Package: plyinteractions (via r-universe)

June 12, 2024

Title Extending tidy verbs to genomic interactions

Description Operate on `GInteractions` objects as tabular data using `dplyr`-like verbs. The functions and methods in `plyinteractions` provide a grammatical approach to manipulate `GInteractions`, to facilitate their integration in genomic analysis workflows.

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URL https://github.com/js2264/plyinteractions

BugReports https://github.com/js2264/plyinteractions/issues

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'methods-AnchoredPinnedGInteractions.R'
'methods-DelegatingGInteractions.R'
'methods-GroupedGInteractions.R'
'methods-PinnedGInteractions.R' 'methods-show.R' 'mutate.R'
'pin.R' 'plyinteractions.R' 'reexports-dplyr.R'
'reexports-plyranges.R' 'reexports.R' 'rename.R'
'replace-anchors.R' 'select.R' 'shift.R' 'slice.R' 'stretch.R'
'summarize.R'

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Contents

plyinteractions-package

plyinteractions: a grammar of data manipulation for genomic interactions

Description

plyinteractions is a dplyr-like API to the GInteractions infrastructure in Bioconductor.

Details

plyinteractions provides a consistent interface for importing and wrangling genomic interactions from a variety of sources. The package defines a grammar of genomic interactions manipulation through a set of verbs. These verbs can be used to construct human-readable analysis pipelines based on `GInteractions`.

- Group genomic interactions with `group_by`;
- Summarize grouped genomic interactions with `summarize`;
- Tally/count grouped genomic interactions with `tally` and `count`;
- Modify genomic interactions with `mutate`;
- Subset genomic interactions with `filter` using `<data-masking>` and logical expressions;
- Pick out any columns from the associated metadata with `select` using `<tidy-select>` arguments;
- Subset using indices with `slice`;
- Order genomic interactions with `arrange` using categorical/numerical variables.

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

Author(s)

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See Also

Useful links:

- https://github.com/js2264/plyinteractions
- Report bugs at https://github.com/js2264/plyinteractions/issues

anchors1 — *Enhanced GInteractions getters*

Description

Enhanced GInteractions getters

Usage

```
anchors1(x)

anchors2(x)

seqnames1(x)

seqnames2(x)

start1(x)

start2(x)

end1(x)

end2(x)

width1(x)

width2(x)

strand1(x)

strand2(x)

ranges1(x)

ranges2(x)

## S4 method for signature 'GInteractions'
x$name

## S4 method for signature 'GInteractions'
anchors1(x)

## S4 method for signature 'GInteractions'
anchors2(x)

## S4 method for signature 'GInteractions'
```

```
seqnames1(x)

## S4 method for signature 'GInteractions'
seqnames2(x)

## S4 method for signature 'GInteractions'
start1(x)

## S4 method for signature 'GInteractions'
start2(x)

## S4 method for signature 'GInteractions'
end1(x)

## S4 method for signature 'GInteractions'
end2(x)

## S4 method for signature 'GInteractions'
width1(x)

## S4 method for signature 'GInteractions'
width2(x)

## S4 method for signature 'GInteractions'
strand1(x)

## S4 method for signature 'GInteractions'
strand2(x)

## S4 method for signature 'GInteractions'
ranges1(x)

## S4 method for signature 'GInteractions'
ranges2(x)
```

Arguments

`x`	a GInteractions object
`name`	The pattern or name of a column stored in the GInteractions metadata (mcols).

Value

One of the core GInteractions fields (e.g. seqnames1, start1, ...) or one of the metadata columns when using `$`. Note that auto-completion works with `$`.

Examples

```
gi <- data.frame(
  seqnames1 = 'chr1', start1 = 1, end1 = 10,
  seqnames2 = 'chr1', start2 = 2, end2 = 20
) |> as_ginteractions() |> mutate(type = 'cis')
anchors1(gi)
anchors2(gi)
seqnames1(gi)
seqnames2(gi)
start1(gi)
start2(gi)
end1(gi)
end2(gi)
width1(gi)
width2(gi)
ranges1(gi)
ranges2(gi)
strand1(gi)
strand2(gi)
gi$type
```

---

annotate *Annotate both anchors of a GInteractions*

Description

For each interaction in a `GInteractions` object, `annotate` returns the pairs of annotations from the `GRanges` object it overlaps with.

Usage

```
annotate(x, y, by)

annotate_directed(x, y, by)

## S4 method for signature 'GInteractions,GRanges,character'
annotate(x, y, by)

## S4 method for signature 'GInteractions,GRanges,character'
annotate_directed(x, y, by)
```

Arguments

`x`	a GInteractions object
`y`	a GRanges object to extract annotations from
`by`	Column name from `y` to use to extract annotations

Value

a GInteractions object with two extra metadata columns named `by.1` and `by.2`.

Examples

```
#####################################################################
# 1. Basic example
#####################################################################

gi <- read.table(text = "
    chr1 11 20 - chr1 21 30 +
    chr1 21 30 + chr2 51 60 +",
    col.names = c(
        "seqnames1", "start1", "end1", "strand1",
        "seqnames2", "start2", "end2", "strand2"
    )
) |> as_ginteractions()

gr <- GenomicRanges::GRanges(c("chr1:20-30:+", "chr2:55-65:+")) |>
    plyranges::mutate(id = 1:2)

annotate(gi, gr, by = 'id')

annotate_directed(gi, gr, by = 'id')

#####################################################################
# 2. Match loops with tiled genomic bins
#####################################################################

data(GM12878_HiCCUPS)
loops <- GM12878_HiCCUPS |>
    pin_by('first') |>
    anchor_center() |>
    mutate(width1 = 500) |>
    pin_by('second') |>
    anchor_center() |>
    mutate(width2 = 500)

genomic_bins <- GenomeInfoDb::getChromInfoFromUCSC(
    'hg19', assembled.molecules.only = TRUE, as.Seqinfo = TRUE
) |>
    GenomicRanges::tileGenome(tilewidth = 10000) |>
    unlist() |>
    plyranges::mutate(binID = seq_len(plyranges::n()))

annotate(loops, genomic_bins, by = 'binID') |>
    select(starts_with('binID'))

#####################################################################
# 3. Annotate interactions by a set of regulatory elements
#####################################################################

data(ce10_ARCC)
data(ce10_REs)
annotate(ce10_ARCC, ce10_REs, by = 'annot') |>
   count(annot.1, annot.2) |>
```

```
    as.data.frame() |>
    dplyr::arrange(desc(n))
```

as_ginteractions *Construct a GInteractions object from a tibble, DataFrame or data.frame*

Description

The `as_ginteractions` function looks for column names in .data called seqnames{1,2}, start{1,2}, end{1,2}, and strand{1,2} in order to construct a GInteractions object. By default other columns in .data are placed into the mcols (metadata columns) slot of the returned object.

Usage

```
as_ginteractions(
  .data,
  ...,
  keep.extra.columns = TRUE,
  starts.in.df.are.0based = FALSE
)
```

Arguments

`.data`	A `data.frame()`, `DataFrame()` or `tibble()` to construct a GInteractions object from.
`...`	Optional named arguments specifying which the columns in .data containin the core components a GInteractions object.
`keep.extra.columns`	TRUE or FALSE (the default). If TRUE, the columns in df that are not used to form the genomic ranges of the returned GRanges object are then returned as metadata columns on the object. Otherwise, they are ignored.
`starts.in.df.are.0based`	TRUE or FALSE (the default). If TRUE, then the start positions of the genomic ranges in df are considered to be 0-based and are converted to 1-based in the returned GRanges object.

Value

a GInteractions object.

See Also

`InteractionSet::GInteractions()`

Examples

```
######################################################################
# 1. GInteractions from bedpe files imported into a data.frame
######################################################################

bedpe <- read.table(text = "
chr1 100 200 chr1 5000 5100 bedpe_example1 30 + -
chr1 1000 5000 chr1 3000 3800 bedpe_example2 100 + -",
col.names = c(
  "chrom1", "start1", "end1",
  "chrom2", "start2", "end2", "name", "score", "strand1", "strand2"))
bedpe |>
  as_ginteractions(seqnames1 = chrom1, seqnames2 = chrom2)

######################################################################
# 2. GInteractions from standard pairs files imported into a data.frame
######################################################################

# Note how the pairs are 0-based and no "end" field is provided
# (the standard pairs file format does not have "end" fields)
# We can provide width1 and width2 to fix this problem.

pairs <- read.table(text = "
pair1 chr1 10000 chr1 20000 + +
pair2 chr1 50000 chr1 70000 + +
pair3 chr1 60000 chr2 10000 + +
pair4 chr1 30000 chr3 40000 + -",
col.names = c(
  "pairID", "chr1", "pos1", "chr2", "pos2", "strand1", "strand2")
)
pairs |>
  as_ginteractions(
    seqnames1 = chr1, start1 = pos1, width1 = 1000,
    seqnames2 = chr2, start2 = pos2, width2 = 1000,
    starts.in.df.are.0based = TRUE
  )

######################################################################
# 3. GInteractions from data.frame with extra fields
######################################################################

df <- read.table(text = "
chr1 100 200 chr1 5000 5100
chr1 1000 5000 chr1 3000 3800",
col.names = c("chr1", "start1", "end1", "chr2", "start2", "end2"))
df |>
  as_ginteractions(seqnames1 = chr1, seqnames2 = chr2)

df <- read.table(text = "
chr1 100 200 chr1 5000 5100
chr1 1000 5000 chr1 3000 3800",
col.names = c("chr1", "start1", "end1", "chr2", "start2", "end2"))
```

```
df |>
  as_ginteractions(
    seqnames1 = chr1, seqnames2 = chr2, strand1 = '+', strand2 = '-'
  )

data.frame(type = "cis", count = 3) |>
  as_ginteractions(
    seqnames1 = 'chr1', start1 = 1, end1 = 10,
    seqnames2 = 'chr1', start2 = 40, end2 = 50
  )

####################################################################
# 4. GInteractions from a real like pairs files
####################################################################

pairsf <- system.file('extdata', 'pairs.gz', package = 'plyinteractions')
pairs <- read.table(pairsf, comment.char = '#', header = FALSE)
head(pairs)
pairs |>
  as_ginteractions(
    seqnames1 = V2, start1 = V3, width1 = 1, strand1 = V6,
    seqnames2 = V4, start2 = V5, width2 = 1, strand2 = V7,
    starts.in.df.are.0based = TRUE
  )
```

`dplyr-arrange` *Arrange a GInteractions by a column*

Description

Arrange a GInteractions by a column

Usage

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

Arguments

`.data`	a GInteractions object
`...`	Variables, or functions of variables. Use dplyr::desc() to sort a variable in descending order.

Value

a GInteractions object.

Examples

```
gi <- read.table(text = "
chr1 1 10 chr1 1 10
chr1 2 10 chr2 1 10
chr3 3 10 chr3 1 10
chr4 4 10 chr4 1 10
chr5 5 10 chr5 1 10",
col.names = c(
  "seqnames1", "start1", "end1",
  "seqnames2", "start2", "end2")
) |>
  as_ginteractions() |>
  mutate(cis = seqnames1 == seqnames2, score = runif(5)*100, gc = runif(5))
gi

####################################################################
# 1. Arrange GInteractions by a numerical column
####################################################################

gi |> arrange(gc)

####################################################################
# 2. Arrange GInteractions by a logical column
####################################################################

gi |> arrange(cis)

####################################################################
# 3. Arrange GInteractions by a factor
####################################################################

gi |>
  mutate(rep = factor(c("rep1", "rep2", "rep1", "rep2", "rep1"))) |>
  arrange(rep)

####################################################################
# 4. Combine sorting variables
####################################################################

gi |>
  mutate(rep = factor(c("rep1", "rep2", "rep1", "rep2", "rep1"))) |>
  arrange(dplyr::desc(rep), score)
```

`dplyr-count` *Count or tally GInteractions per group*

Description

Count or tally GInteractions per group

Usage

```
## S3 method for class 'GroupedGInteractions'
tally(x, wt = NULL, sort = FALSE, name = NULL)

## S3 method for class 'GroupedGInteractions'
count(x, ..., wt = NULL, sort = FALSE, name = NULL)

## S3 method for class 'GInteractions'
count(x, ..., wt = NULL, sort = FALSE, name = NULL)
```

Arguments

`x`	A grouped GInteractions object
`wt`	<`data-masking`> Frequency weights. Can be `NULL` or a variable: • If `NULL` (the default), counts the number of rows in each group. • If a variable, computes `sum(wt)` for each group.
`sort`	If `TRUE`, will show the largest groups at the top.
`name`	The name of the new column in the output.
`...`	<`data-masking`> Variables to group by.

Value

a `S4Vectors::DataFrame()` object, with an added column with the count/tablly per group.

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30 + +
chr1 11 20 chr1 51 55 + +
chr1 11 30 chr1 51 55 - -
chr1 11 30 chr2 51 60 - -",
col.names = c(
  "seqnames1", "start1", "end1",
  "seqnames2", "start2", "end2", "strand1", "strand2")
) |>
  as_ginteractions() |>
  mutate(score = runif(4), type = c('cis', 'cis', 'cis', 'trans'))

####################################################################
# 1. Tally groups
####################################################################

gi

gi |> group_by(strand1) |> tally()

gi |> group_by(type) |> tally()

gi |> group_by(type) |> tally(wt = score)
```

```
####################################################################
# 2. Count per groups
####################################################################

gi |> count(type)

gi |> group_by(type) |> count(strand1)

gi |> group_by(type, strand1) |> count(wt = score)
```

`dplyr-filter` *Subset a GInteractions with tidyverse-like* `filter`

Description

Subset a GInteractions with tidyverse-like `filter`

Usage

```
## S3 method for class 'GInteractions'
filter(.data, ...)
```

Arguments

`.data`	a GInteractions object
`...`	Expressions that return a logical value, and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept.

Value

a GInteractions object.

Examples

```
gi <- read.table(text = "
chr1 1 10 chr1 1 10
chr1 2 10 chr2 1 10
chr3 3 10 chr3 1 10
chr4 4 10 chr4 1 10
chr5 5 10 chr5 1 10",
col.names = c(
    "seqnames1", "start1", "end1",
    "seqnames2", "start2", "end2")
) |>
  as_ginteractions() |>
  mutate(cis = seqnames1 == seqnames2, score = runif(5)*100, gc = runif(5))
```

```
gi

####################################################################
# 1. Filter metadata columns from GInteractions by condition
####################################################################

gi |> filter(gc > 0.1)
gi |> filter(gc > 0.1, score > 50)
gi |> filter(cis)

####################################################################
# 2. On-the-fly calculations
####################################################################

gi
gi |> filter(start1 >= start2 + 3)
gi |> filter(score * gc > score * 0.5)
```

`dplyr-group_by` *Group GInteractions by columns*

Description

Group GInteractions by columns

Usage

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

## S3 method for class 'DelegatingGInteractions'
group_by(.data, ..., .add = FALSE)

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

Arguments

`.data, x`	a (Grouped)GInteractions object
`...`	Column(s) to group by.
`.add`	When FALSE, the default, group_by() will override existing groups. To add to the existing groups, use .add = TRUE.

Value

a `GroupedGInteractions` object. When a `(Anchored)PinnedGInteractions` object is grouped, both anchoring and pinning are dropped.

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30
chr1 11 20 chr1 51 55
chr1 11 30 chr1 51 55
chr1 11 30 chr2 51 60",
col.names = c(
    "seqnames1", "start1", "end1",
    "seqnames2", "start2", "end2")
) |>
  as_ginteractions() |>
  mutate(type = c('cis', 'cis', 'cis', 'trans'), score = runif(4))

####################################################################
# 1. Group by core column
####################################################################

gi |> group_by(end1)

gi |> group_by(end1, end2) |> group_data()

####################################################################
# 2. Group by metadata column
####################################################################

gi |> group_by(type) |> group_data()

####################################################################
# 3. Combine core and metadata column grouping
####################################################################

gi |> group_by(end1, type)
gi |> group_by(end1, type) |> group_data()

####################################################################
# 4. Create a new column and group by this new variable
####################################################################

gi |> group_by(class = c(1, 2, 1, 2))

####################################################################
# 5. Replace or add groups to a GroupedGInteractions
####################################################################

ggi <- gi |> group_by(class = c(1, 2, 1, 2))
ggi |> group_data()
ggi |> group_by(type) |> group_data()
ggi |> group_by(type, .add = TRUE) |> group_data()

####################################################################
# 6. Ungroup GInteractions
####################################################################
```

```
ggi <- gi |> group_by(type, class = c(1, 2, 1, 2))
ggi
ungroup(ggi, type)
ungroup(ggi, class)
```

`dplyr-mutate` *Mutate columns from a GInteractions object*

Description

Mutate columns from a GInteractions object

Usage

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

Arguments

`.data`	a GInteractions object
`...`	Optional named arguments specifying which the columns in .data to create/modify.

Value

a GInteractions object.

Examples

```
gi <- read.table(text = "
chr1 10 20 chr1 50 51
chr1 10 50 chr2 30 40",
col.names = c("chr1", "start1", "end1", "chr2", "start2", "end2")) |>
  as_ginteractions(seqnames1 = chr1, seqnames2 = chr2)

####################################################################
# 1. Add metadata columns to a GInteractions object
####################################################################

gi |>
  mutate(type = c('cis', 'trans'), score = runif(2)) |>
  mutate(type2 = type)

####################################################################
# 2. More complex, nested or inplace changes
####################################################################

gi |>
```

```
    mutate(type = c('cis', 'trans'), score = runif(2)) |>
    mutate(type2 = type) |>
    mutate(count = c(1, 2), score = count * 2, new_col = paste0(type2, score))

  ####################################################################
  # 3. Core GInteractions columns can also be modified
  ####################################################################

  gi |>
    mutate(start1 = 1, end1 = 10, width2 = 30, strand2 = c('-', '+'))

  # Note how the core columns are modified sequentially

  gi |>
    mutate(start1 = 1, end1 = 10)

  gi |>
    mutate(start1 = 1, end1 = 10, width1 = 50)

  ####################################################################
  # 4. Evaluating core GInteractions columns
  ####################################################################

  gi |>
    mutate(
      score = runif(2),
      cis = seqnames1 == seqnames2,
      distance = ifelse(cis, start2 - end1, NA)
    )
```

dplyr-rename   *Rename columns from a GInteractions with tidyverse-like* `rename`

Description

Rename columns from a GInteractions with tidyverse-like `rename`

Usage

```
## S3 method for class 'GInteractions'
rename(.data, ...)
```

Arguments

`.data`	a GInteractions object
`...`	Use `new_name` = `old_name` to rename selected variables.

Value

a GInteractions object.

Examples

```
gi <- read.table(text = "
chr1 10 20 chr1 50 51
chr1 10 50 chr2 30 40",
col.names = c("chr1", "start1", "end1", "chr2", "start2", "end2")) |>
  as_ginteractions(seqnames1 = chr1, seqnames2 = chr2) |>
  mutate(type = c('cis', 'trans'), score = runif(2))

####################################################################
# 1. Rename metadata columns to a GInteractions object
####################################################################

gi |> rename(interaction_type = type, GC = score)
```

`dplyr-select` *Select columns within GInteractions metadata columns*

Description

Select columns within GInteractions metadata columns

Usage

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

Arguments

`.data`	a GInteractions object
`...`	Integer indicating rows to keep.
`.drop_ranges`	if TRUE, returns a DataFrame object. In this case, it enables selection of any column including core GInteractions columns.

Value

a GInteractions object.

Examples

```
gi <- read.table(text = "
chr1 1 10 chr1 1 10
chr2 1 10 chr2 1 10
chr3 1 10 chr3 1 10
chr4 1 10 chr4 1 10
chr5 1 10 chr5 1 10",
col.names = c(
    "seqnames1", "start1", "end1",
      "seqnames2", "start2", "end2")
) |>
  as_ginteractions() |>
  mutate(score = runif(5)*100, cis = TRUE, gc = runif(5))

####################################################################
# 1. Select metadata columns from GInteractions by index
####################################################################

gi |> select(2, 1)
gi |> select(-3)

####################################################################
# 2. Select metadata columns from GInteractions by name
####################################################################

gi |> select(gc, score)

####################################################################
# 3. Select metadata columns from GInteractions with <tidy-select>
####################################################################

gi |> select(contains('s'))
gi |> select(matches('^s'))

####################################################################
# 4. Select core and metadata columns with .drop_ranges = TRUE
####################################################################

gi |> select(matches('^s'), .drop_ranges = TRUE)
```

`dplyr-slice` *Slice a GInteractions rows by their index*

Description

Slice a GInteractions rows by their index

Usage

```
## S3 method for class 'GInteractions'
slice(.data, ...)
```

Arguments

`.data`	a GInteractions object
`...`	Integer indicating rows to keep.

Value

a GInteractions object.

Examples

```
gi <- read.table(text = "
chr1 1 10 chr1 1 10
chr2 1 10 chr2 1 10
chr3 1 10 chr3 1 10
chr4 1 10 chr4 1 10
chr5 1 10 chr5 1 10",
col.names = c(
    "seqnames1", "start1", "end1",
    "seqnames2", "start2", "end2")
) |>
  as_ginteractions()

####################################################################
# 1. Slice a GInteractions
####################################################################

gi |> slice(1, 2, 3)
gi |> slice(-3)
gi |> slice(1:2, 5:4)
```

---

dplyr-summarize *Summarize GInteractions per group*

Description

Summarize GInteractions per group

Usage

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

## S3 method for class 'GroupedGInteractions'
summarize(.data, ...)
```

Arguments

`.data`	a (grouped) GInteractions object
`...`	Name-value pairs of summary functions. The name will be the name of the variable in the result.

Value

a `S4Vectors::DataFrame()` object:

- The rows come from the underlying `group_keys()`.
- The columns are a combination of the grouping keys and the summary expressions that you provide.
- GInteractions class is **not** preserved, as a call to `summarize` fundamentally creates a new data frame

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30 + +
chr1 11 20 chr1 51 55 + +
chr1 11 30 chr1 51 55 - -
chr1 11 30 chr2 51 60 - -",
col.names = c(
  "seqnames1", "start1", "end1",
  "seqnames2", "start2", "end2", "strand1", "strand2")
) |>
  as_ginteractions() |>
  mutate(score = runif(4), type = c('cis', 'cis', 'cis', 'trans'))

####################################################################
# 1. Summarize a single column
####################################################################

gi

gi |> group_by(type) |> summarize(m = mean(score))

gi |> group_by(strand1) |> summarize(m = mean(score))

df <- gi |>
  group_by(strand1) |>
  summarize(m = mean(score), n = table(seqnames2))
df

df$n

####################################################################
# 2. Summarize by multiple columns
####################################################################

gi |>
  group_by(strand1, seqnames2) |>
  summarise(m = mean(score), n = table(type))
```

ginteractions-anchor *Manage GInteractions anchors with plyranges*

Description

Manage GInteractions anchors with plyranges

Usage

```
## S3 method for class 'AnchoredPinnedGInteractions'
anchor(x)

## S3 method for class 'AnchoredPinnedGInteractions'
unanchor(x)

## S3 method for class 'PinnedGInteractions'
anchor_start(x)

## S3 method for class 'PinnedGInteractions'
anchor_end(x)

## S3 method for class 'PinnedGInteractions'
anchor_center(x)

## S3 method for class 'PinnedGInteractions'
anchor_3p(x)

## S3 method for class 'PinnedGInteractions'
anchor_5p(x)

## S3 method for class 'AnchoredPinnedGInteractions'
anchor_start(x)

## S3 method for class 'AnchoredPinnedGInteractions'
anchor_end(x)

## S3 method for class 'AnchoredPinnedGInteractions'
anchor_center(x)

## S3 method for class 'AnchoredPinnedGInteractions'
anchor_3p(x)

## S3 method for class 'AnchoredPinnedGInteractions'
anchor_5p(x)
```

Arguments

x	A PinnedGInteractions object

Value

- `anchor_*` functions return an AnchoredPinnedGInteractions object.
- `anchor` returns a character string indicating where the pinned anchors are anchored at.
- `unanchor` removes the anchoring for a AnchoredPinnedGInteractions object.

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30 + +
chr1 11 20 chr1 51 55 + +
chr1 11 30 chr1 51 55 - -
chr1 11 30 chr2 51 60 - -",
col.names = c(
  "seqnames1", "start1", "end1",
  "seqnames2", "start2", "end2", "strand1", "strand2")
) |>
  as_ginteractions() |>
  mutate(score = runif(4), type = c('cis', 'cis', 'cis', 'trans'))

####################################################################
# 1. Anchoring pinned genomic interactions with plyranges
####################################################################

gi |> pin_by("second") |> anchor_end()
```

`ginteractions-count-overlaps`
Count overlaps between a query GInteractions and a GRanges

Description

Count overlaps between a query GInteractions and a GRanges

Usage

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

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

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

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

Arguments

`x`	A (Pinned)GInteractions object
`y`	A GRanges object
`maxgap, minoverlap`	See ?`countOverlaps` in the **GenomicRanges** package for a description of these arguments

Value

An integer vector of same length as x.

Pinned `GInteractions`

When using `count_overlaps()` with a `PinnedGInteractions` object, only the pinned anchors are used to check for overlap with `y`. This is equivalent to specifying `use.region="both"` in `InteractionSet::findOverlaps()`.

Examples

```
gi <- read.table(text = "
    chr1 11 20 - chr1 21 30 +
    chr1 11 20 - chr1 51 55 +
    chr1 21 30 - chr1 51 55 +
    chr1 21 30 - chr2 51 60 +",
    col.names = c(
        "seqnames1", "start1", "end1", "strand1",
        "seqnames2", "start2", "end2", "strand2"
    )
) |> as_ginteractions() |> mutate(id = 1:4, type = 'gi')

gr <- GenomicRanges::GRanges(
    c("chr1:20-30:+", "chr2:55-65:-")
) |> plyranges::mutate(id = 1:2, type = 'gr')

gi

gr

#####################################################################
# 1. Count overlaps between GInteractions and a subject GRanges
#####################################################################

count_overlaps(gi, gr)

count_overlaps_directed(gi, gr)

#####################################################################
# 2. Count overlaps between PinnedGInteractions and a subject GRanges
#####################################################################

gi |> pin_by("first") |> count_overlaps(gr)
gi |> pin_by("second") |> count_overlaps(gr)

gi |> pin_by("first") |> count_overlaps_directed(gr)

gi |> pin_by("second") |> count_overlaps_directed(gr)
```

`ginteractions-filter-overlaps` *Filter GInteractions overlapping with a GRanges*

Description

Filter GInteractions overlapping with a GRanges

Usage

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

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

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

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

Arguments

`x`	A (Pinned)GInteractions object
`y`	A GRanges object
`maxgap, minoverlap`	See ?`countOverlaps` in the **GenomicRanges** package for a description of these arguments

Value

An integer vector of same length as x.

Pinned `GInteractions`

When using `filter_by_overlaps()` with a `PinnedGInteractions` object, only the pinned anchors are used to check for overlap with `y`. This is equivalent to specifying `use.region="both"` in `InteractionSet::findOverlaps()`.

Examples

```
gi <- read.table(text = "
    chr1 11 20 - chr1 21 30 +
    chr1 11 20 - chr1 51 55 +
    chr1 21 30 - chr1 51 55 +
    chr1 21 30 - chr2 51 60 +",
    col.names = c(
        "seqnames1", "start1", "end1", "strand1",
        "seqnames2", "start2", "end2", "strand2")
) |> as_ginteractions() |> mutate(id = 1:4, type = 'gi')

gr <- GenomicRanges::GRanges(
    c("chr1:20-30:+", "chr2:55-65:-")
) |> plyranges::mutate(id = 1:2, type = 'gr')

gi

gr

####################################################################
# 1. Filter GInteractions overlapping with a subject GRanges
####################################################################

filter_by_overlaps(gi, gr)

filter_by_non_overlaps(gi, gr)

####################################################################
# 2. Filter PinnedGInteractions overlapping with a subject GRanges
####################################################################

gi |> pin_by("first") |> filter_by_overlaps(gr)

gi |> pin_by("first") |> filter_by_non_overlaps(gr)

gi |> pin_by("second") |> filter_by_overlaps(gr)

gi |> pin_by("second") |> filter_by_non_overlaps(gr)
```

`ginteractions-find-overlaps` *Find overlaps between a query GInteractions and a GRanges*

Description

Find overlaps between a query GInteractions and a GRanges

Usage

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

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

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

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

Arguments

x	A (Pinned)GInteractions object
y	A GRanges object
maxgap, minoverlap	See ?findOverlaps in the **GenomicRanges** package for a description of these arguments
suffix	Suffix to add to metadata columns (character vector of length 2, default to c(".x", ".y")).

Value

a GInteractions object with rows corresponding to the GInteractions in x that overlap y.

Rationale

find_overlaps() will search for any overlap between GInteractions in x and GRanges in y. It will return a GInteractions object of length equal to the number of times x overlaps y. This GInteractions will have additional metadata columns corresponding to the metadata from y. find_overlaps_directed() takes the strandness of each object into account.

Pinned `GInteractions`

When using `find_overlaps()` with a `PinnedGInteractions` object, only the pinned anchors are used to check for overlap with `y`. This is equivalent to specifying `use.region="both"` in `InteractionSet::findOverlaps()`.

Examples

```
gi <- read.table(text = "
    chr1 11 20 - chr1 21 30 +
    chr1 11 20 - chr1 51 55 +
    chr1 21 30 - chr1 51 55 +
    chr1 21 30 - chr2 51 60 +",
    col.names = c(
        "seqnames1", "start1", "end1", "strand1",
        "seqnames2", "start2", "end2", "strand2"
    )
) |> as_ginteractions() |> mutate(id = 1:4, type = 'gi')

gr <- GenomicRanges::GRanges(
    c("chr1:20-30:+", "chr2:55-65:-")
) |> plyranges::mutate(id = 1:2, type = 'gr')

gi

gr

#####################################################################
# 1. Find overlaps between GInteractions and a subject GRanges
#####################################################################

find_overlaps(gi, gr)

find_overlaps_directed(gi, gr)

#####################################################################
# 2. Find overlaps between PinnedGInteractions and a subject GRanges
#####################################################################

gi |> pin_by("first") |> find_overlaps(gr)

gi |> pin_by("second") |> find_overlaps(gr)

gi |> pin_by("first") |> find_overlaps_directed(gr)

gi |> pin_by("second") |> find_overlaps_directed(gr)
```

---

ginteractions-join-overlap-left

Join overlaps between a query GInteractions and a GRanges

Description

Join overlaps between a query GInteractions and a GRanges

Usage

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

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

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

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

Arguments

`x`	A (Pinned)GInteractions object
`y`	A GRanges object
`maxgap, minoverlap`	See ?`countOverlaps` in the **GenomicRanges** package for a description of these arguments
`suffix`	Suffix to add to metadata columns (character vector of length 2, default to `c(".x", ".y")`).

Value

An integer vector of same length as x.

Examples

```
gi <- read.table(text = "
    chr1 11 20 - chr1 21 30 +
    chr1 11 20 - chr1 51 55 +
    chr1 21 30 - chr1 51 55 +
    chr1 21 30 - chr2 51 60 +",
col.names = c(
    "seqnames1", "start1", "end1", "strand1",
    "seqnames2", "start2", "end2", "strand2")
) |> as_ginteractions() |> mutate(id = 1:4, type = 'gi')

gr <- GenomicRanges::GRanges(
    c("chr1:20-30:+", "chr2:55-65:-")
) |> plyranges::mutate(id = 1:2, type = 'gr')

gi

gr

####################################################################
# 1. Join overlaps between GInteractions and a subject GRanges
####################################################################

join_overlap_left(gi, gr)

join_overlap_left_directed(gi, gr)

####################################################################
# 2. Join overlaps between PinnedGInteractions and a subject GRanges
####################################################################

gi |> pin_by("first") |> join_overlap_left(gr)

gi |> pin_by("first") |> join_overlap_left_directed(gr)

gi |> pin_by("second") |> join_overlap_left(gr)

gi |> pin_by("second") |> join_overlap_left_directed(gr)
```

`group-group_data` *GInteractions grouping metadata*

Description

GInteractions grouping metadata

Usage

```
## S3 method for class 'GroupedGInteractions'
group_data(.data)

## S3 method for class 'GroupedGInteractions'
group_keys(.tbl, ...)
```

```
## S3 method for class 'GroupedGInteractions'
group_indices(.data, ...)

## S3 method for class 'GInteractions'
group_vars(x)

## S3 method for class 'GroupedGInteractions'
group_vars(x)

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

## S3 method for class 'GroupedGInteractions'
group_size(x)

## S3 method for class 'GroupedGInteractions'
n_groups(x)
```

Arguments

`.data`, `.tbl`, `x`	a GInteractions object
`...`	Ignored.

Value

a GInteractions object.

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30
chr1 11 20 chr1 51 55
chr1 11 30 chr1 51 55
chr1 11 30 chr2 51 60",
col.names = c(
    "seqnames1", "start1", "end1",
    "seqnames2", "start2", "end2")
) |>
  as_ginteractions() |>
  mutate(type = c('cis', 'cis', 'cis', 'trans'), score = runif(4))

ggi <- gi |> group_by(end1)
ggi
group_data(ggi)
group_keys(ggi)
group_rows(ggi)
group_indices(ggi)
group_vars(ggi)
groups(ggi)
group_size(ggi)
n_groups(ggi)
```

`pin` *Pin GInteractions by anchors set (anchors1 or anchors2).*

Description

Pin GInteractions by anchors set (anchors1 or anchors2).

Usage

```
pin(x, anchors)

pin_by(x, anchors)

pinned_anchors(x)

unpin(x)

## S4 method for signature 'GroupedGInteractions,character'
pin(x, anchors)

## S4 method for signature 'GroupedGInteractions,numeric'
pin(x, anchors)

## S4 method for signature 'GInteractions,character'
pin(x, anchors)

## S4 method for signature 'GInteractions,numeric'
pin(x, anchors)

## S4 method for signature 'PinnedGInteractions,missing'
pin(x, anchors)

## S4 method for signature 'PinnedGInteractions,character'
pin(x, anchors)

## S4 method for signature 'PinnedGInteractions,numeric'
pin(x, anchors)

## S4 method for signature 'AnchoredPinnedGInteractions,character'
pin(x, anchors)

## S4 method for signature 'AnchoredPinnedGInteractions,numeric'
pin(x, anchors)

pin_first(x)

pin_second(x)
```

```
pin_anchors1(x)

pin_anchors2(x)

## S4 method for signature 'AnchoredPinnedGInteractions'
unpin(x)

## S4 method for signature 'PinnedGInteractions'
unpin(x)

## S4 method for signature 'GInteractions'
unpin(x)

## S4 method for signature 'PinnedGInteractions'
pinned_anchors(x)

## S4 method for signature 'AnchoredPinnedGInteractions'
pinned_anchors(x)
```

Arguments

`x`	a GInteractions object
`anchors`	Anchors to pin on ("first" or "second")

Value

- `pin_*` functions return a PinnedGInteractions object.
- `pin` returns a numerical value indicating which set of anchors is pinned.
- `unpin` removes the pinning of a PinnedGInteractions object.
- `pinned_anchors` returns an (Anchored)GenomicRanges object corresponding to the pinned anchors of a PinnedGInteractions object.

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30
chr1 11 20 chr1 51 55
chr1 11 30 chr1 51 55
chr1 11 30 chr2 51 60",
col.names = c(
    "seqnames1", "start1", "end1",
    "seqnames2", "start2", "end2")
) |>
  as_ginteractions() |>
  mutate(type = c('cis', 'cis', 'cis', 'trans'), score = runif(4))

####################################################################
# 1. Pin by first anchors
```

```
####################################################################

gi |> pin_by("first")

gi |> pin_first()

gi |> pin_anchors1()

####################################################################
# 2. Pin by second anchors
####################################################################

gi |> pin_by("second")

gi |> pin_second()

gi |> pin_anchors2()

####################################################################
# 3. Unpin
####################################################################

gi |> pin("second") |> unpin()
```

plyranges-flank

Generate flanking regions from pinned anchors of a GInteractions object with plyranges

Description

Generate flanking regions from pinned anchors of a GInteractions object with plyranges

Usage

```
flank_downstream(x, width)

## S3 method for class 'Ranges'
flank_downstream(x, width)

## S3 method for class 'PinnedGInteractions'
flank_downstream(x, width)

flank_upstream(x, width)

## S3 method for class 'Ranges'
flank_upstream(x, width)

## S3 method for class 'PinnedGInteractions'
flank_upstream(x, width)
```

```
flank_right(x, width)

## S3 method for class 'Ranges'
flank_right(x, width)

## S3 method for class 'PinnedGInteractions'
flank_right(x, width)

flank_left(x, width)

## S3 method for class 'Ranges'
flank_left(x, width)

## S3 method for class 'PinnedGInteractions'
flank_left(x, width)
```

Arguments

x	a PinnedGInteractions 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.

Value

A PinnedGInteractions object

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30 + +
chr1 11 20 chr1 51 55 + +
chr1 11 30 chr1 51 55 - -
chr1 11 30 chr2 51 60 - -",
col.names = c(
  "seqnames1", "start1", "end1",
  "seqnames2", "start2", "end2", "strand1", "strand2")
) |>
  as_ginteractions() |>
  mutate(score = runif(4), type = c('cis', 'cis', 'cis', 'trans'))

####################################################################
# 1. Simple flanking
####################################################################

gi

gi |> pin_by("first") |> flank_left(-2)

gi |> pin_by("second") |> flank_upstream(4)
```

```
####################################################################
# 2. Chained flanking of each set of anchors
####################################################################

gi |>
  pin_by("first") |> flank_left(2) |>
  pin_by("second") |> flank_right(2)
```

`plyranges-shift` *Shift pinned anchors of a GInteractions object with plyranges*

Description

Shift pinned anchors of a GInteractions object with plyranges

Usage

```
shift_downstream(x, shift)

## S3 method for class 'Ranges'
shift_downstream(x, shift)

## S3 method for class 'PinnedGInteractions'
shift_downstream(x, shift)

shift_upstream(x, shift)

## S3 method for class 'Ranges'
shift_upstream(x, shift)

## S3 method for class 'PinnedGInteractions'
shift_upstream(x, shift)

shift_right(x, shift)

## S3 method for class 'Ranges'
shift_right(x, shift)

## S3 method for class 'PinnedGInteractions'
shift_right(x, shift)

shift_left(x, shift)

## S3 method for class 'Ranges'
shift_left(x, shift)

## S3 method for class 'PinnedGInteractions'
shift_left(x, shift)
```

Arguments

`x`	a PinnedGInteractions 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.

Value

A PinnedGInteractions object

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30 + +
chr1 11 20 chr1 51 55 + +
chr1 11 30 chr1 51 55 - -
chr1 11 30 chr2 51 60 - -",
col.names = c(
  "seqnames1", "start1", "end1",
  "seqnames2", "start2", "end2", "strand1", "strand2")
) |>
  as_ginteractions() |>
  mutate(score = runif(4), type = c('cis', 'cis', 'cis', 'trans'))

####################################################################
# 1. Simple shifting
####################################################################

gi

gi |> pin_by("first") |> shift_left(15)

gi |> pin_by("second") |> shift_downstream(10)

####################################################################
# 2. Chained shifting of each set of anchors
####################################################################

gi |>
  pin_by("first") |> shift_downstream(20) |>
  pin_by("second") |> shift_upstream(20)
```

`plyranges-stretch` *Stretch pinned anchors of a GInteractions object with plyranges*

Description

Stretch pinned anchors of a GInteractions object with plyranges

Usage

```
## S3 method for class 'AnchoredPinnedGInteractions'
stretch(x, extend)

## S3 method for class 'PinnedGInteractions'
stretch(x, extend)
```

Arguments

`x`	a PinnedGInteractions object
`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 PinnedGInteractions object

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30 + +
chr1 11 20 chr1 51 55 + +
chr1 11 30 chr1 51 55 - -
chr1 11 30 chr2 51 60 - -",
col.names = c(
  "seqnames1", "start1", "end1",
  "seqnames2", "start2", "end2", "strand1", "strand2")
) |>
  as_ginteractions() |>
  mutate(score = runif(4), type = c('cis', 'cis', 'cis', 'trans'))

####################################################################
# 1. Simple stretching
####################################################################

gi

gi |> pin_by("first") |> anchor_start() |> stretch(15)

gi |> pin_by("second") |> anchor_center() |> stretch(10)

gi |> pin_by("second") |> anchor_3p() |> stretch(20)

####################################################################
# 2. Chained stretching of each set of anchors
####################################################################

gi |>
  pin_by("first") |> anchor_start() |> stretch(20) |>
  pin_by("second") |> stretch(20)
```

`replace_anchors` *Replace anchors of a GInteractions*

Description

Replace anchors of a GInteractions

Usage

```
replace_anchors(x, id, value)

## S4 method for signature 'GInteractions,character,GenomicRanges'
replace_anchors(x, id, value)

## S4 method for signature 'GInteractions,numeric,GenomicRanges'
replace_anchors(x, id, value)

## S4 method for signature 'PinnedGInteractions,missing,GenomicRanges'
replace_anchors(x, id, value)

## S4 method for signature 'AnchoredPinnedGInteractions,missing,GRanges'
replace_anchors(x, id, value)

## S4 method for signature 'AnchoredPinnedGInteractions,numeric,GRanges'
replace_anchors(x, id, value)
```

Arguments

`x`	a (Pinned)GInteractions object
`id`	Which anchors to replace ("first" or "second"). Ignored if the GInteractions is already pinned to a specific set of anchors.
`value`	A GRanges object vector the same length as x.

Value

a (Pinned)GInteractions object.

Examples

```
gi <- read.table(text = "
chr1 11 20 chr1 21 30
chr1 11 20 chr1 51 55
chr1 11 30 chr1 51 55
chr1 11 30 chr2 51 60",
col.names = c(
    "seqnames1", "start1", "end1",
    "seqnames2", "start2", "end2")
) |>
  as_ginteractions() |>
  mutate(type = c('cis', 'cis', 'cis', 'trans'), score = runif(4))

####################################################################
# 1. Replace anchors of a GInteractions object
####################################################################

gi |> replace_anchors(2, value = anchors1(gi))

gi |> replace_anchors(1, value = anchors2(gi))

gi |> replace_anchors(1, value = GenomicRanges::GRanges(c(
  "chr1:1-2", "chr1:2-3", "chr1:3-4", "chr1:4-5"
)))

####################################################################
# 2. Replace anchors of a pinned GInteractions object
####################################################################

gi |> pin_by(1) |> replace_anchors(value = anchors1(gi))

gi |> replace_anchors(1, value = anchors2(gi))

gi |>
  pin_by(1) |>
  replace_anchors(value = GenomicRanges::GRanges(c(
    "chr1:1-2", "chr1:2-3", "chr1:3-4", "chr1:4-5"
  ))) |>
  pin_by(2) |>
  replace_anchors(value = GenomicRanges::GRanges(c(
    "chr2:1-2", "chr2:2-3", "chr2:3-4", "chr2:4-5"
  )))
```

Index