Package ‘valr’

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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

```r
bed12_to_exons(x)
```

Arguments

- `x` ivl_df

See Also

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

Examples

```r
x <- read_bed12(valr_example('mm9.refGene.bed.gz'))
bed12_to_exons(x)
```

**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

```r
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, \( .\text{absdist} \) is NA.

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

Both absolute and scaled distances are reported as \( .\text{absdist} \) and \( .\text{absdist}_\text{scaled} \).

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

Value

\texttt{ivl df} with \( .\text{absdist} \) and \( .\text{absdist}_\text{scaled} \) columns.

See Also

\texttt{http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1002529}

Other interval statistics: \texttt{bed_fisher()}, \texttt{bed_jaccard()}, \texttt{bed_projection()}, \texttt{bed_reldist()}

Examples

```r
geno <- read_genome(valr_example('hg19.chrom.sizes.gz'))
x <- bed_random(geno, seed = 1010486)
y <- bed_random(geno, seed = 9203911)
bed_absdist(x, y, geno)
```

---

\textbf{bed closest} \hspace{1cm} \textit{Identify closest intervals.}

Description

Identify closest intervals.

Usage

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

Arguments

- \( x \) \hspace{1cm} \texttt{ivl df}
- \( y \) \hspace{1cm} \texttt{ivl df}
- \( overlap \) \hspace{1cm} report overlapping intervals
- \( suffix \) \hspace{1cm} 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:

- `.dist` distance to closest interval. Negative distances denote upstream intervals.
- `.overlap` overlap with closest interval

See Also

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

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

Examples

```r
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**

```r
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.
**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`

**Examples**

```r
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')
```
Value

ivl_df

See Also

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

Examples

```r
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.
bed_coverage

Usage

bed_coverage(x, y, ...)

Arguments

x  ivl_df
y  ivl_df
... extra arguments (not used)

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

Note

Book-ended intervals are included in coverage calculations.

See Also

http://bedtools.readthedocs.org/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, '-'  )
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::do() to calculate statistics for subsets of data. See vignette('interval-stats') for examples.

Value

ivl_df

See Also

http://bedtools.readthedocs.org/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)
**Description**

Create flanking intervals from input intervals.

**Usage**

```red_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**

http://bedtools.readthedocs.org/en/latest/content/tools/flank.html

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

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

gene <- tibble::tribble(
  ~chrom, ~size,
  'chr1', 130
)

bed_glyph(bed_flank(x, gene, both = 20))
```

```r
x <- tibble::tribble(
  ~chrom, ~start, ~end, ~name, ~score, ~strand,
  'chr1', 500, 1000, '>', '+', '+', '+', '+', '+
  'chr1', 1000, 1500, '>', '>', '>', '>', '>', '>
)

gene <- tibble::tribble(
  ~chrom, ~size,
  'chr1', 5000
)

bed_flank(x, gene, left = 100)
bed_flank(x, gene, right = 100)
bed_flank(x, gene, both = 100)
bed_flank(x, gene, both = 0.5, fraction = TRUE)
```

---

**bed_glyph**  
Create example glyphs for valr functions.

**Description**

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

**Usage**

```r
bed_glyph(expr, label = NULL)
```

**Arguments**

- `expr` expression to evaluate
- `label` column name to use for label values. should be present in the result of the call.
Value

\texttt{ggplot2::ggplot()}

Examples

```r
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, 90, 91, 120)

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

---

**bed_intersect**

Identify intersecting intervals.

**Description**

Report intersecting intervals from x and y tbls. Book-ended intervals have 0 overlap values in the output.

**Usage**

```r
bed_intersect(x, ..., invert = FALSE, suffix = c(".x", ".y"))
```

**Arguments**

- **x**: ivl_df
- **...**: one or more (e.g. a list of) ivl_df()s
- **invert**: report x intervals not in y
- **suffix**: colname suffixes in output
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().

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

http://bedtools.readthedocs.org/en/latest/content/tools/intersect.html

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

Examples

```r
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
)
```
bed_jaccard

Calculate the Jaccard statistic for two sets of intervals.

Description

Quantifies the extent of overlap between 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

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

Arguments

- `x` : ivl_df
- `y` : ivl_df
Details

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

\[ J(x, y) = \frac{|x \cap y|}{|x \cup y|} = \frac{|x \cap y|}{|x| + |y| - |x \cap y|} \]

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

Value

A 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

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

Examples

```r
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))
```

Description

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

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

Arguments

- **x**: ivl_df
- **genome**: this argument has been deprecated and is not used
- **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

```r
x <- tibble::tribble(
  ~chrom, ~start, ~end, ~name, ~score, ~strand,
  "chr1", 100, 200, "A", 0, "-
"
)

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 `count()` 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 = 1)
```

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

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

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

**Arguments**

x  
`ivl_df`

y  
`ivl_df`

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

min_overlap  
minimum overlap for intervals.

.data  
data

sep  
separator character

**Details**

Book-ended intervals can be included by setting `min_overlap = 0`. 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

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

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

Examples

```r
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 converted to 0's

dplyr::mutate(bed_map(x, y, .counts = dplyr::n()), .counts = ifelse(is.na(.counts), 0, .counts))

---

**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**


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

**Examples**

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

bed_glyph(bed_merge(x))
```
```r
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))
```

---

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

Summary operations, such as `min()` or `count()` 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_merge()`, `bed_shift()`, `bed_slop()`

Examples

```r
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))
```
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::do() 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

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

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

```r
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**

```r
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**


Other randomizing operations: `bed_shuffle()`
Examples

```r
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

```r
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::do()` 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

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

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

Examples

```r
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**

```r
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**

http://bedtools.readthedocs.org/en/latest/content/tools/shift.html

Other single set operations: `bed_cluster()`, `bed_complement()`, `bed_flank()`, `bed_merge()`, `bed_partition()`, `bed_slop()`
Examples
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, size = 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

```r
top_hat_rsech
```

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

- [http://bedtools.readthedocs.io/en/latest/content/tools/shuffle.html](http://bedtools.readthedocs.io/en/latest/content/tools/shuffle.html)

Other randomizing operations: `bed_random()`

Examples

```r
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

---

**Description**

Increase the size of input intervals.

**Usage**

```r
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**


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

```r
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**

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

**Arguments**

- `x`  
  ivl_df
- `by_size`  
  sort by interval size
bed_subtract

by_chrom sort within chromosome
reverse reverse sort order

See Also

http://bedtools.readthedocs.org/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)

Arguments

x ivl_df
y ivl_df
any remove any x intervals that overlap y
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

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

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

Examples

```r
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)
```
**Description**

Identify intervals within a specified distance.

**Usage**

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

**Arguments**

- `x`: ivl_df
- `y`: ivl_df
- `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**

http://bedtools.readthedocs.org/en/latest/content/tools/window.html

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

**Examples**

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

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

geneome <- tibble::tribble(
  ~ chrom, ~ size,
  'chr1', 125
)
```
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

```r
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

```r
create_introns(x)
```

Arguments

- `x` - ivl_df in BED12 format

See Also

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

Examples

```r
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()
create_utrs5

Examples

x <- read_bed12(valr_example('mm9.refGene.bed.gz'))
create_utrs3(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
http://www.ensembl.org/info/data/mysql.html

Examples

## Not run:
if(require(RMySQL)) {
  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(RMySQL)) {
  # 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**

```r
flip_strands(x)
```

**Arguments**

- `x` ivl_df

**See Also**

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

**Examples**

```r
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**

```r
gr_to_bed(x)
```

**Arguments**

- `x` GRanges object to convert to bed tibble.

**Value**

`tibble::tibble()`

**Examples**

```r
## 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))
```
interval_spacing

## 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

```r
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

```r
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

```r
read_bed(filename, n_fields = 3, col_types = bed12_coltypes, sort = TRUE, ...)
read_bed12(filename, ...)
read_bedgraph(filename, ...)
read_narrowpeak(filename, ...)
read_broadpeak(filename, ...)
```

### Arguments

- `filename`: file or URL
- `n_fields`: number fields in the BED file
- `col_types`: column type spec for `readr::read_tsv()`
- `sort`: sort the tbl by chrom and start
- `...`: options to pass to `readr::read_tsv()`

### Details

- [https://genome.ucsc.edu/FAQ/FAQformat.html#format1](https://genome.ucsc.edu/FAQ/FAQformat.html#format1)
- [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/goldenPath/help/bedgraph.html)
- [https://genome.ucsc.edu/FAQ/FAQformat.html#format12](https://genome.ucsc.edu/FAQ/FAQformat.html#format12)
- [https://genome.ucsc.edu/FAQ/FAQformat.html#format13](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'))

read_bed(valr_example('6fields.bed.gz'), n_fields = 6)

# 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()
**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**

```r
cvf_file <- valr_example('test.vcf.gz')
read_vcf(vcf_file)
```
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)

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Kent Riemondy kent.riemondy@gmail.com

See Also

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

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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