

# Package ‘genomeIntervals’

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**Title** Operations on genomic intervals

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**Imports** Seqinfo, GenomicRanges (>= 1.21.16), IRanges(>= 2.3.14), S4Vectors (>= 0.7.10)

**Description** This package defines classes for representing genomic intervals and provides functions and methods for working with these.  
Note: The package provides the basic infrastructure for and is enhanced by the package 'girafe'.

**License** Artistic-2.0

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Genome\_intervals-coercion-methods.R Genome\_intervals-package.R  
Genome\_intervals-ordering.R show-methods.R size-methods.R c.R  
core\_annotated.R distance\_to\_nearest-methods.R  
interval\_complement-methods.R interval\_overlap-methods.R  
interval\_intersection-methods.R interval\_union-methods.R  
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genomeIntervals-package

*Operations on genomic intervals*

---

## Description

Tools for operation on genomic intervals.

## Details

Package: genomeIntervals  
 Version: 1.25.3  
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[parseGffAttributes](#) Parse out the gffAttributes column of a `Genome_intervals` object  
[readGff3](#) Make a `Genome_intervals_stranded` object from a GFF file

### Author(s)

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 Maintainer: Julien Gagneur <gagneur@embl.de>

### See Also

[intervals](#)

---

|   |                                                    |
|---|----------------------------------------------------|
| c | <i>c extension for the genomeIntervals package</i> |
|---|----------------------------------------------------|

---

### Description

This function combines several genome intervals (stranded or not) objects into a single one.

### Usage

```
## S4 method for signature 'Genome_intervals'
c(x, ..., recursive = FALSE)
```

### Arguments

|           |                                                                                                                          |
|-----------|--------------------------------------------------------------------------------------------------------------------------|
| x         | a <a href="#">Genome_intervals</a> or <a href="#">Genome_intervals_stranded</a> object - not mandatory.                  |
| ...       | two (one if x is defined) or more <a href="#">Genome_intervals</a> or <a href="#">Genome_intervals_stranded</a> objects. |
| recursive | inherited from the base c function definition and not used.                                                              |

### Details

If the arguments have mixed classes ( both [Genome\\_intervals](#) or [Genome\\_intervals\\_stranded](#)), then they are coerced to [Genome\\_intervals](#) before combination. Otherwise, the common class is used. If a list is provided with NULL entries, these are discarded. If a vector of object is provided with non `genomeIntervals` classes, then a list, ordered as the input vector, is returned.

### Value

- A single [Genome\\_intervals](#) or [Genome\\_intervals\\_stranded](#) object. Input objects are combined in their order of appearance in the the argument list.
- If any input argument is not a [Genome\\_intervals](#), `list(...)` is returned instead.

###

**Examples**

```
##' load toy examples
data("gen_ints")

##' combine i and j returns a Genome_intervals_stranded object
c( i, j )

##' combine a not-stranded and a stranded returns a not-stranded object
c( as(i, "Genome_intervals"), j )
```

---

core\_annotated

*Genome intervals with minimal annotation*


---

**Description**

returns a copy of the input (stranded) genome intervals object with annotations restricted to the minimally required ones.

**Usage**

```
core_annotated(x)
```

**Arguments**

x                      A [Genome\\_intervals](#) or [Genome\\_intervals\\_stranded](#) object.

**Value**

A copy of x with the annotation slot restricted to seq\_name, inter\_base and strand (the latter only if x is a [Genome\\_intervals\\_stranded](#) object).

**Examples**

```
# load toy examples
data("gen_ints")

# add some non-core annotations to i
annotation(i)$comment = "some non-core annotation"

# i with all annotations
i

# core annotations only
core_annotated(i)

## Not run:
# with different annotation columns, i and j cannot be combined
c( i, j )

## End(Not run)

# core annotated versions can
c( core_annotated(i), core_annotated(j) )
```

---

distance\_to\_nearest     *Distance in bases to the closest interval(s)*

---

## Description

Given two objects, from and to, compute the distance in bases of each from interval to the nearest to interval(s). The distance between a base and the next inter-bases on either side values 0.5. Thus, base - base and inter-base - inter-base intervals distances are integer, whereas base - inter-base intervals distances are half-integers.

## Usage

```
## S4 method for signature 'Genome_intervals,Genome_intervals'
distance_to_nearest(from, to)
## S4 method for signature
## 'Genome_intervals_stranded,Genome_intervals_stranded'
distance_to_nearest(from, to)
```

## Arguments

from                    A [Genome\\_intervals](#) or [Genome\\_intervals\\_stranded](#) object.  
to                        A [Genome\\_intervals](#) or [Genome\\_intervals](#) object.

## Details

A wrapper calling [intervals::distance\\_to\\_nearest](#) by seqnames and by strand (if both from and to are [Genome\\_intervals\\_stranded](#) objects). Thus, if both are stranded, distances are computed over each strand separately. One object must be coerced to [Genome\\_intervals](#) if this is not wished.

## Value

A numeric vector of distances with one element for each row of from.

## See Also

[intervals::distance\\_to\\_nearest](#)

## Examples

```
## load toy examples
data(gen_ints)

## i in close_intervals notation
close_intervals(i)

## j in close_intervals notation
close_intervals(j)

## distances from i to j
dn = distance_to_nearest(i,j)
dn
```

```
## distance == 0 if and only if the interval overlaps another one:
io = interval_overlap(i,j)
if( any( ( sapply(io, length) >0 ) != (!is.na(dn) & dn ==0) ) )
  stop("The property 'distance == 0 if and only if the interval overlaps another one' is not followed for at least")

## distances without strand-specificity
distance_to_nearest(
  as(i,"Genome_intervals"),
  as(j,"Genome_intervals")
)
```

---

GenomeIntervals

---

*Constructor function for genomeIntervals objects*


---

## Description

A user-friendly constructor function for creating both `Genome_intervals` and `Genome_intervals_stranded` objects.

## Usage

```
GenomeIntervals(chromosome, start, end, strand = NULL,
  inter.base = NULL, leftOpen = NULL,
  rightOpen = NULL, ...)
```

## Arguments

|                         |                                                                                                                                                                                                                                     |
|-------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>chromosome</code> | character vector of chromosome names of the intervals; will become the <code>seqnames</code> of the resulting object                                                                                                                |
| <code>start</code>      | numeric or integer; start (left-most) coordinate of the intervals                                                                                                                                                                   |
| <code>end</code>        | numeric or integer; end (right-most) coordinate of the intervals                                                                                                                                                                    |
| <code>strand</code>     | character; specifies which strand the intervals are located on; if specified an object of class <code>Genome_intervals_stranded</code> is created; if <code>NULL</code> an object of class <code>Genome_intervals</code> is created |
| <code>inter.base</code> | logical; if <code>TRUE</code> an interval is located between the specified coordinates, instead of spanning them; useful for restriction-enzym cutting sites, for example.                                                          |
| <code>leftOpen</code>   | logical; if <code>TRUE</code> an interval is left-open; if <code>NULL</code> all intervals are assumed to be left-closed.                                                                                                           |
| <code>rightOpen</code>  | logical; if <code>TRUE</code> an interval is right-open; if <code>NULL</code> all intervals are assumed to be right-closed.                                                                                                         |
| <code>...</code>        | any additional annotation for supplied intervals                                                                                                                                                                                    |

## Details

The arguments `chromosome`, `start`, and `end` need to be of the same length, with the first element of each vector corresponding to the first interval, the second element to the second interval, and so on.

The same applies to `strand`, `inter.base`, `leftOpen`, `rightOpen` and any additional vectors in `'...'`, if they are specified.

**Value**

An object of class `Genome_intervals` or `Genome_intervals_stranded` depending on whether strand has been specified.

**Author(s)**

J. Toedling

**See Also**

[Genome\\_intervals-class](#), [Genome\\_intervals\\_stranded-class](#)

**Examples**

```
## constructing a Genome_intervals object
G <- GenomeIntervals(start=c(1,3,4,5,8,10), end=c(5,5,6,8,9,11),
                     chromosome=rep(c("chr2","chrX","chr1"), each=2),
                     leftOpen=rep(c(FALSE, FALSE, TRUE), 2))

show(G)

## constructing a Genome_intervals_stranded object with
## additional interval annotation
GS <- GenomeIntervals(start=c(1,3,4,5,8,10), end=c(5,5,6,8,9,11),
                      chromosome=rep(c("chr2","chrX","chr1"), each=2),
                      strand=c("-", "-", "+", "+", "+", "+"),
                      GC.content=round(runif(6), digits=2))

show(GS)
```

---

genomeIntervals coercion methods

*Coercion methods of the genomeIntervals package*

---

**Description**

**coerce** This method allows to coerce a [genomeIntervals](#) object into a [GRangesList](#) object.

**Usage**

```
## S4 method for signature 'Genome_intervals'
as(from,to)
```

**Arguments**

|      |                                                                      |
|------|----------------------------------------------------------------------|
| from | An object of class <a href="#">Genome_intervals</a>                  |
| to   | a character string: <code>GRanges</code> or <code>GRangesList</code> |

**Value**

**coerce** A [GRanges](#) or [GRangesList](#) containing the result of the coercion.

**Author(s)**

Nicolas Delhomme

**See Also**

- [genomeIntervals](#) object
- [readGff3](#) function

**Examples**

```
## Not run:
annot<-readGff3(system.file("extdata",
                           "Dmel-mRNA-exon-r5.52.gff3",
                           package="RnaSeqTutorial")
gAnnot<-as(annot,"GRangesList") type(annot)

## End(Not run)
```

---

Genome\_intervals deprecated functions

*The following function have been deprecated:*

- `seq_name`
  - `seq_name<-`
- 

**Description**

- The `seq_name` and `seq_name<-` accessor functions have been replaced by the more generic `seqnames` and `seqnames<-` accessor functions, respectively.
- 

Genome\_intervals-class

*Class "Genome\\_intervals"*

---

**Description**

A set of genomic intervals without specified strand. Genomic intervals are intervals over the integers with two further annotations: `seqnames` (a chromosome or more generally a sequence of origin) and `inter_base` (logical) that states whether the interval is to be understood as an interval over bases (such as coding-sequence) or inter-bases (such as restriction sites or insertion positions).

**Slots**

`.Data`: See [Intervals\\_full](#)

`annotation`: A "data.frame" with the same number of rows as `.Data`. It has a column named `seq_name` that is a factor and does not contain missing values. `seq_name` is used to represent the chromosome or more generally the sequence of origin of the intervals. `annotation` has a column named `inter_base` that is logical and does not contain missing values. `inter_base` is FALSE if the interval is to be understood as an interval over bases (such as coding-sequence) and TRUE if it is over inter-bases (such as restriction site or an insertion position). Like base intervals, inter-base interval are encoded over the integers. An inter-base at position `n` indicates the space between base `n` and `n+1`.

`closed`: See [Intervals\\_full](#)

`type`: See [Intervals\\_full](#)



## Extends

Class "[Intervals\\_full](#)", directly. Class "[Intervals\\_virtual](#)", by class "Intervals\full", distance 2. Class "[matrix](#)", by class "Intervals\full", distance 3. Class "[array](#)", by class "Intervals\full", distance 4. Class "[structure](#)", by class "Intervals\full", distance 5. Class "[vector](#)", by class "Intervals\full", distance 6, with explicit coerce.

## Methods

```
[ signature(x = "Genome_intervals"): ...
[[ signature(x = "Genome_intervals"): ...
[[<- signature(x = "Genome_intervals"): ...
\[ signature(x = "Genome_intervals"): ...
\[<- signature(x = "Genome_intervals"): ...
annotation signature(object = "Genome_intervals"): ...
annotation<- signature(object = "Genome_intervals"): ...
coerce signature(from = "Genome_intervals", to = "Intervals_full"): ...
coerce signature(from = "Genome_intervals", to = "character"): ...
coerce signature(from = "Genome_intervals", to = "data.frame"): ...
distance\to\nearest signature(from = "Genome_intervals", to = "Genome_intervals"): ...
inter\base signature(x = "Genome_intervals"): ...
inter\base<- signature(x = "Genome_intervals"): ...
interval\complement signature(x = "Genome_intervals"): ...
interval\intersection signature(x = "Genome_intervals"): ...
interval\overlap signature(from = "Genome_intervals", to = "Genome_intervals"): ...
interval\union signature(x = "Genome_intervals"): ...
seqnames signature(x = "Genome_intervals"): ...
seqnames<- signature(x = "Genome_intervals"): ...
size signature(x = "Genome_intervals"): ...
type<- signature(x = "Genome_intervals"): ...
which\nearest For each interval in Set1, finds nearest (least distant) interval in Set2. Intervals on different chromosomes are never considered 'near' to each other. The returned value is a data.frame with the number of rows equal to the number of intervals in Set1. Each row specifies the distance to the nearest interval in Set2 (a 0 means that the interval overlaps one or more intervals in Set2), and the indices of near and overlapping intervals in Set2. See Intervals\_full for further details.
width Returns the interval length as the number of bp covered (base interval) or spanned(inter-base interval). Similar to the IRanges package widthfunction.
```

## Note

A Genome\_intervals is a "[Intervals\\_full](#)" of type Z (i.e. a set of intervals over the integers). The annotation slot can carry further columns that can serve as annotations.

## See Also

[Genome\\_intervals\\_stranded](#) for a derived class that allows stranded genomic intervals.

**Examples**

```
# The "Genome_intervals" class

i <- new(
  "Genome_intervals",
  matrix(
    c(1,2,
      3,5,
      4,6,
      8,9
    ),
    byrow = TRUE,
                                ncol = 2
  ),
  closed = matrix(
    c(
      TRUE, FALSE,
      TRUE, FALSE,
      TRUE, TRUE,
      TRUE, FALSE
    ),
    byrow = TRUE,
      ncol = 2
    ),
  annotation = data.frame(
    seq_name = factor(c("chr01", "chr01", "chr02", "chr02")),
    inter_base = c(FALSE, FALSE, TRUE, TRUE)
  )
)

colnames(i) <- c( "start", "end" )

# print
print(i)

# size (number of bases per interval)
size(i)

## convert to a data.frame
as(i, "data.frame")

## simpler way to construct a Genome_intervals object:
G <- GenomeIntervals(start=c(1,3,4,5,10,8), end=c(5,5,6,8,11,9),
                     chromosome=rep(c("chr2", "chrX", "chr1"), each=2),
                     leftOpen=rep(c(FALSE, FALSE, TRUE), 2))

show(G)
```

---

Genome\_intervals-ordering

*Ordering methods for Genome intervals*


---

**Description**

An order is defined on genome intervals and stranded genome intervals to allow `sort()`, `order()` and `rank()`.

**Usage**

```
## S4 method for signature 'Genome_intervals'
order(..., na.last=TRUE, decreasing=FALSE)
## S4 method for signature 'Genome_intervals_stranded'
order(..., na.last=TRUE, decreasing=FALSE)

## S4 method for signature 'Genome_intervals'
sort(x, decreasing=FALSE, ...)

## S4 method for signature 'Genome_intervals'
rank(x, na.last=TRUE, ties.method=c("average", "first", "last", "random", "max", "min"), ...)
## S4 method for signature 'Genome_intervals'
xtfrm(x)
```

**Arguments**

|                          |                                                                                                                                |
|--------------------------|--------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>           | Objects of class <a href="#">Genome_intervals</a> or <a href="#">Genome_intervals_stranded</a> .                               |
| <code>...</code>         | Objects of class <a href="#">Genome_intervals</a> , <a href="#">Genome_intervals_stranded</a> or of any other class for order. |
| <code>na.last</code>     | Ignored for ordering <a href="#">Genome_intervals</a> and <a href="#">Genome_intervals_stranded</a> objects                    |
| <code>decreasing</code>  | TRUE or FALSE.                                                                                                                 |
| <code>ties.method</code> | A character string specifying how ties are treated. Only "first" is supported.                                                 |

**Details**

An order on `Genome_intervals` entries is defined by sorting by 1. seqnames 2. start, where closed start & not inter-base < closed start & inter-base < open start & not inter-base < open start & inter-base 3. stop, where open stop & not inter-base < open stop & inter-base < closed stop & not inter-base < closed stop & inter-base 4. strand (for `Genome_intervals_stranded` object)

The factors `seqnames` and `strand` are sorted according to their levels (default R behavior).

The primitive is implemented in `xtfrm` which is then called by the other methods. Hence, the order, sort and rank methods are consistent.

`order(..., na.last=TRUE, decreasing=TRUE)`: return a permutation which rearranges its first argument into ascending or descending order, breaking ties by further arguments. See [order](#) in the base package for more details. `na.last` is ignored for [Genome\\_intervals](#) objects.

`rank(x, na.last=TRUE, ties.method=c("average", "first", "last", "random", "max", "min"), ...)`: Return the sample ranks of the (stranded) genome intervals in `x`. See [rank](#) in the base package for more details.

`sort(x)`: Sort `x`. See [sort](#) in the base package for more details.

`xtfrm(x)`: Auxiliary function that produces a numeric vector which will sort in the same order as 'x' `x`. See [xtfrm](#) in the base package for more details. Workhorse for the other methods

**See Also**

[Genome\\_intervals](#) [Genome\\_intervals\\_stranded](#) [order](#), [sort](#), [rank](#), [xtfrm](#)

## Examples

```
## an example with ties
gi = GenomeIntervals(c("chr2", "chr2", "chr1", "chr1"), c(1,1,10,10), c(5,3,12,12) )

sort(gi)
rank(gi)
order(gi)

## Define order on seqnames at your convenience
## by specifying the order of the levels
## compare:
gi = GenomeIntervals(
  c("chr2", "chr2", "chr10", "chr10"),
  c(1,1,10,10),
  c(5,3,12,12)
)
sort(gi)

## with:
gi2 = GenomeIntervals(
  factor(c("chr2", "chr2", "chr10", "chr10"), levels=c("chr2", "chr10")),
  c(1,1,10,10),
  c(5,3,12,12)
)
sort(gi2)
```

---

Genome\_intervals\_stranded-class

*Class "Genome\intervals\stranded"*

---

## Description

A set of genomic intervals with a specified strand.

## Slots

.Data: See [Genome\\_intervals](#)

annotation: A data.frame (see [Genome\\_intervals](#) for basic requirements). The annotation moreover has a strand column that is a factor with exactly two levels (typically "+" and "-").

closed: See [Genome\\_intervals](#)

type: See [Genome\\_intervals](#)

## Extends

Class "[Genome\\_intervals](#)", directly. Class "[Intervals\\_full](#)", by class "Genome\intervals", distance 2. Class "[Intervals\\_virtual](#)", by class "Genome\intervals", distance 3. Class "[matrix](#)", by class "Genome\intervals", distance 4. Class "[array](#)", by class "Genome\intervals", distance 5. Class "[structure](#)", by class "Genome\intervals", distance 6. Class "[vector](#)", by class "Genome\intervals", distance 7, with explicit coerce.

**Methods**

```

coerce signature(from = "Genome_intervals_stranded", to = "character"): ...
distance\to\nearest signature(from = "Genome_intervals_stranded", to = "Genome_intervals_stranded"): ...
...
interval\complement signature(x = "Genome_intervals_stranded"): ...
interval\intersection signature(x = "Genome_intervals_stranded"): ...
interval\overlap signature(to = "Genome_intervals_stranded", from = "Genome_intervals_stranded"): ...
...
interval\union signature(x = "Genome_intervals_stranded"): ...
strand signature(x = "Genome_intervals_stranded"): ...
strand<- signature(x = "Genome_intervals_stranded"): ...

```

**See Also**

[Genome\\_intervals](#) the parent class without strand.

**Examples**

```

# The "Genome_intervals_stranded" class
j <- new(
  "Genome_intervals_stranded",
  matrix(
    c(1,2,
      3,5,
      4,6,
      8,9
    ),
    byrow = TRUE,
    ncol = 2
  ),
  closed = matrix(
    c(
      FALSE, FALSE,
      TRUE, FALSE,
      TRUE, TRUE,
      TRUE, FALSE
    ),
    byrow = TRUE,
    ncol = 2
  ),
  annotation = data.frame(
    seq_name = factor( c("chr01", "chr01", "chr02", "chr02") ),
    strand = factor( c("+", "+", "+", "-") ),
    inter_base = c(FALSE, FALSE, FALSE, TRUE)
  )
)

## print
print(j)

## size of each interval as count of included bases
size(j)

```

```
## close intervals left and right (canonical representation)
close_intervals(j)

## simpler way to construct a Genome_intervals_stranded object
GS <- GenomeIntervals(start=c(1,3,4,5,8,10), end=c(5,5,6,8,9,11),
                      chromosome=rep(c("chr2","chrX","chr1"), each=2),
                      strand=c("-", "-", "+", "+", "+", "+") )

show(GS)
```

---

|          |                                  |
|----------|----------------------------------|
| gen_ints | <i>Genome Intervals examples</i> |
|----------|----------------------------------|

---

**Description**

Toy examples for testing functions and running examples of the package genomeIntervals.

**Usage**

```
data(gen_ints)
```

**Format**

Two Genome\_intervals\_stranded objects, i and j, without inter-base intervals and a third one, k, with.

---

|                 |                                                                    |
|-----------------|--------------------------------------------------------------------|
| getGffAttribute | <i>Pull one or more key/value pairs from gffAttributes strings</i> |
|-----------------|--------------------------------------------------------------------|

---

**Description**

GFF files contain a string, with key/value pairs separated by “;”, and the key and value separated by “=”. This function quickly extracts one or more key/value pairs.

**Usage**

```
getGffAttribute(gi, attribute)
```

**Arguments**

|           |                                            |
|-----------|--------------------------------------------|
| gi        | A <a href="#">Genome_intervals</a> object. |
| attribute | A vector of key names.                     |

**Value**

A matrix with the same number of rows as gi, and one column per element of attribute.

**See Also**

See [parseGffAttributes](#) for more complete parsing. See the function [readGff3](#) for loading a GFF file.

**Examples**

```
# Get file path
libPath <- installed.packages()["genomeIntervals", "LibPath"]
filePath <- file.path(
  libPath,
  "genomeIntervals",
  "example_files"
)

# Load gff
gff <- readGff3( file.path( filePath, "sgd_simple.gff"), isRightOpen=FALSE)

## head of full gff annotations
head(annotation(gff))

# extract ID and Parent attributes
idpa = getGffAttribute( gff, c( "ID", "Parent" ) )

head(idpa)
```

---

|                  |                                                                    |
|------------------|--------------------------------------------------------------------|
| interval_overlap | <i>Assess overlap from one set of genomic intervals to another</i> |
|------------------|--------------------------------------------------------------------|

---

**Description**

Given two objects, a 'from' and a 'to', assess which intervals in 'to' overlap which of 'from'.

**Usage**

```
## S4 method for signature 'Genome_intervals,Genome_intervals'
interval_overlap(
  from, to,
  check_valid = TRUE
)

## S4 method for signature
## 'Genome_intervals_stranded,Genome_intervals_stranded'
interval_overlap(
  from, to,
  check_valid = TRUE
)
```

**Arguments**

|              |                                                                               |
|--------------|-------------------------------------------------------------------------------|
| from         | A Genome_intervals or Genome_intervals_stranded object.                       |
| to           | A Genome_intervals or Genome_intervals_stranded object.                       |
| check\_valid | Should <a href="#">validObject</a> be called before passing to compiled code? |

## Details

A wrapper calling `intervals:interval_overlap` by `seq_name` and by `strand` (if both `to` and `from` are "Genome\_intervals\_stranded" objects).

## Value

A list, with one element for each row of `from`. The elements are vectors of indices, indicating which `to` rows overlap each `from`. A list element of length 0 indicates a `from` with no overlapping `to` intervals.

## Examples

```
data(gen_ints)
# i as entered
i

# i in close_intervals notation
close_intervals(i)

# j in close_intervals notation
close_intervals(j)

# list of intervals of j overlapping intervals of i
interval_overlap(i,j)
```

---

interval\_union

*Genome interval set operations*

---

## Description

Compute interval set operations on "Genome\_intervals" or "Genome\_intervals\_stranded" objects.

## Usage

```
## S4 method for signature 'Genome_intervals'
interval_union(x, ...)
## S4 method for signature 'Genome_intervals_stranded'
interval_union(x, ...)

## S4 method for signature 'Genome_intervals'
interval_complement(x)
## S4 method for signature 'Genome_intervals_stranded'
interval_complement(x)

## S4 method for signature 'Genome_intervals'
interval_intersection(x,...)
## S4 method for signature 'Genome_intervals_stranded'
interval_intersection(x,...)
```



**Arguments**

`x`                    A "Genome\_intervals" or "Genome\_intervals\_stranded" object.  
`...`                  Optionally, additional objects of the same class as `x`.

**Details**

Wrappers calling the corresponding functions of the package `intervals` by same `seq_name`, `inter_base` and if needed `strand`. Note that the union of single input object `x` returns the reduced form of `x`, i.e. the interval representation of the covered set.

**Value**

A single object of appropriate class, representing the union, complement or intersection of intervals computed over entries with same `seq_name`, `inter_base` and also `strand` if all passed objects are of the class "Genome\_intervals\_stranded".

**See Also**

[interval\\_union](#), [interval\\_complement](#), [interval\\_intersection](#) and [reduce](#) from the package `intervals`.

**Examples**

```
## load toy examples
data(gen_ints)
## content of i object
i

## complement
interval_complement(i)

## reduced form (non-overlapping interval representation of the covered set)
interval_union(i)

## union
interval_union(i[1:2,], i[1:4,])

# map to genome intervals and union again
i.nostrand = as(i, "Genome_intervals")
interval_union(i.nostrand)

## intersection with a second object
# print i and j in closed interval notation
close_intervals(i)
close_intervals(j)

# interval_intersection
interval_intersection(i, j)

# interval intersection non-stranded
interval_intersection(i.nostrand, as(j, "Genome_intervals"))
```

---

|                    |                                                                        |
|--------------------|------------------------------------------------------------------------|
| parseGffAttributes | <i>Parse out the gffAttributes column of a Genome_intervals object</i> |
|--------------------|------------------------------------------------------------------------|

---

## Description

GFF files contain a string, with key/value pairs separated by “;”, and the key and value separated by “=”. This function parses such strings into a list of vectors with named elements.

## Usage

```
parseGffAttributes(gi)
```

## Arguments

gi                    A [Genome\\_intervals](#) object.

## Value

A list, with one element per row of gi. Each element is a character vector with named components. Names correspond to keys, and components correspond to values.

## Note

Key/value pairs which are missing the “=” symbol, or which have nothing between it and the “;” delimiter or end of line, will generate a NA value, with a warning. Any key/value “pairs” with more than one “=” cause an error.

## See Also

In many cases, [getGffAttribute](#), in this package, is easier and faster. See the function [readGff3](#) for loading a GFF file.

## Examples

```
# Get file path
libPath <- installed.packages()[“genomeIntervals”, “LibPath”]
filePath <- file.path(
  libPath,
  “genomeIntervals”,
  “example_files”
)

# Load gff and parse attributes
gff <- readGff3( file.path( filePath, “sgd_simple.gff”), isRightOpen = FALSE )
gfatt <- parseGffAttributes(gff)

head( gfatt )
```

---

```
readGff3,character-method
      readGff3
```

---

## Description

Read (write) a `Genome_intervals_stranded` object from (to) a GFF3 file

## Usage

```
readGff3(file, isRightOpen=FALSE, quiet=FALSE)
readBasePairFeaturesGff3(file, quiet=FALSE)
readZeroLengthFeaturesGff3(file, quiet=FALSE)
writeGff3(object, file)
```

## Arguments

|                          |                                                                                                                                                                                                                                                                                                                                                          |
|--------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>file</code>        | The name of the gff file to read/write.                                                                                                                                                                                                                                                                                                                  |
| <code>isRightOpen</code> | Although it is arguable that a GFF3 file might have a right-open intervals convention - the format description being at best imprecise - most GFF3 file follow a right-closed convention. Hence, as of version 1.25.1, the default has been changed to <code>isRightOpen = FALSE</code> . See the details section on how to restore the older behaviour. |
| <code>quiet</code>       | a boolean to turn verbosity off when reading a Gff3 file                                                                                                                                                                                                                                                                                                 |
| <code>object</code>      | a <code>Genome_intervals</code> object                                                                                                                                                                                                                                                                                                                   |

## Details

- `readGff3` Make a `Genome_intervals_stranded` object from a gff file in gff3 format.
- `readBasePairFeaturesGff3` Same as `readGff3` assuming `isRightOpen='FALSE'`, i.e. no zero length intervals are created. This is the default behaviour since v1.25.1.
- `readZeroLengthFeaturesGff3` Same as `readGff3` assuming `isRightOpen='TRUE'`, i.e. zero length intervals are created when a feature's start is the same as its end. This was the default prior to version 1.25.1.
- `writeGff3` Write a `Genome_intervals` object to a gff file in gff3 format.

The file must follow gff3 format specifications as in <http://www.sequenceontology.org/gff3.shtml>. Due to the imprecise definition and to allow for zero-length features, the default for reading a Gff3 file has been to assume right open intervals (until v1.25.1). As by then, the community consensus has been to use closed intervals, the default behaviour of `readGff3` has been changed accordingly. The `readGff3` file is now a wrapper that dispatches to two sub functions - which may be used directly - `readBasePairFeaturesGff3` and `readZeroLengthFeaturesGff3`. The former assumes closed intervals and hence does not create zero-length intervals. The latter does the opposite and uses right-open intervals!

Some more noteworthy details:

The file is read as a table and meta-information (lines starting with `###`) are not parsed.

A “.” in, for example, the gff file's *score* or *frame* field will be converted to NA.

When the GFF file follows the right-open interval convention (`isRightOpen` is `TRUE`), then GFF entries for which end base equals first base are recognized as zero-length features and loaded as `inter_base` intervals.

Strand entries in the file are expected to be '.', '?', '+' or '-'. The two first are mapped to NA.

It can be that `readGff3` is able to construct a [Genome\\_intervals\\_stranded](#) object from the input file, although not valid. A warning message is then generated and the constructed object is returned to allow inspection of it.

Potential FASTA entries at the end of the file are ignored.

### Value

- `readGff3` and friendsA [Genome\\_intervals\\_stranded](#) object image of the gff file. The GFF3 fields `seqid`, `source`, `type`, `score`, `strand`, `phase` and `attributes` are stored in the annotation slot and renamed as `seq_name`, `source`, `type`, `score`, `strand`, `phase` and `gffAttributes` respectively.
- `writeGff3`It dispatches to `write.table` and hence returns similar values.

### See Also

The functions [getGffAttribute](#) and [parseGffAttributes](#) for parsing GFF attributes.

### Examples

```
# Get file path
libPath <- installed.packages()[ "genomeIntervals", "LibPath" ]
filePath <- file.path(
  libPath,
  "genomeIntervals",
  "example_files"
)

# Load SGD gff
# SGD does not comply to the GFF3 right-open interval convention
gff <- readGff3( file.path( filePath, "sgd_simple.gff"), isRightOpen = FALSE)

head(gff,10)

head(annotation(gff),10)

## Not run:
## write the gff3 file
writeGff3(gff,file="sgd_simple.gff")

## End(Not run)
```

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