

Package ‘plyinteractions’

September 23, 2026

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

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'ginteractions-construct.R' 'ginteractions-env.R'
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'ginteractions-setters.R' 'tbl_vars.R' 'group_data.R'

```
'group_by.R' 'internals.R' 'join-overlap-left.R'
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'methods-DelegatingGInteractions.R'
'methods-GroupedGInteractions.R'
'methods-PinnedGInteractions.R' 'methods-show.R' 'mutate.R'
'pair-granges.R' 'pin.R' 'plyinteractions.R' 'rename.R'
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Author Jacques Serizay [aut, cre]

Maintainer Jacques Serizay <jacquesserizay@gmail.com>

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plyinteractions-package

plyinteractions: Extending tidyomics verbs to genomic interactions

Description

plyinteractions verbs treat 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.

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)

Jacques Serizay

Maintainer: Jacques Serizay <jacquesserizay@gmail.com>

See Also

Useful links:

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

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add_pairedist	<i>Appends distance between interaction anchors</i>
---------------	---

Description

Appends distance between interaction anchors, using `InteractionSet::pairedist`

Usage

```
add_pairedist(x, type = "mid", colname = "pairedist")
```

Arguments

<code>x</code>	The query <code>GInteractions</code>
<code>type</code>	A character string specifying the type of distance to compute. Can take values of "mid", "gap", "span", "diag" or "intra".
<code>colname</code>	name of column to hold pair distance values

Value

The `GInteractions` with an additional column containing the distance between each pair of anchors.

Examples

```
gi <- read.table(text = "
chr1 100 200 chr1 5000 5100 bedpe_example1 30 + -
chr1 1000 5000 chr2 3000 3800 bedpe_example2 100 + -",
col.names = c(
  "seqnames1", "start1", "end1",
  "seqnames2", "start2", "end2", "name", "score", "strand1", "strand2")
) |> as_ginteractions()

add_pairedist(gi)
```

anchors1	<i>Enhanced GInteractions getters</i>
----------	---------------------------------------

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	<i>Annotate both anchors of a GInteractions</i>
----------	---

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:+")) |>
  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() |>
  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() |>
  arrange(desc(n))
```

as_ginteractions	<i>Construct a GInteractions object from a tibble, DataFrame or data.frame</i>
------------------	--

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

<code>.data</code>	A <code>data.frame()</code> , <code>S4Vectors::DataFrame()</code> or <code>tibble()</code> to construct a <code>GInteractions</code> object from.
<code>...</code>	Optional named arguments specifying which the columns in <code>.data</code> contain the core components a <code>GInteractions</code> object.
<code>keep.extra.columns</code>	TRUE or FALSE (the default). If TRUE, the columns in <code>df</code> that are not used to form the genomic ranges of the returned <code>GRanges</code> object are then returned as metadata columns on the object. Otherwise, they are ignored.
<code>starts.in.df.are.0based</code>	TRUE or FALSE (the default). If TRUE, then the start positions of the genomic ranges in <code>df</code> are considered to be 0-based and are converted to 1-based in the returned <code>GRanges</code> 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
  )

```

delegating-ginteractions-methods

Methods for DelegatingGInteractions objects

Description

Methods for DelegatingGInteractions objects

Usage

```
## S4 method for signature 'DelegatingGInteractions'
anchors1(x)
```

```
## S4 method for signature 'DelegatingGInteractions'
ranges1(x)
```

```
## S4 method for signature 'DelegatingGInteractions'
seqnames1(x)
```

```
## S4 method for signature 'DelegatingGInteractions'
start1(x)
```

```
## S4 method for signature 'DelegatingGInteractions'
end1(x)
```

```
## S4 method for signature 'DelegatingGInteractions'
width1(x)

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

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

## S4 method for signature 'DelegatingGInteractions'
ranges2(x)

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

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

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

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

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

## S4 method for signature 'DelegatingGInteractions'
anchors(x)

## S4 method for signature 'DelegatingGInteractions'
regions(x)

## S4 method for signature 'DelegatingGInteractions'
seqinfo(x)

## S4 method for signature 'DelegatingGInteractions'
mcols(x)

## S4 method for signature 'DelegatingGInteractions'
show(object)
```

Value

One of the core GInteractions fields (e.g. seqnames1, start1, ...)

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 de-
           scending 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 <code>sum(wt)</code> 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/tally 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)
```

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

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

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

<code>.data</code>	a GInteractions object
<code>...</code>	Optional named arguments specifying which the columns in <code>.data</code> 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'))

gi

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

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

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

gi |>
  pin_by("first") |> anchor_center() |> stretch(4) |>
  pin_by("second") |> anchor_3p() |> stretch(-2)

```

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:-")
) |> 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)
```

Description

write_* functions are provided to export a GInteractions object into these two file formats. See 4DN documentation (https://github.com/4dn-dcic/pairix/blob/master/pairs_format_specification.md) and UCSC documentation (<https://bedtools.readthedocs.io/en/latest/content/general-usage.html#bedpe-format>) for more details.

Usage

```
write_bedpe(x, file, scores = NULL)

write_pairs(x, file, seqlengths = Seqinfo::seqlengths(x))
```

Arguments

x	a GInteractions object.
file	path to a .bedpe or .pairs file to save the genomic interactions.
scores	Name of column to extract scores from.
seqlengths	Named vector indicating the chromosome sizes.

Value

TRUE

Examples

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

write_bedpe(gi, 'gi.bedpe')
write_pairs(gi, 'gi.pairs')
```

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:-")
) |> 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:-")
) |> 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:-")
) |> 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	<i>GInteractions</i> 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)
```

pair_granges

Pairwise combination of a GRanges object

Description

Create a GInteractions object from a GRanges object, containing all possible entry pairs

Usage

```
pair_granges(x)
```

Arguments

x A GRanges object

Value

A GInteractions object

Examples

```
gr <- read.table(text = "
chr1 100 200
chr1 5000 5100
chr1 1000 5000
chr2 3000 3800",
col.names = c(
  "seqnames", "start", "end"
)) |> plyranges::as_granges()

pair_granges(gr)
```

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()

```

plyinteractions-data *Data files provided in the plyinteractions package*

Description

- Loops identified in GM12878 with HiCCUPS: File obtained from GEO entry GSE63525 (GSE63525_GM12878_primary). Rao SS, Huntley MH, Durand NC, Stamenova EK et al. A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping. Cell 2014 Dec 18;159(7):1665-80. PMID: 25497547

- Interactions identified in L3 *C. elegans* by ARC-C: Supplemental Table 2 obtained from Genome Biology online publication. Huang N, Seow WQ, Appert A, Dong Y, Stempor P and Ahringer J Accessible Region Conformation Capture (ARC-C) gives high-resolution insights into genome architecture and regulation. *Genome Res* 2022 Feb;32(2):357-366. PMID: 34933938
- Annotated regulatory elements in *C. elegans*: Figure 2 - Source data 1 obtained from eLife online publication. Jänes J, Dong Y, Schoof M, Serizay J, Appert A, Cerrato C, Woodbury C, Chen R, Gemma C, Huang N, Kissiov D, Stempor P, Steward A, Zeiser E, Sauer S and Ahringer J Chromatin accessibility dynamics across *C. elegans* development and ageing. *Elife* 2018 Oct 26;7. PMID: 30362940

Usage

```
data(GM12878_HiCCUPS)
```

```
data(GM12878_HiCCUPS)
```

```
data(GM12878_HiCCUPS)
```

Format

```
A GInteractions object
```

```
A GInteractions object
```

```
A GInteractions object
```

Source

```
https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE63525
```

```
https://genome.cshlp.org/content/early/2021/12/21/gr.275669.121
```

```
https://genome.cshlp.org/content/early/2021/12/21/gr.275669.121
```

```
plyinteractions-flank Generate flanking regions from pinned anchors of a GInteractions ob-  
ject
```

Description

```
Generate flanking regions from pinned anchors of a GInteractions object
```

Usage

```
flank_downstream(x, width)
```

```
## S3 method for class 'Ranges'
```

```
flank_downstream(x, width)
```

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

flank_left(x, width)

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

## S3 method for class 'PinnedGInteractions'
flank_left(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)
```

Arguments

<code>x</code>	a <code>PinnedGInteractions</code> object
<code>width</code>	The width of the flanking region relative to the ranges in <code>x</code> . Either an integer vector of length 1 or an integer vector the same length as <code>x</code> . 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_downstream(4)

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

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

```

plyinteractions-shift *Shift pinned anchors of a GInteractions object with plyinteractions*

Description

Shift pinned anchors of a GInteractions object with plyinteractions

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

<code>x</code>	a <code>PinnedGInteractions</code> object
<code>shift</code>	The amount to move the genomic interval in the <code>Ranges</code> object by. Either a non-negative integer vector of length 1 or an integer vector the same length as <code>x</code> .

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	<i>Stretch pinned anchors of a GInteractions object with plyranges</i>
-------------------	--

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	<i>Replace anchors of a GInteractions</i>
-----------------	---

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"
  )))
```

Description

Internal GInteractions setters

Usage

```
set_seqnames1(x, value)

set_seqnames2(x, value)

set_start1(x, value)

set_start2(x, value)

set_end1(x, value)

set_end2(x, value)

set_width1(x, value)

set_width2(x, value)

set_strand1(x, value)

set_strand2(x, value)

## S4 replacement method for signature 'GInteractions'
first(x) <- value

## S4 replacement method for signature 'GInteractions'
second(x) <- value

## S4 method for signature 'GInteractions,factor'
set_seqnames1(x, value)

## S4 method for signature 'GInteractions,factor'
set_seqnames2(x, value)

## S4 method for signature 'GInteractions,numeric'
set_start1(x, value)

## S4 method for signature 'GInteractions,numeric'
set_start2(x, value)

## S4 method for signature 'GInteractions,numeric'
set_end1(x, value)

## S4 method for signature 'GInteractions,numeric'
set_end2(x, value)
```

```
## S4 method for signature 'GInteractions,numeric'
set_width1(x, value)

## S4 method for signature 'GInteractions,numeric'
set_width2(x, value)

## S4 method for signature 'AnchoredPinnedGInteractions,numeric'
set_width1(x, value)

## S4 method for signature 'AnchoredPinnedGInteractions,numeric'
set_width2(x, value)

## S4 method for signature 'GInteractions,character'
set_strand1(x, value)

## S4 method for signature 'GInteractions,character'
set_strand2(x, value)
```

Arguments

x	a GInteractions object
value	a value passed to the corresponding field

Value

A modified GInteractions

show-GInteractions	<i>show method for GInteractions objects</i>
--------------------	--

Description

show method for GInteractions objects

Arguments

object	a (Anchored/Pinned/Grouped)GInteractions object
--------	---

Value

Prints a message to the console describing the contents of a GInteractions' object.

Examples

```
pairsf <- system.file('extdata', 'pairs.gz', package = 'plyinteractions')
pairs <- read.table(pairsf, comment.char = '#', header = FALSE)
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
  )
```

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