Package 'genomeIntervals'

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Imports

Suggests

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'.

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biocViews DataImport, Infrastructure, Genetics

LazyLoad yes

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`genomeIntervals-package`

Operations on genomic intervals

Description

Tools for operation on genomic intervals.

Details

Package:	genomeIntervals
Version:	1.20.1
Date:	2014-06-21
Type:	Package
Depends:	R (>= 2.15.0), intervals (>= 0.13.3), BiocGenerics, methods
Suggests:	
License:	Artistic 2.0
BiocViews:	DataImport, Infrastructure, Genetics
LazyLoad:	yes

Index:

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interval_overlap Assess overlap from one set of genomic intervals to another

interval_complement Compute the complement of a set of genomic intervals

interval_intersection Compute the intersection of one or more sets of genomic intervals

interval_union Compute the union of genomic intervals in one or more genomic interval matrices

parseGffAttributes Parse out the gffAttributes column of a Genome_intervals object

readGff3 Make a Genome_intervals_stranded object from a GFF file

Author(s)

Julien Gagneur <gagneur@embl.de>, Richard Bourgon, Joern Toedling, Nicolas Delhomme.

Maintainer: Julien Gagneur <gagneur@embl.de>

See Also

intervals

---

c *Combine genome intervals objects*

Description

S3 methods for combining several genome intervals into a single one.

Usage

```
## S3 method for class Genome_intervals
c(...)
## S3 method for class Genome_intervals_stranded
c(...)
```

Arguments

...	Genome_intervals or Genome_intervals_stranded objects.

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.

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.

Note

These methods will be converted to S4 once the necessary dispatch on ... is supported.

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 `seq_name` 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 one i

## 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

`chromosome`	character vector of chromosome names of the intervals; will become the `seq_names` of the resulting object
`start`	numeric or integer; start (left-most) coordinate of the intervals
`end`	numeric or integer; end (right-most) coordinate of the intervals
`strand`	chacter; specifies which strand the intervals are located on; if specified an object of class `Genome_intervals_stranded` is created; if `NULL` an object of class `Genome_intervals` is created

inter.base	logical; if TRUE an interval is located between the specified coordinates, instead of spanning them; useful for restriction-enzym cutting sites, for example.
leftOpen	logical; if TRUE an interval is left-open; if NULL all intervals are assumed to be left-closed.
rightOpen	logical; if TRUE an interval is right-open; if NULL all intervals are assumed to be right-closed.
...	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)
```

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: `seq_name` (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")`: ...

seq_name `signature(x = "Genome_intervals")`: ...

seq_name<- `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 chromsomes 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.

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", "random", "max", "min") )
## S4 method for signature Genome_intervals
xtfrm(x)
```

Arguments

x	Objects of class Genome_intervals or Genome_intervals_stranded.
...	Objects of class Genome_intervals, Genome_intervals_stranded or of any other class for order.
na.last	Ignored for ordering Genome_intervals and Genome_intervals_stranded objects
decreasing	TRUE or FALSE.
ties.method	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. seq_name 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 seq_name 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", "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 seq_names 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 *Genome Intervals examples*

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 *Pull one or more key/value pairs from gffAttributes strings*

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 Genome_intervals 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` *Assess overlap from one set of genomic intervals to another*

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 validObject 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` *Parse out the gffAttributes column of a Genome_intervals object*

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

Description

- readGff3 Make a `Genome_intervals_stranded` object from a gff file in gff3 format.
- writeGff3 Write a `Genome_intervals` object to a gff file in gff3 format.

Usage

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

Arguments

`file`	The name of the gff file to read/write.
`isRightOpen`	Although a proper GFF3 file follows the convention of right-open intervals, improper GFF files following the right-closed convention are frequently found. Set `isRightOpen = FALSE` in this case.
`object`	a `Genome_intervals` object
`quiet`	a boolean to turn verbosity off when reading a Gff3 file

Details

The file must follow gff3 format specifications as in `http://www.sequenceontology.org/gff3.shtml`. The file is read as a table. 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.

Value

A 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.

Note

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

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)

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

## End(Not run)
```

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