Package ‘plyinteractions’

March 14, 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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         'ginteractions-construct.R' 'ginteractions-env.R'
         'ginteractions-getters.R' 'ginteractions-scoping.R'
         'ginteractions-setters.R' 'tbl_vars.R' 'group_data.R'
         'group_by.R' 'internals.R' 'join-overlap-left.R'
         'methods- AnchoredPinnedGInteractions.R'
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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](https://github.com/js2264/plyinteractions)
- Report bugs at [https://github.com/js2264/plyinteractions/issues](https://github.com/js2264/plyinteractions/issues)
Enhanced GInteractions getters

**Description**

Enhanced GInteractions getters

**Usage**

anchors1(x)

anchors2(x)

seqnames1(x)

seqnames2(x)

start1(x)

start2(x)

end1(x)

dend2(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'
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

```r
gi <- data.frame(
  seqnames1 = 'chr1', start1 = 1, end1 = 10,
```

```r
class(gi)  # Show class of object
```
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

```r
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

```r
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

```r
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

```r
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

```r
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

```r
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)
```

```r
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
  )

---

**ce10_ARCC**

*Interactions identified in L3 C. elegans by ARC-C*

**Description**

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

**Usage**

ce10_ARCC

**Format**

An object of class GInteractions of length 14992.

**Value**

A GInteractions object

**Source**

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

Figure 2 - Source data 1 obtained from eLife online publication.


Usage

ce10_REs

Format

An object of class GRanges of length 42245.

Value

A GRanges object

Source

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

delegating-ginteractions-methods

Methods for DelegatingGInteractions objects

Description

Methods for DelegatingGInteractions objects

Usage

```r
## 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, ...)

---

**Description**

Arrange a GInteractions by a column

**Usage**

```r
## 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**

```r
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
####################################################################
```
# Count or tally GInteractions per group

### Description

Count or tally GInteractions per group

### Usage

```r
## 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.
**dplyr-filter**

**Value**

A S4Vectors::DataFrame() object, with an added column with the count/tabll per group.

**Examples**

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

```r
gi

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

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

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

---

**Description**

Subset a GInteractions with tidyverse-like filter

**Usage**

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

.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

# 2. On-the-fly calculations

gi |> filter(gc > 0.1)
gi |> filter(gc > 0.1, score > 50)
gi |> filter(cis)
gi |> filter(start1 >= start2 + 3)
gi |> filter(score * gc > score * 0.5)
Usage

```r
## 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

```r
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

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

# 2. Group by metadata column

```r
gi |> group_by(type) |> group_data()
```
# 3. Combine core and metadata column grouping
```r
# Note: the `group_by()` function is used to create a GroupedGInteractions object.

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

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

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

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

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
```r

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**

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

**Arguments**

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

**Value**

A GInteractions object.

**Examples**

```r
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

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

# 2. More complex, nested or inplace changes

```r
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

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

# Note how the core columns are modified sequentially

```r
gi |
  mutate(start1 = 1, end1 = 10)
```

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

# 4. Evaluating core GInteractions columns

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

Description

Rename columns from a GInteractions with tidyverse-like rename

Usage

```r
## 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

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

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

Select columns within GInteractions metadata columns.

### Usage

```r
## 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

```r
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'))

# 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

```r
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

```
# Create a GInteractions object
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 - -",

# Slice the 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**

```
# Read the GInteractions from a file
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'))

# Summarize a single column

# 1. Summarize a single column

# 2. Summarize by multiple columns

# Summarize by multiple columns

# Manage GInteractions anchors with plyranges

---

### Manage GInteractions anchors with plyranges

**Description**

Manage GInteractions anchors with plyranges

**Usage**

```r
## 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**

```r
# Create a PinnedGInteractions object
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

```r
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

```r
## 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().
ginteractions-filter-overlaps

Examples

```r
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)
```

Description

Filter GInteractions overlapping with a GRanges
Usage

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

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

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

```r
## 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

```r
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 65 +",
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
```
### Find overlaps between a query GInteractions and a GRanges

#### Description
Find overlaps between a query GInteractions and a GRanges

#### Usage
```r
## 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(
```

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

```r
# GInteractions
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')

# GRanges
gr <- GenomicRanges::GRanges(  
c("chr1:20-30:+", "chr2:55-65:-")
)
# plyranges::mutate(id = 1:2, type = 'gr')
```
# Find overlaps between GInteractions and a subject GRanges

```r
find_overlaps(gi, gr)
find_overlaps_directed(gi, gr)
```

# Find overlaps between PinnedGInteractions and a subject GRanges

```r
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)
```

---

## Description

Join overlaps between a query GInteractions and a GRanges

## Usage

```r
## 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

```r
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)
```

---

**GM12878_HiCCUPS**

*Loops identified in GM12878 with HiCCUPS*

### Description

File obtained from GEO entry GSE63525 (GSE63525_GM12878_primary+replicate_HiCCUPS_looplist.txt.gz).


### Usage

GM12878_HiCCUPS

### Format

An object of class GInteractions of length 9448.

### Value

A GInteractions object

### Source

Description

GInteractions grouping metadata

Usage

```r
## 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

```r
gi <- read.table(text = "
chr1 11 20 chr1 21 30
chr1 11 20 chr1 51 55")
```


```r
(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))

## 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)
```

---

**Description**

Pin GInteractions by anchors set (anchors1 or anchors2).

**Usage**

- `pin(x, anchors)`
- `pin_by(x, anchors)`
- `pinned_anchors(x)`
- `unpin(x)`

---
pin(x, anchors)

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

# 2. Pin by second anchors

# 3. 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 + +
"
plyranges-shift

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

```r
```
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

```r
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

```r
gi
```
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 28 chr1 21 30 + +
chr1 11 28 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() |>
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)
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)

---

reexports

Objects exported from other packages

Description

These objects are imported from other packages. Follow the links below to see their documentation.

**dplyr** arrange, count, filter, group_by, group_data, group_indices, group_keys, group_rows, group_size, group_vars, groups, mutate, n_groups, rename, select, slice, summarise, summarize, tally, ungroup

**plyranges** anchor, anchor_3p, anchor_5p, anchor_center, anchor_end, anchor_start, count_overlaps, count_overlaps_directed, filter_by_non_overlaps, filter_by_overlaps, find_overlaps, find_overlaps_directed, join_overlap_left, join_overlap_left_directed, stretch, unanchor

Value

Depending on the re-exported function

Examples

```
1 + 1
```
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")
)
# 1. Replace anchors of a GInteractions object

```r
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

```r
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"
)))
```

---

**set_seqnames1**

Internal GInteractions setters

**Description**

Internal GInteractions setters

**Usage**

```r
set_seqnames1(x, value)
set_seqnames2(x, value)
set_start1(x, value)
```
set_seqnames1

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
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