

# Package ‘GenomicTuples’

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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

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'GTuples-comparison.R' 'GTuplesList-class.R' 'GenomicTuples.R'  
'RcppExports.R' 'coverage-methods.R' 'findOverlaps-methods.R'  
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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.

## Author(s)

**Maintainer:** Peter Hickey <peter.hickey@gmail.com>

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- Hervé Pagès [contributor]

## References

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

### See Also

Useful links:

- [www.github.com/PeteHaitch/GenomicTuples](http://www.github.com/PeteHaitch/GenomicTuples)
- Report bugs at <https://github.com/PeteHaitch/GenomicTuples/issues>

---

.allTuplesSortedCpp    *An internal helper function to check that each tuple is sorted in increasing order; only used for tuples of size > 2.*

---

### Description

An internal helper function to check that each tuple is sorted in increasing order; only used for tuples of size > 2.

### Usage

```
.allTuplesSortedCpp(pos1, internal_pos, posm)
```

### Arguments

pos1	An integer vector.
internal_pos	An integer matrix.
posm	An integer vector.

### Details

.allTuplesSorted is adapted from <http://stackoverflow.com/a/7601857>. Strict inequalities are required.

### Value

TRUE if each tuple is sorted in strictly increasing order, FALSE otherwise.

---

.findEqual.GTuples    *An internal function used by the findOverlaps,GTuples,GTuples-method when type = "equal".*

---

### Description

An internal function used by the findOverlaps,GTuples,GTuples-method when type = "equal".

### Usage

```
.findEqual.GTuples(query, subject, select, ignore.strand)
```

### Arguments

query	A GTuples instance
subject	A GTuples instance
select	See findOverlaps in the IRanges package for a description of this argument.
ignore.strand	When set to TRUE, the strand information is ignored in the overlap calculations.

---

.GT2DT	<i>Convert a GTuples object to a data.table.</i>
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---

**Description**

Convert a GTuples object to a data.table.

**Usage**

```
.GT2DT(gt, ignore.strand = FALSE)
```

**Arguments**

gt	A GTuples object
ignore.strand	When set to TRUE, the strand is set to "*".

---

.IPDCpp	<i>An internal function to compute the IPD of a GTuples; ; only used for tuples of size &gt; 2.</i>
---------	---

---

**Description**

An internal function to compute the IPD of a GTuples; ; only used for tuples of size > 2.

**Usage**

```
.IPDCpp(pos1, internal_pos, posm)
```

**Arguments**

pos1	An integer vector.
internal_pos	An integer matrix.
posm	An integer vector.

**Value**

An integer matrix with the same number of rows as internal\_pos and number of columns equal to size - 1.

**Note**

This function silently coerces numeric matrices to integer matrices and does integer subtraction. *This will give unexpected results but it's not a problem for me since I only use it on integer matrices.*

---

.matrixDiffWithRecycling

*Compute column-wise difference of matrices with possibly different number of rows. Do this by iterating over columns, treating them as vectors and then using R's native vector recycling.*

---

### Description

Compute column-wise difference of matrices with possibly different number of rows. Do this by iterating over columns, treating them as vectors and then using R's native vector recycling.

### Usage

```
.matrixDiffWithRecycling(x, y)
```

---

.pcompareGTuplesCpp *An internal function used to pcompare GTuples.*

---

### Description

An internal function used to pcompare GTuples.

### Usage

```
.pcompareGTuplesCpp(int_seqnames, int_strand, int_pos)
```

### Arguments

int_seqnames	An integer vector of length n. An integer representation of the difference in seqnames of each tuple.
int_strand	An integer vector of length n. An integer representation of the difference in strand of each tuple.
int_pos	An integer matrix with n rows. Each row represents the difference in positions of each tuple.

### Details

The tuples should have already been converted to integer representations, namely an integer vector for the difference in chromosome, an integer vector for the difference in strand and an integer matrix for the difference in positions.

### Value

An integer vector where each element is the comparison of a pair of tuples. If the first tuple in the pair is "<" than the second tuple then the return value for that element is < 0, if the first tuple in the pair is "==" the second tuple then the return value is 0, and if the first tuple is ">" that the second tuple then the return value is > 0.

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<code>.zero_range</code>	<i>Check whether all elements of a numeric vector are identical (within machine precision)</i>
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---

### Description

Check whether all elements of a numeric vector are identical (within machine precision)

### Usage

```
.zero_range(x, tol = .Machine$double.eps^0.5)
```

### Arguments

`x` a numeric vector.

### Value

TRUE if all elements of the vector are identical (within machine precision). FALSE in all other cases, including if the vector contains any NAs.

### Note

This function is based on Hadley and John's answer to <http://stackoverflow.com/q/4752275>. No check is made that `x` is a numeric vector.

---

`findOverlaps-methods` *Finding overlapping genomic tuples*

---

### 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](#)
- [GTuples](#)
- [GTuplesList](#)
- [GRanges](#)
- [GRangesList](#)

**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](#) 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 = NULL)`  
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 `pos1` and `posm` 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. `DataFrame` 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

`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](#) objects (defined in the **GenomicRanges** package), [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](#), [Rle](#), [DataFrame](#), [GRanges](#), [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("-", "+", "*+", "+", "-")),
             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

<code>x, table, y</code>	<a href="#">GTuples</a> objects.
<code>incomparables</code>	Not supported.
<code>fromLast, method, nomatch</code>	See <code>?`GenomicRanges-comparison`</code> in the <b>GenomicRanges</b> package for a description of these arguments.
<code>ignore.strand</code>	Whether or not the strand should be ignored when comparing 2 genomic tuples.
<code>...</code>	One or more <a href="#">GTuples</a> objects. The <a href="#">GTuples</a> objects after the first one are used to break ties
<code>na.last</code>	Ignored.
<code>decreasing</code>	TRUE or FALSE.
<code>ties.method</code>	A character string specifying how ties are treated. Only "first" is supported for now.
<code>by</code>	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.
<code>na.rm</code>	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 *strictly* 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.mcols = 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 re-creatable.

### 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. Aboyoun & H. Pagès for all the real work underlying the powerful GRangesList class and methods.

## See Also

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

```

---

intra-tuple-methods     *Intra-tuple transformations of a GTuples or GTuplesLists object*

---

## 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``.

**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))
```

**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.

<code>y</code>	For the distance method, a <code>GTuples</code> or <code>GRanges</code> instance. Cannot be missing. If <code>x</code> and <code>y</code> are not the same length, the shortest will be recycled to match the length of the longest.
<code>select</code>	Logic for handling ties. By default, all methods select a single tuple/range (arbitrary for <code>nearest</code> , the first by order in <code>subject</code> for <code>precede</code> , and the last for <code>follow</code> ). When <code>select = "all"</code> a <code>Hits</code> object is returned with all matches for <code>x</code> . If <code>x</code> does not have a match in <code>subject</code> the <code>x</code> is not included in the <code>Hits</code> object.
<code>ignore.strand</code>	A logical indicating if the strand of the input tuples/ranges should be ignored. When <code>TRUE</code> , <code>strand</code> is set to <code>'+'</code> .
<code>...</code>	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 for `precede` and `follow`:** Orientation 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' behavior on the + and - strand. Using positions 5 and 6 as an example, 5 precedes 6 on the + strand but follows 6 on the - strand.

The table below outlines the orientation when tuples/ranges on different strands are compared. In general, a feature on `*` is considered to belong to both strands. The single exception is when both `x` and `subject` are `*` in which case both are treated as `+`.

	<code>x</code>		<code>subject</code>		orientation
a)	+		+		--->
b)	+		-		NA
c)	+		*		--->
d)	-		+		NA
e)	-		-		<---
f)	-		*		<---
g)	*		+		--->
h)	*		-		<---
i)	*		*		---> (the only situation where * arbitrarily means +)

**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 `aHits` 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.
- `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 gtlis 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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