

# Package ‘GenomicTuples’

April 16, 2019

**Type** Package

**Title** Representation and Manipulation of Genomic Tuples

**Version** 1.16.0

**Date** 2018-07-18

**Encoding** UTF-8

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**Description** GenomicTuples defines general purpose containers for storing genomic tuples. It aims to provide functionality for tuples of genomic co-ordinates that are analogous to those available for genomic ranges in the GenomicRanges Bioconductor package.

**URL** [www.github.com/PeteHaitch/GenomicTuples](http://www.github.com/PeteHaitch/GenomicTuples)

**BugReports** <https://github.com/PeteHaitch/GenomicTuples/issues>

**biocViews** Infrastructure, DataRepresentation, Sequencing

**VignetteBuilder** knitr

**Depends** R (>= 3.3.0), GenomicRanges (>= 1.31.8), GenomeInfoDb (>= 1.15.2), S4Vectors (>= 0.17.25)

**Imports** methods, BiocGenerics (>= 0.21.2), Rcpp (>= 0.11.2), IRanges (>= 2.13.13), data.table, stats4

**Suggests** testthat, knitr, BiocStyle, rmarkdown

**LinkingTo** Rcpp

**License** Artistic-2.0

**Collate** 'AllGenerics.R' 'AllUtilities.R' 'GTuples-class.R'  
'GTuples-comparison.R' 'GTuplesList-class.R' 'GenomicTuples.R'  
'RcppExports.R' 'coverage-methods.R' 'findOverlaps-methods.R'  
'inter-tuple-methods.R' 'intra-tuple-methods.R'  
'nearest-methods.R' 'setops-methods.R' 'tile-methods.R' 'zzz.R'

**RoxygenNote** 6.0.1

**git\_url** <https://git.bioconductor.org/packages/GenomicTuples>

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** 3a2cd2b

**git\_last\_commit\_date** 2018-10-30

**Date/Publication** 2019-04-15

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GenomicTuples-package *Representation and manipulation of genomic tuples.*

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### Description

**GenomicTuples** defines general purpose containers for storing genomic tuples. It aims to provide functionality for tuples of genomic co-ordinates that are analogous to those available for genomic ranges in the GenomicRanges Bioconductor package.

### Details

Please refer to the vignettes to see how to use the **GenomicTuples** package.

### References

Peter F Hickey (2016). Representation and Manipulation of Genomic Tuples in R. *JOSS*. URL <http://dx.doi.org/10.21105/joss.00020>

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findOverlaps-methods *Finding overlapping genomic tuples*

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### Description

Various methods for finding/counting overlaps between objects containing genomic tuples. This man page describes the methods that operate on **GTuples** and **GTuplesList** objects.

NOTE: The **findOverlaps** generic function is defined and documented in the **IRanges** package. The **findOverlaps** method for **GenomicRanges** and **GRangesList** objects are defined and documented in the **GenomicRanges** package.

**GTuples** and **GTuplesList** objects also support **countOverlaps**, **overlapsAny**, and **subsetByOverlaps** thanks to the default methods defined in the **IRanges** package and to the **findOverlaps** and **countOverlaps** methods defined in this package and documented below.

**Usage**

```
## S4 method for signature 'GTuples,GTuples'
findOverlaps(query, subject,
             maxgap = -1L, minoverlap = 0L,
             type = c("any", "start", "end", "within", "equal"),
             select = c("all", "first", "last", "arbitrary"),
             ignore.strand = FALSE)

## S4 method for signature 'GTuples,GTuples'
countOverlaps(query, subject,
              maxgap = -1L, minoverlap = 0L,
              type = c("any", "start", "end", "within", "equal"),
              ignore.strand = FALSE)
```

**Arguments**

`query`, `subject` A [GTuples](#) or [GTuplesList](#) object.

`type` See details below.

`maxgap`, `minoverlap` See [?findOverlaps](#) in the **IRanges** package for a description of these arguments.

`select` When `select` is "all" (the default), the results are returned as a [Hits](#) object. Otherwise the returned value is an integer vector parallel to `query` (i.e. same length) containing the first, last, or arbitrary overlapping interval in `subject`, with NA indicating intervals that did not overlap any intervals in `subject`.

`ignore.strand` When set to TRUE, the strand information is ignored in the overlap calculations.

**Details**

The `findOverlaps`-based methods involving genomic tuples, either through [GTuples](#) or [GTuplesList](#) objects, can search for *tuple-tuple*, *tuple-range* and *range-tuple* overlaps. Each of these are described below, with attention paid to the important special case of finding "equal tuple-tuple overlaps".

**Equal tuple-tuple overlaps** When the query and the subject are both [GTuples](#) objects and `type = "equal"`, `findOverlaps` uses the `seqnames` ([seqnames](#)), positions ([tuples](#), [GTuples-method](#)) and strand (`strand`) to determine which tuples from the query exactly match those in the subject, where a strand value of "\*" is treated as occurring on both the "+" and "-" strand. An overlap is recorded when a tuple in the query and a tuple in the subject have the same sequence name, have a compatible pairing of strands (e.g. "+"/"+"", "-"/"-", "\*"/"+", "\*"/"-", etc.), and have identical positions.

**NOTE:** Equal tuple-tuple overlaps can only be computed if `size(query)` is equal to `size(subject)`.

**Other tuple-tuple overlaps** When the query and the subject are [GTuples](#) or [GTuplesList](#) objects and `type = "any"`, "start", "end" or "within", `findOverlaps` treats the tuples as if they were ranges, with ranges given by  $[pos_1, pos_m]$  and where  $m$  is the `size`, [GTuples-method](#) of the tuples. This is done via inheritance so that a [GTuples](#) (resp. [GTuplesList](#)) object is treated as a [GRanges](#) (resp. [GRangesList](#)) and the appropriate `findOverlaps` method is dispatched upon.

**NOTE:** This is the only type of overlap finding available when either the query and subject are [GTuplesList](#) objects. This is following the behaviour of [findOverlaps](#), [GRangesList](#), [GRangesList-method](#) that allows `type = "any"`, "start", "end" or "within" but does not allow `type = "equal"`.

**tuple-range and range-tuple overlaps** When one of the query and the subject is not a [GTuples](#) or [GTuplesList](#) objects, `findOverlaps` treats the tuples as if they were ranges, with ranges given by  $[pos_1, pos_m]$  and where  $m$  is the [size, GTuples-method](#) of the tuples. This is done via inheritance so that a [GTuples](#) (resp. [GTuplesList](#)) object is treated as a [GRanges](#) (resp. [GRangesList](#)) and the appropriate `findOverlaps` method is dispatched upon.

In the context of `findOverlaps`, a feature is a collection of tuples/ranges that are treated as a single entity. For [GTuples](#) objects, a feature is a single tuple; while for [GTuplesList](#) objects, a feature is a list element containing a set of tuples. In the results, the features are referred to by number, which run from 1 to `length(query)/length(subject)`.

### Value

For `findOverlaps`, either a [Hits](#) object when `select = "all"` or an integer vector otherwise.

For `countOverlaps`, an integer vector containing the tabulated query overlap hits.

For `overlapsAny` a logical vector of length equal to the number of tuples/ranges in query indicating those that overlap any of the tuples/ranges in subject.

For `subsetByOverlaps` an object of the same class as query containing the subset that overlapped at least one entity in subject.

### Author(s)

Peter Hickey for methods involving [GTuples](#) and [GTuplesList](#). P. Aboyoun, S. Falcon, M. Lawrence, N. Gopalakrishnan, H. Pagès and H. Corrada Bravo for all the real work underlying the powerful `findOverlaps` functionality.

### See Also

- Please see the package vignette for an extended discussion of overlaps involving genomic tuples, which is available by typing `vignette(topic = 'GenomicTuplesIntroduction', package = 'GenomicTuples')` at the R prompt.
- [findOverlaps](#)
- [findOverlaps](#)
- [Hits-class](#)
- [GTuples-class](#)
- [GTuplesList-class](#)
- [GRanges-class](#)
- [GRangesList-class](#)

### Examples

```
## GTuples object containing 3-tuples:
gt3 <- GTuples(seqnames = c('chr1', 'chr1', 'chr1', 'chr1', 'chr2'),
              tuples = matrix(c(10L, 10L, 10L, 10L, 10L, 20L, 20L, 20L, 25L,
                               20L, 30L, 30L, 35L, 30L, 30L), ncol = 3),
              strand = c('+', '-', '*', '+', '+'))

## GTuplesList object
gtl3 <- GTuplesList(A = gt3[1:3], B = gt3[4:5])

## Find equal genomic tuples:
```

```

findOverlaps(gt3, gt3, type = 'equal')
## Note that this is different to the results if the tuples are treated as
## ranges since this ignores the "internal positions" (pos2):
findOverlaps(granges(gt3), granges(gt3), type = 'equal')

## Scenarios where tuples are treated as ranges:
findOverlaps(gt3, gt3, type = 'any')
findOverlaps(gt3, gt3, type = 'start')
findOverlaps(gt3, gt3, type = 'end')
findOverlaps(gt3, gt3, type = 'within')

## Overlapping a GTuples and a GTuplesList object (tuples treated as ranges):
table(!is.na(findOverlaps(gt13, gt3, select="first")))
countOverlaps(gt13, gt3)
findOverlaps(gt13, gt3)
subsetByOverlaps(gt13, gt3)
countOverlaps(gt13, gt3, type = "start")
findOverlaps(gt13, gt3, type = "start")
subsetByOverlaps(gt13, gt3, type = "start")
findOverlaps(gt13, gt3, select = "first")

```

---

GTuples-class

*GTuples objects*


---

## Description

The GTuples class is a container for the genomic tuples and their associated annotations.

## Details

GTuples extends [GRanges](#) as a container for genomic tuples rather than genomic ranges. GTuples is a vector of genomic locations and associated annotations. Each element in the vector is comprised of a sequence name, a tuple, a [strand](#), and optional metadata columns (e.g. score, GC content, etc.). This information is stored in four components:

`seqnames` a 'factor' [Rle](#) object containing the sequence names.

`tuples` externally, a matrix-link object containing the tuples. Internally, an [IRanges](#) object storing the first and last position of each tuple and, if required, a matrix storing the "internal" positions of each tuple (see description of `internalPos` below).

`strand` a [Rle](#) [Rle](#) object containing the strand information.

`mcols` a [DataFrame](#) object containing the metadata columns. Columns cannot be named "seqnames", "ranges", "tuples", "internalPos", "size", "strand", "seqlevels", "seqlengths", "isCircular", "start", "end", "width", or "element".

`seqinfo` a [DataFrame](#) object containing information about the set of genomic sequences present in the GTuples object.

## Slots

Since the GTuples class extends the [GRanges](#) class it contains the `seqnames`, `ranges`, `strand`, `elementMetadata`, `seqinfo` and `metadata`. The GTuples class also contains two additional slots, `size` and `internalPos`.

`size` An integer. The size of the genomic tuples stored in the `GTuples` object.

`internalPos` If the size of the genomic tuples is greater than 2, `internalPos` is an integer matrix storing the "internal" positions of each genomic tuple. Otherwise `internalPos` is `NULL`.

### Constructor

`GTuples(seqnames = Rle(), tuples = matrix(), strand = Rle("*", length(seqnames)), ..., seqlengths)`  
Creates a `GTuples` object.

`seqnames` `Rle` object, character vector, or factor containing the sequence names.

`tuples` matrix object containing the positions of the tuples. The first column should refer to `pos1`, the second to `pos2`, etc.

`strand` `Rle` object, character vector, or factor containing the strand information.

`...` Optional metadata columns. These columns cannot be named "start", "end", "width", or "element". A named integer vector "seqlength" can be used instead of `seqinfo`.

`seqlengths` an integer vector named with the sequence names and containing the lengths (or `NA`) for each `level(seqnames)`.

`seqinfo` a `DataFrame` object containing allowed sequence names and lengths (or `NA`) for each `level(seqnames)`.

### Coercion

In the code snippets below, `x` is a `GTuples` object.

`as.data.frame(x, row.names = NULL, optional = FALSE, ...)`: Creates a `data.frame` with columns `seqnames` (factor), `tuples` (integer), `strand` (factor), as well as the additional metadata columns stored in `mcols(x)`. Pass an explicit `stringsAsFactors=TRUE/FALSE` argument via `...` to override the default conversions for the metadata columns in `mcols(x)`.

`as.character(x, ignore.strand=FALSE)`: Turn `GTuples` object `x` into a character vector where each tuples in `x` is represented by a string in format `chr1:100,109,115:+`. If `ignore.strand` is `TRUE` or if *all* the ranges in `x` are unstranded (i.e. their strand is set to `*`), then all the strings in the output are in format `chr1:100,109,115`.

The names on `x` are propagated to the returned character vector. Its metadata (`metadata(x)`) and metadata columns (`mcols(x)`) are ignored.

`as.factor(x)`: Equivalent to

```
factor(as.character(x), levels=as.character(sort(unique(x))))
```

`as(x, "GRanges"), granges(x)`: Creates a `GRanges` object from a `GTuples` object. **WARNING:** This is generally a *destructive* operation because all "internal" positions will be dropped.

### Accessors

In the following code snippets, `x` is a `GTuples` object.

`size(x)`: Get the size of the genomic tuples stored in `x`.

`length(x)`: Get the number of elements.

`seqnames(x), seqnames(x) <- value`: Get or set the sequence names. `value` can be an `Rle` object, a character vector, or a factor.

`tuples(x), tuples(x) <- value`: Get the positions of the tuples, which are returned as an integer matrix. `value` can be an integer matrix.

`ranges(x, use.mcols = FALSE)`, `ranges(x) <- value`: Get or set the ranges in the form of a `CompressedIRangesList`. `value` can be a `IntegerRangesList` object.

**WARNING:** The use of `ranges` with `GTuples` objects is **strongly** discouraged. It will only get/set  $pos_1$  and  $pos_m$  of the tuples, where  $m$  is the size of the tuples, as these are what are stored in the "ranges" slot of a `GTuples` object.

`names(x)`, `names(x) <- value`: Get or set the names of the elements.

`strand(x)`, `strand(x) <- value`: Get or set the strand. `value` can be an `Rle` object, character vector, or factor.

`mcols(x, use.names=FALSE)`, `mcols(x) <- value`: Get or set the metadata columns. If `use.names=TRUE` and the metadata columns are not `NULL`, then the names of `x` are propagated as the row names of the returned `DataFrame` object. When setting the metadata columns, the supplied value must be `NULL` or a data.frame-like object (i.e. `DataTable` or `data.frame`) object holding element-wise metadata.

`elementMetadata(x)`, `elementMetadata(x) <- value`, `values(x)`, `values(x) <- value`: Alternatives to `mcols` functions. Their use is discouraged.

`seqinfo(x)`, `seqinfo(x) <- value`: Get or set the information about the underlying sequences. `value` must be a `DataFrame` object.

`seqlevels(x)`, `seqlevels(x, force=FALSE) <- value`: Get or set the sequence levels. `seqlevels(x)` is equivalent to `seqlevels(seqinfo(x))` or to `levels(seqnames(x))`, those 2 expressions being guaranteed to return identical character vectors on a `GTuples` object. `value` must be a character vector with no NAs. See `?seqlevels` for more information.

`seqlengths(x)`, `seqlengths(x) <- value`: Get or set the sequence lengths. `seqlengths(x)` is equivalent to `seqlengths(seqinfo(x))`. `value` can be a named non-negative integer or numeric vector eventually with NAs.

`isCircular(x)`, `isCircular(x) <- value`: Get or set the circularity flags. `isCircular(x)` is equivalent to `isCircular(seqinfo(x))`. `value` must be a named logical vector eventually with NAs.

`genome(x)`, `genome(x) <- value`: Get or set the genome identifier or assembly name for each sequence. `genome(x)` is equivalent to `genome(seqinfo(x))`. `value` must be a named character vector eventually with NAs.

`seqlevelsStyle(x)`, `seqlevelsStyle(x) <- value`: Get or set the seqname style for `x`. See the `seqlevelsStyle` generic getter and setter in the **GenomeInfoDb** package for more information.

`score(x)`, `score(x) <- value`: Get or set the "score" column from the element metadata.

## Tuples methods

In the following code snippets, `x` is a `GTuples` object. **WARNING:** The preferred setter is `tuples(x) <- value` and the use of `start(x) <- value`, `end(x) <- value` and `width(x) <- value` is discouraged.

`start(x)`, `start(x) <- value`: Get or set  $pos_1$  of the tuples. **WARNING:** The use of `width(x) <- value` is discouraged; instead, construct the tuples as the appropriate integer matrix, `mvalue`, and use `tuples(x) <- mvalue`.

`end(x)`, `end(x) <- value`: Get or set  $pos_m$  of the tuples, where  $m$  is the size of the tuples. **WARNING:** The use of `end(x) <- value` is discouraged; instead, construct the tuples as the appropriate integer matrix, `mvalue`, and use `tuples(x) <- mvalue`.

`IPD(x)`: Get the intra-pair distances (IPD). IPD is only defined for tuples with size  $> 1$ . The IPD of a tuple with size =  $m$  is the vector of intra-pair distances,  $(pos_2 - pos_1, \dots, pos_m - pos_{m-1})$ .

`width(x), width(x) <- value`: Get or set  $pos_m - pos_1$  of the tuples, where  $m$  is the size of the tuples. If using `width(x) <- value`,  $pos_1$  is held fixed and  $pos_m$  is altered. **WARNING**: The use of `width(x) <- value` is discouraged; instead, construct the tuples as the appropriate integer matrix, `mvalue`, and use `tuples(x) <- mvalue`.

### Splitting and Combining

In the following code snippets, `x` is a GTuples object.

`append(x, values, after = length(x))`: Inserts the values into `x` at the position given by `after`, where `x` and `values` are of the same class.

`c(x, ...)`: Combines `x` and the GTuples objects in `...` together. Any object in `...` must belong to the same class as `x`, or to one of its subclasses, or must be NULL. The result is an object of the same class as `x`.

`c(x, ..., ignore.mcols=FALSE)` If the GTuples objects have metadata columns (represented as one `DataFrame` per object), each such `DataFrame` must have the same columns in order to combine successfully. In order to circumvent this restraint, you can pass in an `ignore.mcols=TRUE` argument which will combine all the objects into one and drop all of their metadata columns.

`split(x, f, drop=FALSE)`: Splits `x` according to `f` to create a GTuplesList object. If `f` is a list-like object then `drop` is ignored and `f` is treated as if it was `rep(seq_len(length(f)), sapply(f, length))`, so the returned object has the same shape as `f` (it also receives the names of `f`). Otherwise, if `f` is not a list-like object, empty list elements are removed from the returned object if `drop` is TRUE.

### Subsetting

In the following code snippets, `x` is a GTuples object.

`x[i, j], x[i, j] <- value`: Get or set elements `i` with optional metadata columns `mcols(x)[, j]`, where `i` can be missing; an NA-free logical, numeric, or character vector; or a 'logical' Rle object.

`x[i, j] <- value`: Replaces elements `i` and optional metadata columns `j` with `value`.

`head(x, n = 6L)`: If `n` is non-negative, returns the first `n` elements of the GTuples object. If `n` is negative, returns all but the last `abs(n)` elements of the GTuples object.

`rep(x, times, length.out, each)`: Repeats the values in `x` through one of the following conventions:

`times` Vector giving the number of times to repeat each element if of length `length(x)`, or to repeat the whole vector if of length 1.

`length.out` Non-negative integer. The desired length of the output vector.

`each` Non-negative integer. Each element of `x` is repeated `each` times.

`subset(x, subset)`: Returns a new object of the same class as `x` made of the subset using logical vector `subset`, where missing values are taken as FALSE.

`tail(x, n = 6L)`: If `n` is non-negative, returns the last `n` elements of the GTuples object. If `n` is negative, returns all but the first `abs(n)` elements of the GTuples object.

`window(x, start = NA, end = NA, width = NA, frequency = NULL, delta = NULL, ...)`: Extracts the subsequence window from the GTuples object using:

`start, end, width` The start, end, or width of the window. Two of the three are required.

`frequency, delta` Optional arguments that specify the sampling frequency and increment within the window.



In general, this is more efficient than using "[" operator.

`window(x, start = NA, end = NA, width = NA, keepLength = TRUE) <- value`: Replaces the subsequence window specified on the left (i.e. the subsequence in `x` specified by `start`, `end` and `width`) by `value`. `value` must either be of class `class(x)`, belong to a subclass of `class(x)`, be coercible to `class(x)`, or be `NULL`. If `keepLength` is `TRUE`, the elements of `value` are repeated to create a `GTuples` object with the same number of elements as the width of the subsequence window it is replacing. If `keepLength` is `FALSE`, this replacement method can modify the length of `x`, depending on how the length of the left subsequence window compares to the length of `value`.

`x$name, x$name <- value`: Shortcuts for `mcols(x)$name` and `mcols(x)$name <- value`, respectively. Provided as a convenience, from `GRanges` as the result of strong popular demand. Note that those methods are not consistent with the other `$` and `$<-` methods in the `IRanges/ GenomicRanges` infrastructure, and might confuse some users by making them believe that a `GRanges` object can be manipulated as a data.frame-like object. Therefore we recommend using them only interactively, and we discourage their use in scripts or packages. For the latter, use `mcols(x)$name` and `mcols(x)$name <- value`, instead of `x$name` and `x$name <- value`, respectively.

### Other methods

`item show(x)`: By default the `show` method displays 5 head and 5 tail elements. This can be changed by setting the global options `showHeadLines` and `showTailLines`. If the object length is less than (or equal to) the sum of these 2 options plus 1, then the full object is displayed. Note that these options also affect the display of `GRanges`, `GAlignments` and `GAlignmentPairs` objects (defined in the `GenomicAlignments` package), as well as other objects defined in the `IRanges` and `Biostrings` packages (e.g. `IRanges` and `DNASTringSet` objects).

### Author(s)

Peter Hickey

### See Also

[GTuplesList-class](#), [seqinfo](#), [Vector-class](#), [Rle-class](#), [DataFrame](#), [GRanges-class](#), [intra-tuple-methods](#), [findOverlaps-methods](#), [nearest-methods](#),

### Examples

```
## Create example 4-tuples
seqinfo <- Seqinfo(paste0("chr", 1:3), c(1000, 2000, 1500), NA, "mock1")
gt4 <- GTuples(seqnames = Rle(c("chr1", "chr2", "chr1", "chr3"),
                             c(1, 3, 2, 4)),
              tuples = matrix(c(1:10, 2:11, 3:12, 4:13), ncol = 4),
              strand = Rle(strand(c("-", "+", "x", "+", "-")),
                           c(1, 2, 2, 3, 2)),
              score = 1:10, GC = seq(1, 0, length = 10), seqinfo = seqinfo)

gt4

## Summarizing elements
table(seqnames(gt4))
sum(width(gt4))
summary(mcols(gt4)[, "score"])
```

```

## Renaming the underlying sequences
seqlevels(gt4)
seqlevels(gt4) <- sub("chr", "Chrom", seqlevels(gt4))
gt4
seqlevels(gt4) <- sub("Chrom", "chr", seqlevels(gt4)) # revert

## Combining objects
gt4_a <- GTuples(seqnames = Rle(c("chr1", "chr2", "chr1", "chr3"),
                               c(1, 3, 2, 4)),
                tuples = matrix(c(1:10, 21:30, 31:40, 41:50), ncol = 4),
                strand = Rle(strand(c("-", "+", "x", "+", "-")),
                             c(1, 2, 2, 3, 2)),
                score = 1:10, seqinfo = seqinfo)

gt4_b <- GTuples(seqnames = Rle(c("chr1", "chr2", "chr1", "chr3"),
                               c(1, 3, 2, 4)),
                tuples = matrix(c(101:110, 121:130, 131:140, 141:150),
                               ncol = 4),
                strand = Rle(strand(c("-", "+", "x", "+", "-")),
                             c(1, 2, 2, 3, 2)),
                score = 1:10, seqinfo = seqinfo)

some_gt4 <- c(gt4_a, gt4_b)

## all_gt4 <- c(gt4, gt4_a, gt4_b) ## (This would fail)
all_gt4 <- c(gt4, gt4_a, gt4_b, ignore.mcols=TRUE)

## The number of lines displayed in the 'show' method
## are controlled with two global options.
options("showHeadLines" = 7)
options("showTailLines" = 2)
all_gt4

## Revert to default values
options("showHeadLines"=NULL)
options("showTailLines"=NULL)

## Get the size of the tuples stored in the GTuples object
size(gt4)

## Get the tuples
tuples(gt4)

## Get the matrix of intra-pair distances (IPD)
IPD(all_gt4)

## Can't combine genomic tuples of different sizes
gt1 <- GTuples('chr1', matrix(30:40))
gt1
## Not run:
## Returns error
c(gt4, gt1)

## End(Not run)

```

---

 GTuples-comparison      *Comparing and ordering genomic tuples*


---

## Description

Methods for comparing and ordering the elements in one or more [GTuples](#) objects.

## Usage

```
## duplicated()
## -----

## S4 method for signature 'GTuples'
duplicated(x, incomparables = FALSE, fromLast = FALSE)

## match() and selfmatch()
## -----

## S4 method for signature 'GTuples,GTuples'
match(x, table, nomatch = NA_integer_,
      incomparables = NULL, ignore.strand = FALSE)
## S4 method for signature 'GTuples'
selfmatch(x, ignore.strand = FALSE, ...)

## order() and related methods
## -----

## S4 method for signature 'GTuples'
order(..., na.last = TRUE, decreasing = FALSE, method = c("auto", "shell", "radix"))

## S4 method for signature 'GTuples'
sort(x, decreasing = FALSE, ignore.strand = FALSE, by)

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

## S4 method for signature 'GTuples'
is.unsorted(x, na.rm=FALSE, strictly=FALSE, ignore.strand = FALSE)

## Generalized element-wise (aka "parallel") comparison of 2 GTuples
## objects
## -----

## S4 method for signature 'GTuples,GTuples'
pcompare(x, y)
```

## Arguments

`x`, `table`, `y`      [GTuples](#) objects.  
`incomparables`      Not supported.

fromLast, method, nomatch	See ?`GenomicRanges-comparison` in the <b>GenomicRanges</b> package for a description of these arguments.
ignore.strand	Whether or not the strand should be ignored when comparing 2 genomic tuples.
...	One or more <b>GTuples</b> objects. The <b>GTuples</b> objects after the first one are used to break ties
na.last	Ignored.
decreasing	TRUE or FALSE.
ties.method	A character string specifying how ties are treated. Only "first" is supported for now.
by	An optional formula that is resolved against <code>as.env(x)</code> ; the resulting variables are passed to <code>order</code> to generate the ordering permutation.
na.rm	logical. Should missing values be removed before checking? <b>WARNING:</b> This currently has no effect and is ignored.
strictly	logical indicating if the check should be for <i>strictly</i> increasing values.

## Details

Two elements of a **GTuples** object (i.e. two genomic tuples) are considered equal if and only if they are on the same underlying sequence and strand, and have the same positions (**tuples**). `duplicated()` and `unique()` on a **GTuples** object are conforming to this.

The "natural order" for the elements of a **GTuples** object is to order them (a) first by sequence level, (b) then by strand, (c) then by  $pos_1, \dots, pos_m$ . This way, the space of genomic tuples is totally ordered.

`order()`, `sort()`, `is.unsorted()`, and `rank()` on a **GTuples** object are using this "natural order".

Also `==`, `!=`, `<=`, `>=`, `<` and `>` on **GTuples** objects are using this "natural order".

`pcompare(x, y)`: Performs "generalized range-wise comparison" of `x` and `y`, that is, returns an integer vector where the *i*-th element is a code describing how the *i*-th element in `x` is qualitatively positioned relatively to the *i*-th element in `y`.

A code that is `< 0`, `= 0`, or `> 0`, corresponds to `x[i] < y[i]`, `x[i] == y[i]`, or `x[i] > y[i]`, respectively.

**WARNING:** These predefined codes are not as detailed as those for **IPosRanges-comparison**. Specifically, only the sign of the code matters, not the actual value.

`match(x, table, nomatch = NA_integer_)`: Returns an integer vector of the length of `x`, containing the index of the first matching range in `table` (or `nomatch` if there is no matching range) for each tuple in `x`.

`duplicated(x, fromLast = FALSE, method = c("hash", "base"))`: Determines which elements of `x` are equal to elements with smaller subscripts, and returns a logical vector indicating which elements are duplicates. See `duplicated` in the **base** package for more details.

`unique(x, fromLast = FALSE, method = c("hash", "base"))`: Removes duplicate tuples from `x`. See `unique` in the **base** package for more details.

`x %in% table`: A shortcut for finding the ranges in `x` that match any of the tuples in `table`. Returns a logical vector of length equal to the number of tuples in `x`.

`findMatches(x, table)`: An enhanced version of `match` that returns all the matches in a **Hits** object.

`countMatches(x, table)`: Returns an integer vector of the length of `x` containing the number of matches in `table` for each element in `x`.

`order(...)`: Returns a permutation which rearranges its first argument (a `GTuples` object) into ascending order, breaking ties by further arguments. See `order` in the **BiocGenerics** package for more information.

`sort(x)`: Sorts `x`. See `sort` in the **base** package for more details.

`rank(x, na.last = TRUE, ties.method = c("average", "first", "random", "max", "min"))`  
Returns the sample ranks of the tuples in `x`. See `rank` in the **base** package for more details.

### Value

For `pcompare`: see Details section above.

For `selfmatch`: an integer vector of the same length as `x`.

For `duplicated`, `unique`, and `%in%`: see `?BiocGenerics::duplicated`, `?BiocGenerics::unique`, and `?%in%`.

For `findMatches`: a `Hits` object by default (i.e. if `select="all"`).

For `countMatches`: an integer vector of the length of `x` containing the number of matches in `table` for each element in `x`.

For `sort`: see `?BiocGenerics::sort`.

### Author(s)

Peter Hickey

### See Also

- The `GTuples` class.
- `GenomicRanges-comparison` in the **GRanges** package for comparing and ordering genomic ranges.
- `intra-tuple-methods` for intra-tuple transformations.
- `findOverlaps-methods` for finding overlapping genomic ranges.

### Examples

```
## GTuples object containing 3-tuples:
gt3 <- GTuples(seqnames = c('chr1', 'chr1', 'chr1', 'chr1', 'chr2'),
               tuples = matrix(c(10L, 10L, 10L, 10L, 10L, 20L, 20L, 20L, 25L,
                                20L, 30L, 30L, 35L, 30L, 30L), ncol = 3),
               strand = c('+', '-', '*', '+', '+'))
gt3 <- c(gt3, rev(gt3[3:5]))

## -----
## A. ELEMENT-WISE (AKA "PARALLEL") COMPARISON OF 2 GTuples OBJECTS
## -----
gt3[2] == gt3[2] # TRUE
gt3[2] == gt3[5] # FALSE
gt3 == gt3[4]
gt3 >= gt3[3]

## -----
## B. duplicated(), unique()
## -----
duplicated(gt3)
unique(gt3)
```

```

## -----
## C. match(), %in%
## -----
table <- gt3[2:5]
match(gt3, table)
match(gt3, table, ignore.strand = TRUE)

## -----
## D. findMatches(), countMatches()
## -----
findMatches(gt3, table)
countMatches(gt3, table)

findMatches(gt3, table, ignore.strand = TRUE)
countMatches(gt3, table, ignore.strand = TRUE)

gt3_levels <- unique(gt3)
countMatches(gt3_levels, gt3)

## -----
## E. order() AND RELATED METHODS
## -----
is.unsorted(gt3)
order(gt3)
sort(gt3)
is.unsorted(sort(gt3))

is.unsorted(gt3, ignore.strand=TRUE)
gt3_2 <- sort(gt3, ignore.strand=TRUE)
is.unsorted(gt3_2) # TRUE
is.unsorted(gt3_2, ignore.strand=TRUE) # FALSE

## TODO (TODO copied from GenomicRanges): Broken. Please fix!
#sort(gt3, by = ~ seqnames + start + end) # equivalent to (but slower than) above

score(gt3) <- rev(seq_len(length(gt3)))

## TODO (TODO copied from GenomicRanges): Broken. Please fix!
#sort(gt3, by = ~ score)

rank(gt3)

## -----
## F. GENERALIZED ELEMENT-WISE COMPARISON OF 2 GTuples OBJECTS
## -----
pcompare(gt3[3], gt3)

```

---

GTuplesList-class

*GTuplesList* objects

---

### Description

The `GTuplesList` class is a container for storing a collection of `GTuples` objects. It is derived from `GRangesList`.

**Constructor**

`GTuplesList(...)`: Creates a `GTuplesList` object using `GTuples` objects supplied in ...

**Accessors**

In the following code snippets, `x` is a `GTuplesList` object.

`length(x)`: Get the number of list elements.

`names(x)`, `names(x) <- value`: Get or set the names on `x`.

`elementNROWS(x)`: Get the length of each of the list elements.

`isEmpty(x)`: Returns a logical indicating either if the `GTuplesList` has no elements or if all its elements are empty.

`seqnames(x)`, `seqnames(x) <- value`: Get or set the sequence names in the form of an `RleList`. `value` can be an `RleList` or `CharacterList` object.

`tuples(x)`, `tuples(x) <- value`: Get or set the tuples in the form of a `SimpleList` of integer matrices. `value` can be a single integer matrix.

`ranges(x, use.mcols = FALSE)`, `ranges(x) <- value`: Get or set the ranges in the form of a `CompressedIRangesList`. `value` can be a `IntegerRangesList` object.

**WARNING:** The use of `ranges` with `GTuplesList` objects is **strongly** discouraged. It will only get/set  $pos_1$  and  $pos_m$  of the tuples, where  $m$  is the size of the tuples, as these are what are stored in the "ranges" slot of the `GTuples` objects.

`strand(x)`, `strand(x) <- value`: Get or set the strand in the form of an `RleList`. `value` can be an `RleList`, `CharacterList` or single character. `value` as a single character converts all ranges in `x` to the same value; for selective strand conversion (i.e., mixed "+" and "-") use `RleList` or `CharacterList`.

`mcols(x, use.names=FALSE)`, `mcols(x) <- value`: Get or set the metadata columns. `value` can be `NULL`, or a data.frame-like object (i.e. `DataFrame` or `data.frame`) holding element-wise metadata.

`elementMetadata(x)`, `elementMetadata(x) <- value`, `values(x)`, `values(x) <- value`: Alternatives to `mcols` functions. Their use is discouraged.

`seqinfo(x)`, `seqinfo(x) <- value`: Get or set the information about the underlying sequences. `value` must be a `Seqinfo` object.

`seqlevels(x)`, `seqlevels(x, force=FALSE) <- value`: Get or set the sequence levels. `seqlevels(x)` is equivalent to `seqlevels(seqinfo(x))` or to `levels(seqnames(x))`, those 2 expressions being guaranteed to return identical character vectors on a `GTuplesList` object. `value` must be a character vector with no NAs. See `?seqlevels` for more information.

`seqlengths(x)`, `seqlengths(x) <- value`: Get or set the sequence lengths. `seqlengths(x)` is equivalent to `seqlengths(seqinfo(x))`. `value` can be a named non-negative integer or numeric vector eventually with NAs.

`isCircular(x)`, `isCircular(x) <- value`: Get or set the circularity flags. `isCircular(x)` is equivalent to `isCircular(seqinfo(x))`. `value` must be a named logical vector eventually with NAs.

`genome(x)`, `genome(x) <- value`: Get or set the genome identifier or assembly name for each sequence. `genome(x)` is equivalent to `genome(seqinfo(x))`. `value` must be a named character vector eventually with NAs.

`seqlevelsStyle(x)`, `seqlevelsStyle(x) <- value`: Get or set the seqname style for `x`. See the `seqlevelsStyle` generic getter and setter in the `GenomeInfoDb` package for more information.

`score(x)`, `score(x) <- value`: Get or set the "score" metadata column.

## Tuples methods

In the following code snippets, `x` is a `GTuplesList` object.

**WARNING:** The preferred setter is `tuples(x) <- value` and the use of `start(x) <- value`, `end(x) <- value` and `width(x) <- value` is discouraged.

`start(x)`, `start(x) <- value`: Get or set  $pos_1$  of the tuples. **WARNING:** The use of `start(x) <- value` is discouraged; instead, construct the tuples as the appropriate `List` of integer matrices, `mvalue`, and use `tuples(x) <- mvalue`.

`end(x)`, `end(x) <- value`: Get or set  $pos_m$  of the tuples, where  $m$  is the size of the tuples. **WARNING:** The use of `end(x) <- value` is discouraged; instead, construct the tuples as the appropriate `List` of integer matrices, `mvalue`, and use `tuples(x) <- mvalue`.

`IPD(x)`: Get the intra-pair distances (IPD) in the form of a `SimpleList` of integer matrices. IPD is only defined for tuples with size  $> 1$ . The IPD of a tuple with size  $= m$  is the vector of intra-pair distances,  $(pos_2 - pos_1, \dots, pos_m - pos_{m-1})$ .

`width(x)`, `width(x) <- value`: Get or set  $pos_m - pos_1$  of the tuples, where  $m$  is the size of the tuples. If using `width(x) <- value`,  $pos_1$  is held fixed and  $pos_m$  is altered. **WARNING:** The use of `width(x) <- value` is discouraged; instead, instead, construct the tuples as the appropriate `List` of integer matrices, `mvalue`, and use `tuples(x) <- mvalue`.

## Coercion

In the code snippets below, `x` is a `GTuplesList` object.

`as.data.frame(x, row.names = NULL, optional = FALSE, ..., value.name = "value", use.outer = FALSE)`: Coerces `x` to a `data.frame`. See `as.data.frame` on the `List` man page for details (`?List`).

`as.list(x, use.names = TRUE)`: Creates a list containing the elements of `x`.

`as(x, "GRangesList")`: Creates a `GRangesList` object from a `GTuplesList` object. **WARNING:** This is generally a *destructive* operation, as the original `GTuplesList` may not be recreatable.

## Subsetting

In the following code snippets, `x` is a `GTuplesList` object.

`x[i, j]`, `x[i, j] <- value`: Get or set elements `i` with optional metadata columns `mcols(x)[, j]`, where `i` can be missing; an NA-free logical, numeric, or character vector; a 'logical' Rle object, or an `AtomicList` object.

`x[[i]]`, `x[[i]] <- value`: Get or set element `i`, where `i` is a numeric or character vector of length 1.

`x$name`, `x$name <- value`: Get or set element name, where `name` is a name or character vector of length 1.

`head(x, n = 6L)`: If `n` is non-negative, returns the first `n` elements of the `GTuplesList` object. If `n` is negative, returns all but the last `abs(n)` elements of the `GTuplesList` object.

`rep(x, times, length.out, each)`: Repeats the values in `x` through one of the following conventions:

`times` Vector giving the number of times to repeat each element if of length `length(x)`, or to repeat the whole vector if of length 1.

`length.out` Non-negative integer. The desired length of the output vector.

`each` Non-negative integer. Each element of `x` is repeated `each` times.



`subset(x, subset)`: Returns a new object of the same class as `x` made of the subset using logical vector `subset`, where missing values are taken as `FALSE`.

`tail(x, n = 6L)`: If `n` is non-negative, returns the last `n` elements of the `GTuples` object. If `n` is negative, returns all but the first `abs(n)` elements of the `GTuples` object.

### Combining

In the code snippets below, `x` is a `GTuplesList` object.

`c(x, ...)`: Combines `x` and the `GTuplesList` objects in `...` together. Any object in `...` must belong to the same class as `x`, or to one of its subclasses, or must be `NULL`. The result is an object of the same class as `x`.

`append(x, values, after = length(x))`: Inserts the values into `x` at the position given by `after`, where `x` and `values` are of the same class.

`unlist(x, recursive = TRUE, use.names = TRUE)`: Concatenates the elements of `x` into a single `GTuples` object.

### Looping

In the code snippets below, `x` is a `GTuplesList` object.

`endoapply(X, FUN, ...)`: Similar to `lapply`, but performs an endomorphism, i.e. returns an object of `class(X)`.

`lapply(X, FUN, ...)`: Like the standard `lapply` function defined in the base package, the `lapply` method for `GTuplesList` objects returns a list of the same length as `X`, with each element being the result of applying `FUN` to the corresponding element of `X`.

`Map(f, ...)`: Applies a function to the corresponding elements of given `GTuplesList` objects.

`mapply(FUN, ..., MoreArgs = NULL, SIMPLIFY = TRUE, USE.NAMES = TRUE)`: Like the standard `mapply` function defined in the base package, the `mapply` method for `GTuplesList` objects is a multivariate version of `sapply`.

`mendoapply(FUN, ..., MoreArgs = NULL)`: Similar to `mapply`, but performs an endomorphism across multiple objects, i.e. returns an object of `class(list(...)[[1]])`.

`Reduce(f, x, init, right = FALSE, accumulate = FALSE)`: Uses a binary function to successively combine the elements of `x` and a possibly given initial value.

**f** A binary argument function.

**init** An R object of the same kind as the elements of `x`.

**right** A logical indicating whether to proceed from left to right (default) or from right to left.

**nomatch** The value to be returned in the case when "no match" (no element satisfying the predicate) is found.

`sapply(X, FUN, ..., simplify=TRUE, USE.NAMES=TRUE)`: Like the standard `sapply` function defined in the base package, the `sapply` method for `GTuplesList` objects is a user-friendly version of `lapply` by default returning a vector or matrix if appropriate.

### Author(s)

Peter Hickey for `GTuplesList` definition and methods. P. Aboyou & H. Pagès for all the real work underlying the powerful `GRangesList` class and methods.

**See Also**

[GTuples-class](#) [seqinfo](#), [GRangesList-class](#), [Vector-class](#), [IntegerRangesList-class](#), [RleList-class](#), [DataFrameList-class](#), [findOverlaps-methods](#)

**Examples**

```
## Construction of GTuplesList of 4-tuples with GTuplesList():
seqinfo <- Seqinfo(paste0("chr", 1:3), c(1000, 2000, 1500), NA, "mock1")
gt4 <- GTuples(seqnames = Rle(c("chr1", "chr2", "chr1", "chr3"),
                             c(1, 3, 2, 4)),
              tuples = matrix(c(1:10, 2:11, 3:12, 4:13), ncol = 4),
              strand = Rle(strand(c("-", "+", "*", "+", "-")),
                           c(1, 2, 2, 3, 2)),
              score = 1:10, GC = seq(1, 0, length = 10), seqinfo = seqinfo)
gtl4 <- GTuplesList(A = gt4[1:4], B = gt4[5:10])
gtl4

## Summarizing elements:
elementNROWS(gtl4)
table(seqnames(gtl4))

## Extracting subsets:
gtl4[seqnames(gtl4) == "chr1", ]
gtl4[seqnames(gtl4) == "chr1" & strand(gtl4) == "+", ]

## Renaming the underlying sequences:
seqlevels(gtl4)
seqlevels(gtl4) <- sub("chr", "Chrom", seqlevels(gtl4))
gtl4

## Coerce to GRangesList ("internal positions" information is lost):
as(gtl4, "GRangesList")

## Get the size of the tuples stored in the GTuplesList object
size(gtl4)

## Get the tuples
tuples(gtl4)

## Get the matrix of intra-pair distances (IPD)
IPD(gtl4)

## Can't combine genomic tuples of different sizes
gt1 <- GTuples('chr1', matrix(30:40))
gt1
## Not run:
## Returns error
GTuplesList(A = gt4, gt1)

## End(Not run)
```

## Description

This man page documents intra-tuple transformations of a [GTuples](#) or a [GTuplesList](#) object.

**WARNING:** These are not exactly the same as the intra-range methods defined in the **GenomicRanges** package (`?GenomicRanges::intra-range-methods`) or in the **IRanges** package (`?IRanges::intra-range-m`

## Usage

```
## S4 method for signature 'GTuples'
shift(x, shift = 0L, use.names = TRUE)
## S4 method for signature 'GTuplesList'
shift(x, shift = 0L, use.names = TRUE)

## S4 method for signature 'GTuples'
trim(x, use.names = TRUE)
```

## Arguments

`x` A [GTuples](#) or [GTuplesList](#) object.  
`shift, use.names` See `?`intra-range-methods``.  
`...` Additional arguments to methods.

## Details

- `shift` behaves like the `shift` method for [GRanges](#) objects, except that any `internalPos` are also shifted. See `?`intra-range-methods`` for further details of the `shift` method.
- `trim` trims out-of-bound tuples located on non-circular sequences whose length is not NA.

## Value

See Details section above.

## Author(s)

Peter Hickey for methods involving [GTuples](#) and [GTuplesList](#). P. Aboyoun and V. Obenchain <[vobencha@fhcrc.org](mailto:vobencha@fhcrc.org)> for all the real work underlying the powerful intra-range methods.

## See Also

- [GTuples](#) and [GTuplesList](#) objects.
- The [intra-range-methods](#) man page in the **GenomicRanges** package.

## Examples

```
## -----
## A. ON A GTuples OBJECT
## -----
gt3 <- GTuples(seqnames = c('chr1', 'chr1', 'chr1', 'chr1', 'chr2'),
              tuples = matrix(c(10L, 10L, 10L, 10L, 10L, 20L, 20L, 20L, 25L,
                               20L, 30L, 30L, 35L, 30L, 30L), ncol = 3),
              strand = c('+', '-', '*', '+', '+'))
gt3
```

```

shift(gt3, 10)

## -----
## B. ON A GTuplesList OBJECT
## -----
gtl3 <- GRangesList(A = gt3, B = rev(gt3))
gtl3

shift(gtl3, IntegerList(10, 100))

```

---

nearest-methods

*Finding the nearest genomic tuple/range neighbour*


---

### Description

The nearest, precede, follow, distance and distanceToNearest methods for [GTuples](#) objects and subclasses.

**NOTE:** These methods treat the tuples as if they were ranges, with ranges given by  $[pos_1, pos_m]$  and where  $m$  is the [size, GTuples-method](#) of the tuples. This is done via inheritance so that a [GTuples](#) object is treated as a [GRanges](#) and the appropriate method is dispatched upon.

### Usage

```

## S4 method for signature 'GTuples,GTuples'
precede(x, subject, select = c("arbitrary", "all"),
        ignore.strand = FALSE, ...)
## S4 method for signature 'GTuples,missing'
precede(x, subject, select = c("arbitrary", "all"),
        ignore.strand = FALSE, ...)

## S4 method for signature 'GTuples,GTuples'
follow(x, subject, select = c("arbitrary", "all"),
        ignore.strand=FALSE, ...)
## S4 method for signature 'GTuples,missing'
follow(x, subject, select = c("arbitrary", "all"),
        ignore.strand = FALSE, ...)

## S4 method for signature 'GTuples,GTuples'
nearest(x, subject, select = c("arbitrary", "all"),
        ignore.strand = FALSE, ...)
## S4 method for signature 'GTuples,missing'
nearest(x, subject, select = c("arbitrary", "all"),
        ignore.strand = FALSE, ...)

## S4 method for signature 'GTuples,GTuples'
distanceToNearest(x, subject, ignore.strand = FALSE,
                  ...)
## S4 method for signature 'GTuples,missing'
distanceToNearest(x, subject, ignore.strand = FALSE,
                  ...)

```

```
## S4 method for signature 'GTuples,GTuples'
distance(x, y, ignore.strand = FALSE, ...)
```

### Arguments

x	The query <a href="#">GTuples</a> instance.
subject	The subject <a href="#">GTuples</a> instance within which the nearest neighbours are found. Can be missing, in which case x is also the subject.
y	For the distance method, a <a href="#">GTuples</a> or <a href="#">GRanges</a> instance. Cannot be missing. If x and y are not the same length, the shortest will be recycled to match the length of the longest.
select	Logic for handling ties. By default, all methods select a single tuple/range (arbitrary for nearest, the first by order in subject for precede, and the last for follow). When select = "all" a <a href="#">Hits</a> object is returned with all matches for x. If x does not have a match in subject the x is not included in the <a href="#">Hits</a> object.
ignore.strand	A logical indicating if the strand of the input tuples/ranges should be ignored. When TRUE, strand is set to '+'.
...	Additional arguments for methods.

### Details

- nearest: Performs conventional nearest neighbour finding. Returns an integer vector containing the index of the nearest neighbour tuple/range in subject for each range in x. If there is no nearest neighbour NA is returned. For details of the algorithm see the man page in [IRanges](#), ?nearest.
- precede: For each range in x, precede returns the index of the tuple/range in subject that is directly preceded by the tuple/range in x. Overlapping tuples/ranges are excluded. NA is returned when there are no qualifying tuples/ranges in subject.
- follow: The opposite of precede, follow returns the index of the tuple/range in subject that is directly followed by the tuple/range in x. Overlapping tuples/ranges are excluded. NA is returned when there are no qualifying tuples/ranges in subject.
- Orientation and Strand: The relevant orientation for precede and follow is 5' to 3', consistent with the direction of translation. Because positional numbering along a chromosome is from left to right and transcription takes place from 5' to 3', precede and follow can appear to have 'opposite' behaviour on the + and - strand. Using positions 5 and 6 as an example, 5 precedes 6 on the + strand but follows 6 on the - strand.  
A tuple/range with strand \* can be compared to tuples/ranges on either the + or - strand. Below we outline the priority when tuples/ranges on multiple strands are compared. When ignore.strand=TRUE all tuples/ranges are treated as if on the + strand.
  - x on + strand can match to tuples/ranges on both + and \* strands. In the case of a tie the first tuple/range by order is chosen.
  - x on - strand can match to tuples/ranges on both - and \* strands. In the case of a tie the first tuple/range by order is chosen.
  - x on \* strand can match to tuples/ranges on any of +, - or \* strands. In the case of a tie the first tuple/range by order is chosen.
- distanceToNearest: Returns the distance for each tuple/range in x to its nearest neighbour in the subject.

- `distance`: Returns the distance for each tuple/range in `x` to the range in `y`. The behaviour of `distance` has changed in Bioconductor 2.12. See the man page `?distance` in `IRanges` for details.

### Value

For `nearest`, `precede` and `follow`, an integer vector of indices in `subject`, or a `Hits` if `select = "all"`.

For `distanceToNearest`, a `Hits` object with a column for the query index (`from`), subject index (`to`) and the distance between the pair.

For `distance`, an integer vector of distances between the tuples/ranges in `x` and `y`.

### Author(s)

Peter Hickey for methods involving `GTuples`. P. Aboyoun and V. Obenchain <[vobencha@fhcrc.org](mailto:vobencha@fhcrc.org)> for all the real work underlying the powerful nearest methods.

### See Also

- The `GTuples` and `GRanges` classes.
- The `GenomicRanges` and `GRanges` classes in the `GenomicRanges` package.
- The `IPosRanges` class in the `IRanges` package.
- The `Hits` class in the `S4Vectors` package.
- The `nearest-methods` man page in the `GenomicRanges` package.
- `findOverlaps-methods` for finding just the overlapping ranges.

### Examples

```
## -----
## precede() and follow()
## -----
query <- GTuples("A", matrix(c(5L, 20L, 6L, 21L), ncol = 2), strand = "+")
subject <- GTuples("A", matrix(c(rep(c(10L, 15L), 2), rep(c(11L, 16L), 2)),
                             ncol = 2),
                       strand = c("+", "+", "-", "-"))
precede(query, subject)
follow(query, subject)

strand(query) <- "-"
precede(query, subject)
follow(query, subject)

## ties choose first in order
query <- GTuples("A", matrix(c(10L, 11L), ncol = 2), c("+", "-", "*"))
subject <- GTuples("A", matrix(c(rep(c(5L, 15L), each = 3),
                               rep(c(6L, 16L), each = 3)), ncol = 2),
                    rep(c("+", "-", "*"), 2))
precede(query, subject)
precede(query, rev(subject))

## ignore.strand = TRUE treats all ranges as '+'
precede(query[1], subject[4:6], select="all", ignore.strand = FALSE)
precede(query[1], subject[4:6], select="all", ignore.strand = TRUE)
```

```

## -----
## nearest()
## -----
## When multiple tuples overlap an "arbitrary" tuple is chosen
query <- GTuples("A", matrix(c(5L, 15L), ncol = 2))
subject <- GTuples("A", matrix(c(1L, 15L, 5L, 19L), ncol = 2))
nearest(query, subject)

## select = "all" returns all hits
nearest(query, subject, select = "all")

## Tuples in 'x' will self-select when 'subject' is present
query <- GTuples("A", matrix(c(1L, 10L, 6L, 15L), ncol = 2))
nearest(query, query)

## Tuples in 'x' will not self-select when 'subject' is missing
nearest(query)

## -----
## distance(), distanceToNearest()
## -----
## Adjacent, overlap, separated by 1
query <- GTuples("A", matrix(c(1L, 2L, 10L, 5L, 8L, 11L), ncol = 2))
subject <- GTuples("A", matrix(c(6L, 5L, 13L, 10L, 10L, 15L), ncol = 2))
distance(query, subject)

## recycling
distance(query[1], subject)

query <- GTuples(c("A", "B"), matrix(c(1L, 5L, 2L, 6L), ncol = 2))
distanceToNearest(query, subject)

```

---

tuples-squeezers

*Squeeze the tuples out of a tuples-based object*


---

## Description

S4 generic functions for squeezing the tuples out of a tuples-based object. Similar to the S4 generic functions for squeezing the ranges out of a ranged-based object, see [granges](#) and [grglist](#).

gtuples returns them as a [GTuples](#) object, and gtlist as a [GTuplesList](#) object.

## Usage

```

gtuples(x, use.mcols=FALSE, ...)
gtlist(x, use.mcols=FALSE, ...)

```

## Arguments

x	A tuples-based object.
use.mcols	TRUE or FALSE (the default). Whether the metadata columns on x (accessible with <code>mcols(x)</code> ) should be propagated to the returned object or not.
...	Additional arguments, for use in specific methods.

## Details

The **MethylationTuples** (<https://github.com/PeteHaitch/MethylationTuples>) package defines and document methods for various types of tuples-based objects.

Other Bioconductor packages might as well.

Note that these functions can be seen as a specific kind of *object getters* as well as functions performing coercion.

## Value

A **GTuples** object for `gtuples`.

A **GTuplesList** object for `gtlist`.

If `x` is a vector-like object, the returned object is expected to be *parallel* to `x`, that is, the *i*-th element in the output corresponds to the *i*-th element in the input. If `x` has names on it, they're propagated to the returned object. If `use.mcols` is `TRUE` and `x` has metadata columns on it (accessible with `mcols(x)`), they're propagated to the returned object.

## Author(s)

Peter Hickey

## See Also

- **GTuples** and **GTuplesList** objects.

## Examples

```
## See ?MethPat in the MethylationTuples package (GitHub-only package) for some
## examples.
```

---

Undefined methods

*Undefined methods*

---

## Description

These are methods defined for **GRanges** and **GRangesList** objects that have no well-defined equivalent for **GTuples** or **GTuplesList**. Therefore, I have explicitly written methods for these that return errors when called.

## Examples

```
gt3 <- GTuples(seqnames = c('chr1', 'chr1', 'chr1', 'chr1', 'chr2'),
              tuples = matrix(c(10L, 10L, 10L, 10L, 10L, 20L, 20L, 20L, 25L,
                               20L, 30L, 30L, 35L, 30L, 30L), ncol = 3),
              strand = c('+', '-', '*', '+', '+'))

## Not run:
# Will return errors
narrow(gt3)
reduce(gt3)

## End(Not run)
```



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