(x,y) = \frac{|\, x \bigcap y \,|}{|\, x \bigcup y \,|} = \frac{|\, x \bigcap y \,|}{|\, x \,| + |\, y \,| - |\, x \bigcap y \,|}$$

Interval statistics can be used in combination with `dplyr::group_by()` and `dplyr::reframe()` to calculate statistics for subsets of data. See `vignette('interval-stats')` for examples.

Value

tibble with the following columns:

- `len_i` length of the intersection in base-pairs
- `len_u` length of the union in base-pairs
- `jaccard` value of jaccard statistic
- `n_int` number of intersecting intervals between `x` and `y`

If inputs are grouped, the return value will contain one set of values per group.

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/jaccard.html

Other interval statistics: `bed_absdist()`, `bed_fisher()`, `bed_projection()`, `bed_reldist()`

Examples

```
genome <- read_genome(valr_example("hg19.chrom.sizes.gz"))

x <- bed_random(genome, seed = 1010486)
y <- bed_random(genome, seed = 9203911)

bed_jaccard(x, y)

# calculate jaccard per chromosome
bed_jaccard(
  dplyr::group_by(x, chrom),
  dplyr::group_by(y, chrom)
)
```

---

bed_makewindows *Divide intervals into new sub-intervals ("windows").*

Description

Divide intervals into new sub-intervals ("windows").

Usage

```
bed_makewindows(x, win_size = 0, step_size = 0, num_win = 0, reverse = FALSE)
```

Arguments

`x`	ivl_df
`win_size`	divide intervals into fixed-size windows
`step_size`	size to step before next window
`num_win`	divide intervals to fixed number of windows
`reverse`	reverse window numbers

Value

ivl_df with `.win_id` column that contains a numeric identifier for the window.

Note

The `name` and `.win_id` columns can be used to create new interval names (see 'namenum' example below) or in subsequent `group_by` operations (see vignette).

See Also

Other utilities: `bed12_to_exons()`, `bound_intervals()`, `flip_strands()`, `interval_spacing()`

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end, ~name, ~score, ~strand,
  "chr1", 100,    200,  "A",   ".",    "+"
)

bed_glyph(bed_makewindows(x, num_win = 10), label = ".win_id")

# Fixed number of windows
bed_makewindows(x, num_win = 10)

# Fixed window size
bed_makewindows(x, win_size = 10)

# Fixed window size with overlaps
bed_makewindows(x, win_size = 10, step_size = 5)

# reverse win_id
bed_makewindows(x, win_size = 10, reverse = TRUE)

# bedtools 'namenum'
wins <- bed_makewindows(x, win_size = 10)
dplyr::mutate(wins, namenum = stringr::str_c(name, "_", .win_id))
```

---

bed_map *Calculate summaries from overlapping intervals.*

Description

Apply functions like `min()` and `max()` to intersecting intervals. `bed_map()` uses `bed_intersect()` to identify intersecting intervals, so output columns will be suffixed with `.x` and `.y`. Expressions that refer to input columns from `x` and `y` columns must take these suffixes into account.

Usage

```
bed_map(x, y, ..., min_overlap = 1L)

concat(.data, sep = ",")

values_unique(.data, sep = ",")

values(.data, sep = ",")
```

Arguments

x	ivl_df
y	ivl_df, or a path or URL to a bigWig (`.bw`) or bigBed (`.bb`) file. When a file is supplied, only the regions spanned by `x` are read from it (local files and `http(s)://` URLs are both supported), avoiding the cost of loading the entire file.
...	name-value pairs specifying column names and expressions to apply
min_overlap	minimum overlap in base pairs required for mapping. Default is `1`, meaning book-ended intervals (touching but not overlapping) are not included. Set to `0` to include book-ended intervals.
.data	data
sep	separator character

Details

Non-intersecting intervals from `x` are included in the result with `NA` values.

input tbls are grouped by `chrom` by default, and additional groups can be added using `dplyr::group_by()`. For example, grouping by `strand` will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the y tbl can first be inverted using `flip_strands()`.

Value

ivl_df

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/map.html

Other multiple set operations: `bed_closest()`, `bed_coverage()`, `bed_intersect()`, `bed_subtract()`, `bed_window()`

Examples

```
x <- tibble::tribble(
  ~chrom ,
  ~start ,
  ~end   ,
  'chr1' ,
```

```
    100 ,
    250 ,
  'chr2' ,
    250 ,
    500
)

y <- tibble::tribble(
  ~chrom ,
  ~start ,
  ~end   ,
  ~value ,
  'chr1' ,
    100 ,
    250 ,
     10 ,
  'chr1' ,
    150 ,
    250 ,
     20 ,
  'chr2' ,
    250 ,
    500 ,
    500
)

bed_glyph(bed_map(x, y, value = sum(value)), label = 'value')

# summary examples
bed_map(x, y, .sum = sum(value))

bed_map(x, y, .min = min(value), .max = max(value))

# identify non-intersecting intervals to include in the result
res <- bed_map(x, y, .sum = sum(value))
x_not <- bed_intersect(x, y, invert = TRUE)
dplyr::bind_rows(res, x_not)

# create a list-column
bed_map(x, y, .values = list(value))

# use `nth` family from dplyr
bed_map(x, y, .first = dplyr::first(value))

bed_map(x, y, .absmax = abs(max(value)))

bed_map(x, y, .count = length(value))

bed_map(x, y, .vals = values(value))

# count defaults are NA not 0; differs from bedtools2 ...
bed_map(x, y, .counts = dplyr::n())
```

```
# ... but NA counts can be coverted to 0's
dplyr::mutate(
  bed_map(x, y, .counts = dplyr::n()),
  .counts = ifelse(is.na(.counts), 0, .counts)
)

# a bigWig or bigBed file path (or `http(s)://` URL) can be used in place of
# `y`; only the regions spanned by `x` are read from the file
peaks <- tibble::tribble(
  ~chrom  , ~start   , ~end     ,
  "chr22" , 16100000 , 16150000 ,
  "chr22" , 16500000 , 16550000
)

bed_map(peaks, valr_example("hg19.dnase1.bw"), .signal = sum(value))
```

`bed_merge` *Merge overlapping intervals.*

Description

Operations can be performed on merged intervals by specifying name-value pairs. Default `max_dist` of `0` means book-ended intervals are merged.

Usage

```
bed_merge(x, max_dist = 0, ...)
```

Arguments

`x`	ivl_df
`max_dist`	maximum distance between intervals to merge
`...`	name-value pairs that specify operations on merged intervals

Details

input tbls are grouped by `chrom` by default, and additional groups can be added using `dplyr::group_by()`. For example, grouping by `strand` will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the y tbl can first be inverted using `flip_strands()`.

Value

ivl_df

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/merge.html

Other single set operations: `bed_cluster()`, `bed_complement()`, `bed_flank()`, `bed_genomecov()`, `bed_partition()`, `bed_shift()`, `bed_slop()`

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 1, 50,
  "chr1", 10, 75,
  "chr1", 100, 120
)

bed_glyph(bed_merge(x))

x <- tibble::tribble(
  ~chrom, ~start, ~end, ~value, ~strand,
  "chr1", 1,      50,   1,      "+",
  "chr1", 100,    200,  2,      "+",
  "chr1", 150,    250,  3,      "-",
  "chr2", 1,      25,   4,      "+",
  "chr2", 200,    400,  5,      "-",
  "chr2", 400,    500,  6,      "+",
  "chr2", 450,    550,  7,      "+"
)

bed_merge(x)

bed_merge(x, max_dist = 100)

# merge intervals on same strand
bed_merge(dplyr::group_by(x, strand))

bed_merge(x, .value = sum(value))
```

---

bed_partition *Partition intervals into elemental intervals*

Description

Convert a set of intervals into elemental intervals that contain each start and end position in the set.

Usage

```
bed_partition(x, ...)
```

Arguments

x	ivl_df
...	name-value pairs specifying column names and expressions to apply

Details

Summary operations, such as `min()` or `max()` can be performed on elemental intervals by specifying name-value pairs.

This function is useful for calculating summaries across overlapping intervals without merging the intervals.

input tbls are grouped by `chrom` by default, and additional groups can be added using `dplyr::group_by()`. For example, grouping by `strand` will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the `y` tbl can first be inverted using `flip_strands()`.

Value

`ivl_df()`

See Also

https://bedops.readthedocs.io/en/latest/content/reference/set-operations/bedops.html#partition-p-partition

Other single set operations: `bed_cluster()`, `bed_complement()`, `bed_flank()`, `bed_genomecov()`, `bed_merge()`, `bed_shift()`, `bed_slop()`

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end, ~value, ~strand,
  "chr1", 100, 500, 10, "+",
  "chr1", 200, 400, 20, "-",
  "chr1", 300, 550, 30, "+",
  "chr1", 550, 575, 2, "+",
  "chr1", 800, 900, 5, "+"
)


bed_glyph(bed_partition(x))
bed_glyph(bed_partition(x, value = sum(value)), label = "value")

bed_partition(x)

# compute summary over each elemental interval
bed_partition(x, value = sum(value))

# partition and compute summaries based on group
x <- dplyr::group_by(x, strand)
bed_partition(x, value = sum(value))

# combine values across multiple tibbles
y <- tibble::tribble(
  ~chrom, ~start, ~end, ~value, ~strand,
  "chr1", 10, 500, 100, "+",
  "chr1", 250, 420, 200, "-",
  "chr1", 350, 550, 300, "+",
```

```
  "chr1", 550, 555, 20, "+",
  "chr1", 800, 900, 50, "+"
)

x <- dplyr::bind_rows(x, y)
bed_partition(x, value = sum(value))
```

`bed_projection` *Projection test for query interval overlap.*

Description

Projection test for query interval overlap.

Usage

```
bed_projection(x, y, genome, by_chrom = FALSE)
```

Arguments

x	ivl_df
y	ivl_df
genome	genome_df
by_chrom	compute test per chromosome

Details

Interval statistics can be used in combination with `dplyr::group_by()` and `dplyr::reframe()` to calculate statistics for subsets of data. See `vignette('interval-stats')` for examples.

Value

ivl_df with the following columns:

- `chrom` the name of chromosome tested if `by_chrom = TRUE`, otherwise has a value of `whole_genome`
- `p.value` p-value from a binomial test. p-values > 0.5 are converted to `1 - p-value` and `lower_tail` is `FALSE`
- `obs_exp_ratio` ratio of observed to expected overlap frequency
- `lower_tail` `TRUE` indicates the observed overlaps are in the lower tail of the distribution (e.g., less overlap than expected). `FALSE` indicates that the observed overlaps are in the upper tail of the distribution (e.g., more overlap than expected)

See Also

https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1002529

Other interval statistics: `bed_absdist()`, `bed_fisher()`, `bed_jaccard()`, `bed_reldist()`

Examples

```
genome <- read_genome(valr_example("hg19.chrom.sizes.gz"))

x <- bed_random(genome, seed = 1010486)
y <- bed_random(genome, seed = 9203911)

bed_projection(x, y, genome)

bed_projection(x, y, genome, by_chrom = TRUE)
```

`bed_random` *Generate randomly placed intervals on a genome.*

Description

Generate randomly placed intervals on a genome.

Usage

```
bed_random(genome, length = 1000, n = 1e+06, seed = 0, sorted = TRUE)
```

Arguments

`genome`	genome_df
`length`	length of intervals
`n`	number of intervals to generate
`seed`	seed RNG for reproducible intervals
`sorted`	return sorted output

Details

Sorting can be suppressed with `sorted = FALSE`.

Value

ivl_df

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/random.html

Other randomizing operations: `bed_shuffle()`

Examples

```
genome <- tibble::tribble(
  ~chrom,  ~size,
  "chr1",  10000000,
  "chr2",  50000000,
  "chr3",  60000000,
  "chrX",  5000000
)

bed_random(genome, seed = 10104)

# sorting can be suppressed
bed_random(genome, sorted = FALSE, seed = 10104)

# 500 random intervals of length 500
bed_random(genome, length = 500, n = 500, seed = 10104)
```

---

bed_reldist *Compute relative distances between intervals.*

Description

Compute relative distances between intervals.

Usage

```
bed_reldist(x, y, detail = FALSE)
```

Arguments

x	ivl_df
y	ivl_df
detail	report relative distances for each x interval.

Details

Interval statistics can be used in combination with `dplyr::group_by()` and `dplyr::reframe()` to calculate statistics for subsets of data. See `vignette('interval-stats')` for examples.

Value

If `detail = FALSE`, a ivl_df that summarizes calculated `.reldist` values with the following columns:

- `.reldist` relative distance metric
- `.counts` number of metric observations
- `.total` total observations
- `.freq` frequency of observation

If `detail = TRUE`, the `.reldist` column reports the relative distance for each input `x` interval.

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/reldist.html

Other interval statistics: bed_absdist(), bed_fisher(), bed_jaccard(), bed_projection()

Examples

```
genome <- read_genome(valr_example("hg19.chrom.sizes.gz"))

x <- bed_random(genome, seed = 1010486)
y <- bed_random(genome, seed = 9203911)

bed_reldist(x, y)

bed_reldist(x, y, detail = TRUE)
```

---

bed_shift *Adjust intervals by a fixed size.*

Description

Out-of-bounds intervals are removed by default.

Usage

```
bed_shift(x, genome, size = 0, fraction = 0, trim = FALSE)
```

Arguments

x	ivl_df
genome	ivl_df
size	number of bases to shift. positive numbers shift right, negative shift left.
fraction	define size as a fraction of interval
trim	adjust coordinates for out-of-bounds intervals

Value

ivl_df

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/shift.html

Other single set operations: bed_cluster(), bed_complement(), bed_flank(), bed_genomecov(), bed_merge(), bed_partition(), bed_slop()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 25, 50,
  "chr1", 100, 125
)

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 125
)

bed_glyph(bed_shift(x, genome, size = -20))

x <- tibble::tribble(
  ~chrom, ~start, ~end, ~strand,
  "chr1", 100,    150,  "+",
  "chr1", 200,    250,  "+",
  "chr2", 300,    350,  "+",
  "chr2", 400,    450,  "-",
  "chr3", 500,    550,  "-",
  "chr3", 600,    650,  "-"
)

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 1000,
  "chr2", 2000,
  "chr3", 3000
)

bed_shift(x, genome, 100)

bed_shift(x, genome, fraction = 0.5)

# shift with respect to strand
stranded <- dplyr::group_by(x, strand)
bed_shift(stranded, genome, 100)
```

---

bed_shuffle *Shuffle input intervals.*

Description

Shuffle input intervals.

Usage

```
bed_shuffle(
  x,
  genome,
  incl = NULL,
  excl = NULL,
  max_tries = 1000,
  within = FALSE,
  seed = 0
)
```

Arguments

x	ivl_df
genome	genome_df
incl	ivl_df of included intervals
excl	ivl_df of excluded intervals
max_tries	maximum tries to identify a bounded interval
within	shuffle within chromosomes
seed	seed for reproducible intervals

Value

ivl_df

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/shuffle.html

Other randomizing operations: bed_random()

Examples

```
genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 1e6,
  "chr2", 2e6,
  "chr3", 4e6
)

x <- bed_random(genome, seed = 1010486)

bed_shuffle(x, genome, seed = 9830491)
```

bed_slop *Increase the size of input intervals.*

Description

Increase the size of input intervals.

Usage

```
bed_slop(
  x,
  genome,
  both = 0,
  left = 0,
  right = 0,
  fraction = FALSE,
  strand = FALSE,
  trim = FALSE,
  ...
)
```

Arguments

x	ivl_df
genome	genome_df
both	number of bases on both sizes
left	number of bases on left side
right	number of bases on right side
fraction	define flanks based on fraction of interval length
strand	define `left` and `right` based on strand
trim	adjust coordinates for out-of-bounds intervals
...	extra arguments (not used)

Value

ivl_df

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/slop.html

Other single set operations: `bed_cluster()`, `bed_complement()`, `bed_flank()`, `bed_genomecov()`, `bed_merge()`, `bed_partition()`, `bed_shift()`

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 110,    120,
  "chr1", 225,    235
)

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 400
)

bed_glyph(bed_slop(x, genome, both = 20, trim = TRUE))

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 5000
)

x <- tibble::tribble(
  ~chrom, ~start, ~end, ~name, ~score, ~strand,
  "chr1", 500, 1000, ".", ".", "+",
  "chr1", 1000, 1500, ".", ".", "-"
)

bed_slop(x, genome, left = 100)

bed_slop(x, genome, right = 100)

bed_slop(x, genome, both = 100)

bed_slop(x, genome, both = 0.5, fraction = TRUE)
```

---

bed_sort *Sort a set of intervals.*

Description

Sort a set of intervals.

Usage

```
bed_sort(x, by_size = FALSE, by_chrom = FALSE, reverse = FALSE)
```

Arguments

x	ivl_df
by_size	sort by interval size

by_chrom	sort within chromosome
reverse	reverse sort order

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/sort.html

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr8", 500,    1000,
  "chr8", 1000,   5000,
  "chr8", 100,    200,
  "chr1", 100,    300,
  "chr1", 100,    200
)

# sort by chrom and start
bed_sort(x)

# reverse sort order
bed_sort(x, reverse = TRUE)

# sort by interval size
bed_sort(x, by_size = TRUE)

# sort by decreasing interval size
bed_sort(x, by_size = TRUE, reverse = TRUE)

# sort by interval size within chrom
bed_sort(x, by_size = TRUE, by_chrom = TRUE)
```

---

bed_subtract *Subtract two sets of intervals.*

Description

Subtract y intervals from x intervals.

Usage

```
bed_subtract(x, y, any = FALSE, min_overlap = 1L)
```

Arguments

x	ivl_df
y	ivl_df, or a path or URL to a bigWig (.bw) or bigBed (.bb) file. When a file is supplied, only the regions spanned by x are read from it (local files and http(s):// URLs are both supported), avoiding the cost of loading the entire file.
any	remove any x intervals that overlap y
min_overlap	minimum overlap in base pairs required for the operation. Defaults to 1, which excludes book-ended intervals (those that touch but do not overlap), matching bedtools behavior. Set to 0 to include book-ended intervals (the legacy valr behavior).

Details

input tbls are grouped by chrom by default, and additional groups can be added using dplyr::group_by(). For example, grouping by strand will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the y tbl can first be inverted using flip_strands().

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/subtract.html

Other multiple set operations: bed_closest(), bed_coverage(), bed_intersect(), bed_map(), bed_window()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 1,      100
)

y <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 50,     75
)

bed_glyph(bed_subtract(x, y))

x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 100,    200,
  "chr1", 250,    400,
  "chr1", 500,    600,
  "chr1", 1000,   1200,
  "chr1", 1300,   1500
)

y <- tibble::tribble(
  ~chrom, ~start, ~end,
```

```
  "chr1", 150,    175,
  "chr1", 510,    525,
  "chr1", 550,    575,
  "chr1", 900,    1050,
  "chr1", 1150,   1250,
  "chr1", 1299,   1501
)

bed_subtract(x, y)

bed_subtract(x, y, any = TRUE)
```

---

bed_window *Identify intervals within a specified distance.*

Description

Identify intervals within a specified distance.

Usage

```
bed_window(x, y, genome, ...)
```

Arguments

x	ivl_df
y	ivl_df, or a path or URL to a bigWig (.bw) or bigBed (.bb) file. When a file is supplied, only the windowed regions around x are read from it (local files and http(s):// URLs are both supported), avoiding the cost of loading the entire file.
genome	genome_df
...	params for bed_slop and bed_intersect

Details

input tbls are grouped by chrom by default, and additional groups can be added using dplyr::group_by(). For example, grouping by strand will constrain analyses to the same strand. To compare opposing strands across two tbls, strands on the y tbl can first be inverted using flip_strands().

See Also

https://bedtools.readthedocs.io/en/latest/content/tools/window.html

Other multiple set operations: bed_closest(), bed_coverage(), bed_intersect(), bed_map(), bed_subtract()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 25,     50,
  "chr1", 100,    125
)

y <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 60,     75
)

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 125
)

bed_glyph(bed_window(x, y, genome, both = 15))

x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 10, 100,
  "chr2", 200, 400,
  "chr2", 300, 500,
  "chr2", 800, 900
)

y <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 150,    400,
  "chr2", 230,    430,
  "chr2", 350,    430
)

genome <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 500,
  "chr2", 1000
)

bed_window(x, y, genome, both = 100)

# `y` can be a bigWig/bigBed file path or `http(s)://` URL; only the
# windowed regions around `x` are read from the file
xf <- tibble::tribble(
  ~chrom, ~start,   ~end,
  "chr1", 4840000, 4841000
)

gf <- read_genome(valr_example("hg19.chrom.sizes.gz"))

bed_window(xf, valr_example("test.bb"), gf, both = 10000)
```

```
# add a `.dist` column to the output
## Not run:
bed_window(x, y, genome, both = 200) |>
 mutate(
   .dist = case_when(
     .overlap == 0 ~ abs(pmax(start.x, start.y) - pmin(end.x, end.y)),
     .default = 0
   )
 )

## End(Not run)
```

---

bound_intervals *Select intervals bounded by a genome.*

Description

Used to remove out-of-bounds intervals, or trim interval coordinates using a genome.

Usage

```
bound_intervals(x, genome, trim = FALSE)
```

Arguments

x	ivl_df
genome	genome_df
trim	adjust coordinates for out-of-bounds intervals

Value

ivl_df

See Also

Other utilities: bed12_to_exons(), bed_makewindows(), flip_strands(), interval_spacing()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", -100,   500,
  "chr1", 100,    1e9,
  "chr1", 500,    1000
)

genome <- read_genome(valr_example("hg19.chrom.sizes.gz"))
```

```
# out-of-bounds are removed by default ...
bound_intervals(x, genome)

# ... or can be trimmed within the bounds of a genome
bound_intervals(x, genome, trim = TRUE)
```

`create_introns` *Create intron features.*

Description

Numbers in the `score` column are intron numbers from 5' to 3' independent of strand. I.e., the first introns for `+` and `-` strand genes both have `score` values of `1`.

Usage

```
create_introns(x)
```

Arguments

x	ivl_df in BED12 format

See Also

Other feature functions: `create_tss()`, `create_utrs3()`, `create_utrs5()`

Examples

```
x <- read_bed12(valr_example("mm9.refGene.bed.gz"))

create_introns(x)
```

`create_tss` *Create transcription start site features.*

Description

Create transcription start site features.

Usage

```
create_tss(x)
```

Arguments

x	ivl_df in BED format

See Also

Other feature functions: `create_introns()`, `create_utrs3()`, `create_utrs5()`

Examples

```
x <- read_bed12(valr_example("mm9.refGene.bed.gz"))

create_tss(x)
```

`create_utrs3` *Create 3' UTR features.*

Description

Create 3' UTR features.

Usage

```
create_utrs3(x)
```

Arguments

x	ivl_df in BED12 format

See Also

Other feature functions: `create_introns()`, `create_tss()`, `create_utrs5()`

Examples

```
x <- read_bed12(valr_example("mm9.refGene.bed.gz"))

create_utrs3(x)
```

create_utrs5 *Create 5' UTR features.*

Description

Create 5' UTR features.

Usage

```
create_utrs5(x)
```

Arguments

x	ivl_df in BED12 format

See Also

Other feature functions: `create_introns()`, `create_tss()`, `create_utrs3()`

Examples

```
x <- read_bed12(valr_example("mm9.refGene.bed.gz"))

create_utrs5(x)
```

db *Fetch data from remote databases.*

Description

Currently `db_ucsc` and `db_ensembl` are available for connections.

Usage

```
db_ucsc(
  dbname,
  host = "genome-mysql.cse.ucsc.edu",
  user = "genomep",
  password = "password",
  port = 3306,
  ...
)

db_ensembl(
  dbname,
```

```
  host = "ensembldb.ensembl.org",
  user = "anonymous",
  password = "",
  port = 3306,
  ...
)
```

Arguments

dbname	name of database
host	hostname
user	username
password	password
port	MySQL connection port
...	params for connection

See Also

https://genome.ucsc.edu/goldenpath/help/mysql.html

https://www.ensembl.org/info/data/mysql.html

Examples

```
## Not run:
if (require(RMariaDB)) {
  library(dplyr)
  ucsc <- db_ucsc("hg38")

  # fetch the `refGene` tbl
  tbl(ucsc, "refGene")

  # the `chromInfo` tbls have size information
  tbl(ucsc, "chromInfo")
}

## End(Not run)
## Not run:
if (require(RMariaDB)) {
  library(dplyr)
  # squirrel genome
  ensembl <- db_ensembl("spermophilus_tridecemlineatus_core_67_2")

  tbl(ensembl, "gene")
}

## End(Not run)
```

flip_strands *Flip strands in intervals.*

Description

Flips positive (+) stranded intervals to negative (-) strands, and vice-versa. Facilitates comparisons among intervals on opposing strands.

Usage

```
flip_strands(x)
```

Arguments

x	ivl_df

See Also

Other utilities: `bed12_to_exons()`, `bed_makewindows()`, `bound_intervals()`, `interval_spacing()`

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end, ~strand,
  "chr1", 1,      100,  "+",
  "chr2", 1,      100,  "-"
)

flip_strands(x)
```

gr_to_bed *Convert Granges to bed tibble*

Description

Convert Granges to bed tibble

Usage

```
gr_to_bed(x)
```

Arguments

x	GRanges object to convert to bed tibble.

Value

tibble::tibble()

Examples

```
## Not run:
gr <- GenomicRanges::GRanges(
  seqnames = S4Vectors::Rle(
    c("chr1", "chr2", "chr1", "chr3"),
    c(1, 1, 1, 1)
  ),
  ranges = IRanges::IRanges(
    start = c(1, 10, 50, 100),
    end = c(100, 500, 1000, 2000),
    names = head(letters, 4)
  ),
  strand = S4Vectors::Rle(
    c("-", "+"), c(2, 2)
  )
)

gr_to_bed(gr)

# There are two ways to convert a bed-like data.frame to GRanges:

gr <- GenomicRanges::GRanges(
  seqnames = S4Vectors::Rle(x$chrom),
  ranges = IRanges::IRanges(
    start = x$start + 1,
    end = x$end,
    names = x$name
  ),
  strand = S4Vectors::Rle(x$strand)
)
# or:

gr <- GenomicRanges::makeGRangesFromDataFrame(dplyr::mutate(x, start = start + 1))

## End(Not run)
```

---

interval_spacing *Calculate interval spacing.*

Description

Spacing for the first interval of each chromosome is undefined (NA). The leading interval of an overlapping interval pair has a negative value.

Usage

```
interval_spacing(x)
```

Arguments

x	ivl_df

Value

ivl_df with .spacing column.

See Also

Other utilities: bed12_to_exons(), bed_makewindows(), bound_intervals(), flip_strands()

Examples

```
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 1,      100,
  "chr1", 150,    200,
  "chr2", 200,    300
)

interval_spacing(x)
```

---

ivl_df *Bed-like data.frame requirements for valr functions*

Description

Required column names for interval dataframes are chrom, start and end. Internally interval dataframes are validated using check_interval()

Required column names for genome dataframes are chrom and size. Internally genome dataframes are validated using check_genome().

Usage

```
check_interval(x)

check_genome(x)
```

Arguments

x	A data.frame or tibble::tibble

Examples

```
# using tibble
x <- tibble::tribble(
  ~chrom, ~start, ~end,
  "chr1", 1, 50,
  "chr1", 10, 75,
  "chr1", 100, 120
)

check_interval(x)

# using base R data.frame
x <- data.frame(
  chrom = "chr1",
  start = 0,
  end = 100,
  stringsAsFactors = FALSE
)

check_interval(x)

# example genome input

x <- tibble::tribble(
  ~chrom, ~size,
  "chr1", 1e6
)

check_genome(x)
```

`read_bed` *Read BED and related files.*

Description

read functions for BED and related formats. Filenames can be local file or URLs. The read functions load data into tbls with consistent `chrom`, `start` and `end` colnames.

Usage

```
read_bed(
  filename,
  col_types = bed12_coltypes,
  sort = TRUE,
  ...,
  n_fields = NULL
)
```

```
read_bed12(filename, ...)

read_bedgraph(filename, ...)

read_narrowpeak(filename, ...)

read_broadpeak(filename, ...)
```

Arguments

filename	file or URL
col_types	column type spec for readr::read_tsv()
sort	sort the tbl by chrom and start
...	options to pass to readr::read_tsv()
n_fields	**[Defunct]**

Details

https://genome.ucsc.edu/FAQ/FAQformat.html#format1

https://genome.ucsc.edu/FAQ/FAQformat.html#format1

https://genome.ucsc.edu/goldenPath/help/bedgraph.html

https://genome.ucsc.edu/FAQ/FAQformat.html#format12

https://genome.ucsc.edu/FAQ/FAQformat.html#format13

Value

ivl_df

See Also

Other read functions: read_genome(), read_vcf()

Examples

```
# read_bed assumes 3 field BED format.
read_bed(valr_example("3fields.bed.gz"))

# result is sorted by chrom and start unless `sort = FALSE`
read_bed(valr_example("3fields.bed.gz"), sort = FALSE)


read_bed12(valr_example("mm9.refGene.bed.gz"))


read_bedgraph(valr_example("test.bg.gz"))


read_narrowpeak(valr_example("sample.narrowPeak.gz"))
```

```
read_broadpeak(valr_example("sample.broadPeak.gz"))
```

`read_genome` *Read genome files.*

Description

Genome files (UCSC "chromSize" files) contain chromosome name and size information. These sizes are used by downstream functions to identify computed intervals that have coordinates outside of the genome bounds.

Usage

```
read_genome(path)
```

Arguments

`path`	containing chrom/contig names and sizes, one-pair-per-line, tab-delimited

Value

genome_df, sorted by `size`

Note

URLs to genome files can also be used.

See Also

Other read functions: `read_bed()`, `read_vcf()`

Examples

```
read_genome(valr_example("hg19.chrom.sizes.gz"))

## Not run:
# `read_genome` accepts a URL
read_genome("https://genome.ucsc.edu/goldenpath/help/hg19.chrom.sizes")

## End(Not run)
```

read_gtf *Import and convert a GTF/GFF file into a valr compatible bed tbl format*

Description

[Deprecated]

This function will output a tibble with the required chrom, start, and end columns, as well as other columns depending on content in GTF/GFF file.

Usage

```
read_gtf(path, zero_based = TRUE)
```

Arguments

path	path to gtf or gff file
zero_based	if TRUE, convert to zero based

Examples

```
## Not run:
gtf <- read_gtf(valr_example("hg19.gencode.gtf.gz"))
head(gtf)

## End(Not run)
```

read_vcf *Read a VCF file.*

Description

Read a VCF file.

Usage

```
read_vcf(vcf)
```

Arguments

vcf	vcf filename

Value

data_frame

Note

return value has `chrom`, `start` and `end` columns. Interval lengths are the size of the 'REF' field.

See Also

Other read functions: `read_bed()`, `read_genome()`

Examples

```
vcf_file <- valr_example("test.vcf.gz")
read_vcf(vcf_file)
```

`valr` *valr: genome interval arithmetic in R*

Description

valr provides tools to read and manipulate intervals and signals on a genome reference. valr was developed to facilitate interactive analysis of genome-scale data sets, leveraging the power of dplyr and piping.

Details

To learn more about valr, start with the vignette: `browseVignettes(package = "valr")`

Author(s)

Jay Hesselberth jay.hesselberth@gmail.com

Kent Riemondy kent.riemondy@gmail.com

See Also

Report bugs at `https://github.com/rnabioco/valr/issues`

`valr_example` *Provide working directory for valr example files.*

Description

Provide working directory for valr example files.

Usage

```
valr_example(path)
```

Arguments

`path`	path to file

Examples

```
valr_example("hg19.chrom.sizes.gz")
```

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