

# Package ‘IRanges’

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**Title** Foundation of integer range manipulation in Bioconductor

**Description** Provides efficient low-level and highly reusable S4 classes for storing, manipulating and aggregating over annotated ranges of integers. Implements an algebra of range operations, including efficient algorithms for finding overlaps and nearest neighbors. Defines efficient list-like classes for storing, transforming and aggregating large grouped data, i.e., collections of atomic vectors and DataFrames.

**biocViews** Infrastructure, DataRepresentation

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RleViewsList-utils.R RangedSelection-class.R

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 CompressedList-comparison.R CompressedHitsList-class.R  
 CompressedDataFrameList-class.R CompressedAtomicList-class.R  
 CompressedGrouping-class.R CompressedRangesList-class.R  
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 windows-methods.R intra-range-methods.R inter-range-methods.R  
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AtomicList

*Lists of Atomic Vectors in Natural and Rle Form*

---

## Description

An extension of [List](#) that holds only atomic vectors in either a natural or run-length encoded form.

## Details

The lists of atomic vectors are [LogicalList](#), [IntegerList](#), [NumericList](#), [ComplexList](#), [CharacterList](#), and [RawList](#). There is also an [RleList](#) class for run-length encoded versions of these atomic vector types.

Each of the above mentioned classes is virtual with [Compressed\\*](#) and [Simple\\*](#) non-virtual representations.

## Constructors

[LogicalList](#)(..., compress = TRUE): Concatenates the logical vectors in ... into a new [LogicalList](#).  
If compress, the internal storage of the data is compressed.

[IntegerList](#)(..., compress = TRUE): Concatenates the integer vectors in ... into a new [IntegerList](#).  
If compress, the internal storage of the data is compressed.

[NumericList](#)(..., compress = TRUE): Concatenates the numeric vectors in ... into a new [NumericList](#).  
If compress, the internal storage of the data is compressed.

[ComplexList](#)(..., compress = TRUE): Concatenates the complex vectors in ... into a new [ComplexList](#).  
If compress, the internal storage of the data is compressed.

`CharacterList(..., compress = TRUE)`: Concatenates the character vectors in ... into a new `CharacterList`. If `compress`, the internal storage of the data is compressed.

`RawList(..., compress = TRUE)`: Concatenates the raw vectors in ... into a new `RawList`. If `compress`, the internal storage of the data is compressed.

`RleList(..., compress = TRUE)`: Concatenates the run-length encoded atomic vectors in ... into a new `RleList`. If `compress`, the internal storage of the data is compressed.

`FactorList(..., compress = TRUE)`: Concatenates the factor objects in ... into a new `FactorList`. If `compress`, the internal storage of the data is compressed.

### Coercion

`as(from, "CompressedSplitDataFrameList"), as(from, "SimpleSplitDataFrameList")`: Creates a [CompressedSplitDataFrameList/SimpleSplitDataFrameList](#) instance from an `AtomicList` instance.

`as(from, "IRangesList"), as(from, "CompressedIRangesList"), as(from, "SimpleIRangesList")`: Creates a [CompressedIRangesList/SimpleIRangesList](#) instance from a `LogicalList` or `logical RleList` instance. Note that the elements of this instance are guaranteed to be normal.

`as(from, "NormalIRangesList"), as(from, "CompressedNormalIRangesList"), as(from, "SimpleNormalIRangesList")`: Creates a [CompressedNormalIRangesList/SimpleNormalIRangesList](#) instance from a `LogicalList` or `logical RleList` instance.

`as(from, "CharacterList"), as(from, "ComplexList"), as(from, "IntegerList"), as(from, "LogicalList"), as(from, "RleList")`: Coerces an `AtomicList` from to another derivative of `AtomicList`.

`as(from, "AtomicList")`: If `from` is a vector, converts it to an `AtomicList` of the appropriate type.

`drop(x)`: Checks if every element of `x` is of length one, and, if so, unlists `x`. Otherwise, an error is thrown.

`as(from, "RleViews")`: Creates an `RleViews` where each view corresponds to an element of `from`. The subject is `unlist(from)`.

`as.matrix(x, col.names=NULL)`: Maps the elements of the list to rows of a matrix. The column mapping depends on whether there are inner names (either on the object or provided via `col.names` as a `List` object). If there are no inner names, each row is padded with NAs to reach the length of the longest element. If there are inner names, there is a column for each unique name and the mapping is by name. To provide inner names, the `col.names` argument should be a `List`, usually a `CharacterList` or `FactorList` (which is particularly efficient). If `col.names` is a character vector, it names the columns of the result, but does not imply inner names.

### Compare, Order, Tabulate

The following methods are provided for element-wise comparison of 2 `AtomicList` objects, and ordering or tabulating of each list element of an `AtomicList` object: `is.na`, `duplicated`, `unique`, `match`, `%in%`, `table`, `order`, `sort`.

### RleList Methods

`RleList` has a number of methods that are not shared by other `AtomicList` derivatives.

`runLength(x)`: Gets the run lengths of each element of the list, as an `IntegerList`.

`runValue(x)`, `runValue(x) <- value`: Gets or sets the run values of each element of the list, as an AtomicList.

`ranges(x)`: Gets the run ranges as a IntegerRangesList.

### Author(s)

P. Aboyoun

### See Also

- [AtomicList-utils](#) for common operations on AtomicList objects.
- [List](#) objects in the **S4Vectors** package for the parent class.

### Examples

```
int1 <- c(1L,2L,3L,5L,2L,8L)
int2 <- c(15L,45L,20L,1L,15L,100L,80L,5L)
collection <- IntegerList(int1, int2)

## names
names(collection) <- c("one", "two")
names(collection)
names(collection) <- NULL # clear names
names(collection)
names(collection) <- "one"
names(collection) # c("one", NA)

## extraction
collection[[1]] # range1
collection[["1"]] # NULL, does not exist
collection[["one"]] # range1
collection[[NA_integer_]] # NULL

## subsetting
collection[numeric()] # empty
collection[NULL] # empty
collection[] # identity
collection[c(TRUE, FALSE)] # first element
collection[2] # second element
collection[c(2,1)] # reversed
collection[-1] # drop first
collection$one

## replacement
collection$one <- int2
collection[[2]] <- int1

## concatenating
col1 <- IntegerList(one = int1, int2)
col2 <- IntegerList(two = int2, one = int1)
col3 <- IntegerList(int2)
append(col1, col2)
```

```

append(col1, col2, 0)
col123 <- c(col1, col2, col3)
col123

## revElements
revElements(col123)
revElements(col123, 4:5)

```

AtomicList-utils

*Common operations on AtomicList objects***Description**

Common operations on [AtomicList](#) objects.

**Group Generics**

AtomicList objects have support for S4 group generic functionality to operate within elements across objects:

Arith "+", "-", "\*", "^", "%%", "%/%", "/"

Compare "=", ">", "<", "!=", "<=", ">="

Logic "&", "|"

Ops "Arith", "Compare", "Logic"

Math "abs", "sign", "sqrt", "ceiling", "floor", "trunc", "cummax", "cummin", "cumprod",  
 "cumsum", "log", "log10", "log2", "log1p", "acos", "acosh", "asin", "asinh", "atan",  
 "atanh", "exp", "expm1", "cos", "cosh", "sin", "sinh", "tan", "tanh", "gamma", "lgamma",  
 "digamma", "trigamma"

Math2 "round", "signif"

Summary "max", "min", "range", "prod", "sum", "any", "all"

Complex "Arg", "Conj", "Im", "Mod", "Re"

See [S4groupGeneric](#) for more details.

**Other Methods**

The AtomicList objects also support a large number of basic methods. Like the group generics above, these methods perform the corresponding operation on each element of the list separately. The methods are:

**Logical** !, which, which.max, which.min

**Numeric** diff, pmax, pmax.int, pmin, pmin.int, mean, var, cov, cor, sd, median, quantile,  
 mad, IQR

**Running Window** smoothEnds, runmed, runmean, runsum, runwtsum, runq

**Character** nchar, chartr, tolower, toupper, sub, gsub, startsWith, endsWith

The `which.min` and `which.max` functions have an extra argument, `global=FALSE`, which controls whether the returned subscripts are global (compatible with the unlisted form of the input) or local (compatible with the corresponding list element).

The `rank` method only supports tie methods “average”, “first”, “min” and “max”.

Since `ifelse` relies on non-standard evaluation for arguments that need to be in the generic signature, we provide `ifelse2`, which has eager but otherwise equivalent semantics.

### Specialized Methods

`unstrsplit(x, sep="")`: : A fast `sapply(x, paste0, collapse=sep)`. See `?unstrsplit` for the details.

### Author(s)

P. Aboyoun

### See Also

- [AtomicList](#) objects.

### Examples

```
## group generics
int1 <- c(1L,2L,3L,5L,2L,8L)
int2 <- c(15L,45L,20L,1L,15L,100L,80L,5L)
col1 <- IntegerList(one = int1, int2)
2 * col1
col1 + col1
col1 > 2
sum(col1) # equivalent to (but faster than) 'sapply(col1, sum)'
mean(col1) # equivalent to 'sapply(col1, mean)'
```

---

CompressedHitsList-class

*CompressedHitsList* objects

---

### Description

An efficient representation of [HitsList](#) objects. See `?HitsList` for more information about [HitsList](#) objects.

### Note

This class is highly experimental. It has not been well tested and may disappear at any time.

### Author(s)

Michael Lawrence

**See Also**

[HitsList](#) objects.

---

CompressedList-class    *CompressedList objects*

---

**Description**

Like the [SimpleList](#) class defined in the **S4Vectors** package, the `CompressedList` class extends the `List` virtual class.

**Details**

Unlike the [SimpleList](#) class, `CompressedList` is virtual, that is, it cannot be instantiated. Many concrete (i.e. non-virtual) `CompressedList` subclasses are defined and documented in this package (e.g. [CompressedIntegerList](#), [CompressedCharacterList](#), [CompressedRleList](#), etc...), as well as in other packages (e.g. [GRangesList](#) in the **GenomicRanges** package, [GAlignmentsList](#) in the **GenomicAlignments** package, etc...). It's easy for developers to extend `CompressedList` to create a new `CompressedList` subclass and there is generally very little work involved to make this new subclass fully operational.

In a `CompressedList` object the list elements are concatenated together in a single vector-like object. The *partitioning* of this single vector-like object (i.e. the information about where each original list element starts and ends) is also kept in the `CompressedList` object. This internal representation is generally more memory efficient than [SimpleList](#), especially if the object has many list elements (e.g. thousands or millions). Also it makes it possible to implement many basic list operations very efficiently.

Many objects like [LogicalList](#), [IntegerList](#), [CharacterList](#), [RleList](#), etc... exist in 2 flavors: `CompressedList` and `SimpleList`. Each flavor is incarnated by a concrete subclass: [CompressedLogicalList](#) and [SimpleLogicalList](#) for virtual class [LogicalList](#), [CompressedIntegerList](#) and [SimpleIntegerList](#) for virtual class [IntegerList](#), etc... It's easy to switch from one representation to the other with `as(x, "CompressedList")` and `as(x, "SimpleList")`. Also the constructor function for those virtual classes have a switch that lets the user choose the representation at construction time e.g. `CharacterList(..., compress=TRUE)` or `CharacterList(..., compress=FALSE)`. See below for more information.

**Constructor**

See the [List](#) man page in the **S4Vectors** package for a quick overview of how to construct `List` objects in general.

Unlike for [SimpleList](#) objects, there is no `CompressedList` constructor function.

However, many constructor functions for `List` derivatives provide the `compress` argument that lets the user choose between the `CompressedList` and [SimpleList](#) representations at construction time. For example, depending on whether the `compress` argument of the `CharacterList()` constructor is set to `TRUE` or `FALSE`, a [CompressedCharacterList](#) or [SimpleCharacterList](#) instance will be returned.

Finally let's mention that the most efficient way to construct a `CompressedList` derivative is with



```
relist(unlisted, partitioning)
```

where `unlisted` is a vector-like object and `partitioning` a [PartitioningByEnd](#) object describing a partitioning of `unlisted`. The cost of this `relist` operation is virtually zero because `unlisted` and `partitioning` get stored *as-is* in the returned object.

### Accessors

Same as for [List](#) objects. See the [List](#) man page in the **S4Vectors** package for more information.

### Coercion

All the coercions documented in the [List](#) man page apply to `CompressedList` objects.

### Subsetting

Same as for [List](#) objects. See the [List](#) man page for more information.

### Looping and functional programming

Same as for [List](#) objects. See `?`List-utils`` in the **S4Vectors** package for more information.

### Displaying

When a `CompressedList` object is displayed, the "Compressed" prefix is removed from the real class name of the object. See [classNameForDisplay](#) in the **S4Vectors** package for more information about this.

### See Also

- [List](#) in the **S4Vectors** package for an introduction to `List` objects and their derivatives (`CompressedList` is a direct subclass of `List` which makes `CompressedList` objects `List` derivatives).
- The [SimpleList](#) class defined and documented in the **S4Vectors** package for an alternative to `CompressedList`.
- [relist](#) and [extractList](#) for efficiently constructing a [List](#) derivative from a vector-like object.
- The [CompressedNumericList](#) class for an example of a concrete `CompressedList` subclass.
- [PartitioningByEnd](#) objects. These objects are used inside `CompressedList` derivatives to keep track of the *partitioning* of the single vector-like object made of all the list elements concatenated together.

### Examples

```
## Fastest way to construct a CompressedList object:
unlisted <- runif(12)
partitioning <- PartitioningByEnd(c(5, 5, 10, 12), names=LETTERS[1:4])
partitioning

x1 <- relist(unlisted, partitioning)
x1
```

```

stopifnot(identical(lengths(partitioning), lengths(x1)))

## Note that the class of the CompressedList derivative returned by
## relist() is determined by relistToClass():
relistToClass(unlisted)
stopifnot(relistToClass(unlisted) == class(x1))

## Displaying a CompressedList object:
x2 <- IntegerList(11:12, integer(0), 3:-2, compress=TRUE)
class(x2)

## The "Simple" prefix is removed from the real class name of the
## object:
x2

## This is controlled by internal helper classNameForDisplay():
classNameForDisplay(x2)
classNameForDisplay(x1)

```

---

coverage-methods

*Coverage of a set of ranges*


---

## Description

For each position in the space underlying a set of ranges, counts the number of ranges that cover it.

## Usage

```

coverage(x, shift=0L, width=NULL, weight=1L, ...)

## S4 method for signature 'IntegerRanges'
coverage(x, shift=0L, width=NULL, weight=1L,
         method=c("auto", "sort", "hash", "naive"))

## S4 method for signature 'IntegerRangesList'
coverage(x, shift=0L, width=NULL, weight=1L,
         method=c("auto", "sort", "hash", "naive"))

```

## Arguments

|               |  |
|---------------|--|
| x             | A <a href="#">IntegerRanges</a> , <a href="#">Views</a> , or <a href="#">IntegerRangesList</a> object. See <code>?coverage-methods</code> in the <b>GenomicRanges</b> package for coverage methods for other objects.  |
| shift, weight | shift specifies how much each range in x should be shifted before the coverage is computed. A positive shift value will shift the corresponding range in x to the right, and a negative value to the left. NAs are not allowed.<br>weight assigns a weight to each range in x. |

- If `x` is an `IntegerRanges` or `Views` object: each of these arguments must be an integer or numeric vector parallel to `x` (will get recycled if necessary). Alternatively, each of these arguments can also be specified as a single string naming a metadata column in `x` (i.e. a column in `mcols(x)`) to be used as the `shift` (or `weight`) vector. Note that when `x` is an `IPos` object, each of these arguments can only be a single number.
- If `x` is an `IntegerRangesList` object: each of these arguments must be a numeric vector or list-like object of the same length as `x` (will get recycled if necessary). If it's a numeric vector, it's first turned into a list with `as.list`. After recycling, each list element `shift[[i]]` (or `weight[[i]]`) must be an integer or numeric vector parallel to `x[[i]]` (will get recycled if necessary).

If `weight` is an integer vector or list-like object of integer vectors, the coverage vector(s) will be returned as integer-`Rle` object(s). If it's a numeric vector or list-like object of numeric vectors, the coverage vector(s) will be returned as numeric-`Rle` object(s).

`width`

Specifies the length of the returned coverage vector(s).

- If `x` is an `IntegerRanges` object: `width` must be `NULL` (the default), an `NA`, or a single non-negative integer. After being shifted, the ranges in `x` are always clipped on the left to keep only their positive portion i.e. their intersection with the `[1, +inf)` interval. If `width` is a single non-negative integer, then they're also clipped on the right to keep only their intersection with the `[1, width]` interval. In that case coverage returns a vector of length `width`. Otherwise, it returns a vector that extends to the last position in the underlying space covered by the shifted ranges.
- If `x` is a `Views` object: Same as for a `IntegerRanges` object, except that, if `width` is `NULL` then it's treated as if it was `length(subject(x))`.
- If `x` is a `IntegerRangesList` object: `width` must be `NULL` or an integer vector parallel to `x` (i.e. with one element per list element in `x`). If not `NULL`, the vector must contain `NA`s or non-negative integers and it will get recycled to the length of `x` if necessary. If `NULL`, it is replaced with `NA` and recycled to the length of `x`. Finally `width[i]` is used to compute the coverage vector for `x[[i]]` and is therefore treated like explained above (when `x` is a `IntegerRanges` object).

`method`

If `method` is set to `"sort"`, then `x` is sorted previous to the calculation of the coverage. If `method` is set to `"hash"` or `"naive"`, then `x` is hashed directly to a vector of length `width` without previous sorting.

The `"hash"` method is faster than the `"sort"` method when `x` is large (i.e. contains a lot of ranges). When `x` is small and `width` is big (e.g. `x` represents a small set of reads aligned to a big chromosome), then `method="sort"` is faster and uses less memory than `method="hash"`.

The `"naive"` method is a slower version of the `"hash"` method that has the advantage of avoiding floating point artefacts in the no-coverage regions of the numeric-`Rle` object returned by `coverage()` when the weights are supplied as a numeric vector of type `double`. See `"FLOATING POINT ARITHMETIC CAN BRING A SURPRISE"` section in the Examples below for more information.

Using method="auto" selects between the "sort" and "hash" methods, picking the one that is predicted to be faster based on length(x) and width.

... Further arguments to be passed to or from other methods.

### Value

If x is a [IntegerRanges](#) or [Views](#) object: An integer- or numeric-[Rle](#) object depending on whether weight is an integer or numeric vector.

If x is a [IntegerRangesList](#) object: An [RleList](#) object with one coverage vector per list element in x, and with x names propagated to it. The i-th coverage vector can be either an integer- or numeric-[Rle](#) object, depending on the type of weight[[i]] (after weight has gone thru as.list and recycling, like described previously).

### Author(s)

H. Pagès and P. Aboyoun

### See Also

- [coverage-methods](#) in the [GenomicRanges](#) package for more coverage methods.
- The [slice](#) function for slicing the [Rle](#) or [RleList](#) object returned by coverage.
- [IntegerRanges](#), [IPos](#), [IntegerRangesList](#), [Rle](#), and [RleList](#) objects.

### Examples

```
## -----
## A. COVERAGE OF AN IRanges OBJECT
## -----
x <- IRanges(start=c(-2L, 6L, 9L, -4L, 1L, 0L, -6L, 10L),
             width=c( 5L, 0L, 6L,  1L, 4L, 3L,  2L,  3L))
coverage(x)
coverage(x, shift=7)
coverage(x, shift=7, width=27)
coverage(x, shift=c(-4, 2)) # 'shift' gets recycled
coverage(x, shift=c(-4, 2), width=12)
coverage(x, shift=-max(end(x)))

coverage(restrict(x, 1, 10))
coverage(reduce(x), shift=7)
coverage(gaps(shift(x, 7), start=1, end=27))

## With weights:
coverage(x, weight=as.integer(10^(0:7))) # integer-Rle
coverage(x, weight=c(2.8, -10)) # numeric-Rle, 'shift' gets recycled

## -----
## B. FLOATING POINT ARITHMETIC CAN BRING A SURPRISE
## -----
## Please be aware that rounding errors in floating point arithmetic can
## lead to some surprising results when computing a weighted coverage:
```

```

y <- IRanges(c(4, 10), c(18, 15))
w1 <- 0.958
w2 <- 1e4
cvg <- coverage(y, width=100, weight=c(w1, w2))
cvg # non-zero coverage at positions 19 to 100!

## This is an artefact of floating point arithmetic and the algorithm
## used to compute the weighted coverage. It can be observed with basic
## floating point arithmetic:
w1 + w2 - w2 - w1 # very small non-zero value!

## Note that this only happens with the "sort" and "hash" methods but
## not with the "naive" method:
coverage(y, width=100, weight=c(w1, w2), method="sort")
coverage(y, width=100, weight=c(w1, w2), method="hash")
coverage(y, width=100, weight=c(w1, w2), method="naive")

## These very small non-zero coverage values in the no-coverage regions
## of the numeric-Rle object returned by coverage() are not always
## present. But when they are, they can cause problems downstream or
## in unit tests. For example downstream code that relies on things
## like 'cvg != 0' to find regions with coverage won't work properly.
## This can be mitigated either by selecting the "naive" method (be aware
## that this can slow down things significantly) or by "cleaning" 'cvg'
## first e.g. with something like 'cvg <- round(cvg, digits)' where
## 'digits' is a carefully chosen number of digits:
cvg <- round(cvg, digits=3)

## Note that this rounding will also have the interesting side effect of
## reducing the memory footprint of the Rle object in general (because
## some runs might get merged into a single run as a consequence of the
## rounding).

## -----
## C. COVERAGE OF AN IPos OBJECT
## -----
pos_runs <- IRanges(c(1, 5, 9), c(10, 8, 15))
ipos <- IPos(pos_runs)
coverage(ipos)

## -----
## D. COVERAGE OF AN IRangesList OBJECT
## -----
x <- IRangesList(A=IRanges(3*(4:-1), width=1:3), B=IRanges(2:10, width=5))
cvg <- coverage(x)
cvg

stopifnot(identical(cvg[[1]], coverage(x[[1]])))
stopifnot(identical(cvg[[2]], coverage(x[[2]])))

coverage(x, width=c(50, 9))
coverage(x, width=c(NA, 9))
coverage(x, width=9) # 'width' gets recycled

```

```

## Each list element in 'shift' and 'weight' gets recycled to the length
## of the corresponding element in 'x'.
weight <- list(as.integer(10^(0:5)), -0.77)
cvg2 <- coverage(x, weight=weight)
cvg2 # 1st coverage vector is an integer-Rle, 2nd is a numeric-Rle

identical(mapply(coverage, x=x, weight=weight), as.list(cvg2))

## -----
## E. SOME MATHEMATICAL PROPERTIES OF THE coverage() FUNCTION
## -----

## PROPERTY 1: The coverage vector is not affected by reordering the
## input ranges:
set.seed(24)
x <- IRanges(sample(1000, 40, replace=TRUE), width=17:10)
cvg0 <- coverage(x)
stopifnot(identical(coverage(sample(x)), cvg0))

## Of course, if the ranges are shifted and/or assigned weights, then
## this doesn't hold anymore, unless the 'shift' and/or 'weight'
## arguments are reordered accordingly.

## PROPERTY 2: The coverage of the concatenation of 2 IntegerRanges
## objects 'x' and 'y' is the sum of the 2 individual coverage vectors:
y <- IRanges(sample(-20:280, 36, replace=TRUE), width=28)
stopifnot(identical(coverage(c(x, y), width=100),
                    coverage(x, width=100) + coverage(y, width=100)))

## Note that, because adding 2 vectors in R recycles the shortest to
## the length of the longest, the following is generally FALSE:
identical(coverage(c(x, y)), coverage(x) + coverage(y)) # FALSE

## It would only be TRUE if the 2 coverage vectors that we add had the
## same length, which would only happen by chance. By using the same
## 'width' value when we computed the 2 coverages previously, we made
## sure they had the same length.

## Because of properties 1 & 2, we have:
x1 <- x[c(TRUE, FALSE)] # pick up 1st, 3rd, 5th, etc... ranges
x2 <- x[c(FALSE, TRUE)] # pick up 2nd, 4th, 6th, etc... ranges
cvg1 <- coverage(x1, width=100)
cvg2 <- coverage(x2, width=100)
stopifnot(identical(coverage(x, width=100), cvg1 + cvg2))

## PROPERTY 3: Multiplying the weights by a scalar has the effect of
## multiplying the coverage vector by the same scalar:
weight <- runif(40)
cvg3 <- coverage(x, weight=weight)
stopifnot(all.equal(coverage(x, weight=-2.68 * weight), -2.68 * cvg3))

## Because of properties 1 & 2 & 3, we have:

```

```

stopifnot(identical(coverage(x, width=100, weight=c(5L, -11L)),
                    5L * cvg1 - 11L * cvg2))

## PROPERTY 4: Using the sum of 2 weight vectors produces the same
## result as using the 2 weight vectors separately and summing the
## 2 results:
weight2 <- 10 * runif(40) + 3.7
stopifnot(all.equal(coverage(x, weight=weight + weight2),
                    cvg3 + coverage(x, weight=weight2)))

## PROPERTY 5: Repeating any input range N number of times is
## equivalent to multiplying its assigned weight by N:
times <- sample(0:10L, length(x), replace=TRUE)
stopifnot(all.equal(coverage(rep(x, times), weight=rep(weight, times)),
                    coverage(x, weight=weight * times)))

## In particular, if 'weight' is not supplied:
stopifnot(identical(coverage(rep(x, times)), coverage(x, weight=times)))

## PROPERTY 6: If none of the input range actually gets clipped during
## the "shift and clip" process, then:
##
##      sum(cvg) = sum(width(x) * weight)
##
stopifnot(sum(cvg3) == sum(width(x) * weight))

## In particular, if 'weight' is not supplied:
stopifnot(sum(cvg0) == sum(width(x)))

## Note that this property is sometimes used in the context of a
## ChIP-Seq analysis to estimate "the number of reads in a peak", that
## is, the number of short reads that belong to a peak in the coverage
## vector computed from the genomic locations (a.k.a. genomic ranges)
## of the aligned reads. Because of property 6, the number of reads in
## a peak is approximately the area under the peak divided by the short
## read length.

## PROPERTY 7: If 'weight' is not supplied, then disjoining or reducing
## the ranges before calling coverage() has the effect of "shaving" the
## coverage vector at elevation 1:
table(cvg0)
shaved_cvg0 <- cvg0
runValue(shaved_cvg0) <- pmin(runValue(cvg0), 1L)
table(shaved_cvg0)

stopifnot(identical(coverage(disjoin(x)), shaved_cvg0))
stopifnot(identical(coverage(reduce(x)), shaved_cvg0))

## -----
## F. SOME SANITY CHECKS
## -----
dummy_coverage <- function(x, shift=0L, width=NULL)
{

```

```

y <- IRanges::unlist_as_integer(shift(x, shift))
if (is.null(width))
  width <- max(c(0L, y))
Rle(tabulate(y, nbins=width))
}

check_real_vs_dummy <- function(x, shift=0L, width=NULL)
{
  res1 <- coverage(x, shift=shift, width=width)
  res2 <- dummy_coverage(x, shift=shift, width=width)
  stopifnot(identical(res1, res2))
}
check_real_vs_dummy(x)
check_real_vs_dummy(x, shift=7)
check_real_vs_dummy(x, shift=7, width=27)
check_real_vs_dummy(x, shift=c(-4, 2))
check_real_vs_dummy(x, shift=c(-4, 2), width=12)
check_real_vs_dummy(x, shift=-max(end(x)))

## With a set of distinct single positions:
x3 <- IRanges(sample(50000, 20000), width=1)
stopifnot(identical(sort(start(x3)), which(coverage(x3) != 0L)))

```

---

DataFrameList-class    *List of DataFrames*

---

## Description

Represents a list of [DataFrame](#) objects. The `SplitDataFrameList` class contains the additional restriction that all the columns be of the same name and type. Internally it is stored as a list of `DataFrame` objects and extends [List](#).

## Accessors

In the following code snippets, `x` is a `DataFrameList`.

`dims(x)`: Get the two-column matrix indicating the number of rows and columns over the entire dataset.

`dimnames(x)`: Get the list of two `CharacterLists`, the first holding the rownames (possibly `NULL`) and the second the column names.

In the following code snippets, `x` is a `SplitDataFrameList`.

`commonColnames(x)`: Get the character vector of column names present in the individual `DataFrames` in `x`.

`commonColnames(x) <- value`: Set the column names of the `DataFrames` in `x`.

`columnMetadata(x)`: Get the `DataFrame` of metadata along the columns, i.e., where each column in `x` is represented by a row in the metadata. The metadata is common across all elements of `x`. Note that calling `mcols(x)` returns the metadata on the `DataFrame` elements of `x`.

`columnMetadata(x) <- value`: Set the `DataFrame` of metadata for the columns.



### Subsetting

In the following code snippets, `x` is a `SplitDataFrameList`. In general `x` follows the conventions of `SimpleList/CompressedList` with the following addition:

`x[i, j, drop]`: If matrix subsetting is used, `i` selects either the list elements or the rows within the list elements as determined by the `[]` method for `SimpleList/CompressedList`, `j` selects the columns, and `drop` is used when one column is selected and output can be coerced into an `AtomicList` or `IntegerRangesList` subclass.

`x[i, j] <- value`: If matrix subsetting is used, `i` selects either the list elements or the rows within the list elements as determined by the `[<-` method for `SimpleList/CompressedList`, `j` selects the columns and `value` is the replacement value for the selected region.

### Constructor

`DataFrameList(...)`: Concatenates the `DataFrame` objects in `...` into a new `DataFrameList`.

`SplitDataFrameList(..., compress = TRUE, cbindArgs = FALSE)`: If `cbindArgs` is `FALSE`, the `...` arguments are coerced to `DataFrame` objects and concatenated to form the result. The arguments must have the same number and names of columns. If `cbindArgs` is `TRUE`, the arguments are combined as columns. The arguments must then be the same length, with each element of an argument mapping to an element in the result. If `compress = TRUE`, returns a `CompressedSplitDataFrameList`; else returns a `SimpleSplitDataFrameList`.

### Combining

In the following code snippets, objects in `...` are of class `DataFrameList`.

`rbind(...)`: Creates a new `DataFrameList` containing the element-by-element row concatenation of the objects in `...`

`cbind(...)`: Creates a new `DataFrameList` containing the element-by-element column concatenation of the objects in `...`

### Transformation

`transform('_data', ...)`: Transforms a `SplitDataFrame` in a manner analogous to the base `transform`, where the columns are `List` objects adhering to the structure of `_data`.

### Coercion

In the following code snippets, `x` is a `DataFrameList`.

`as(from, "DataFrame")`: Coerces a `SplitDataFrameList` to a `DataFrame`, which has a column for every column in `from`, except each column is a `List` with the same structure as `from`.

`as(from, "SplitDataFrameList")`: By default, simply calls the `SplitDataFrameList` constructor on `from`. If `from` is a `List`, each element of `from` is passed as an argument to `SplitDataFrameList`, like calling `as.list` on a vector. If `from` is a `DataFrame`, each row becomes an element in the list.

`stack(x, index.var = "name")`: Unlists `x` and adds a column named `index.var` to the result, indicating the element of `x` from which each row was obtained.

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

### Author(s)

Michael Lawrence, with contributions from Aaron Lun

### See Also

[DataFrame](#)

### Examples

```
# Making a DataFrameList, which has different columns.
out <- DataFrameList(DataFrame(X=1, Y=2), DataFrame(A=1:2, B=3:4))
out[[1]]

# A more interesting SplitDataFrameList, which is guaranteed
# to have the same columns.
out <- SplitDataFrameList(DataFrame(X=1, Y=2), DataFrame(X=1:2, Y=3:4))
out[[1]]
out[, "X"]
out[, "Y"]

commonColnames(out)
commonColnames(out) <- c("x", "y")
out[[1]]

# We can also create these split objects using various split() functions:
out <- splitAsList(DataFrame(X=runif(100), Y=rpois(100, 5)),
  sample(letters, 100, replace=TRUE))
out[['a']]
```

---

extractList

*Group elements of a vector-like object into a list-like object*

---

### Description

relist and split are 2 common ways of grouping the elements of a vector-like object into a list-like object. The **IRanges** and **S4Vectors** packages define relist and split methods that operate on a [Vector](#) object and return a [List](#) object.

Because relist and split both impose restrictions on the kind of grouping that they support (e.g. every element in the input object needs to go in a group and can only go in one group), the **IRanges** package introduces the extractList generic function for performing *arbitrary* groupings.

**Usage**

```
## relist()
## -----

## S4 method for signature 'ANY,List'
relist(flesh, skeleton)

## S4 method for signature 'Vector,list'
relist(flesh, skeleton)

## extractList()
## -----

extractList(x, i)

## regroup()
## -----

regroup(x, g)
```

**Arguments**

|          |  |
|----------|--|
| flesh, x | A vector-like object.  |
| skeleton | A list-like object. Only the "shape" (i.e. element lengths) of skeleton matters. Its exact content is ignored.   |
| i        | A list-like object. Unlike for skeleton, the content here matters (see Details section below). Note that i can be a <a href="#">IntegerRanges</a> object (a particular type of list-like object), and, in that case, extractList is particularly fast (this is a common use case). |
| g        | A <a href="#">Grouping</a> or an object coercible to one. For regroup, g groups the elements of x.   |

**Details**

Like split, relist and extractList have in common that they return a list-like object where all the list elements have the same class as the original vector-like object.

Methods that return a [List](#) derivative return an object of class `relistToClass(x)`.

By default, `extractList(x, i)` is equivalent to:

```
relist(x[unlist(i)], i)
```

An exception is made when x is a data-frame-like object. In that case x is subsetted along the rows, that is, `extractList(x, i)` is equivalent to:

```
relist(x[unlist(i), ], i)
```

This is more or less how the default method is implemented, except for some optimizations when `i` is a [IntegerRanges](#) object.

`relist` and `split` can be seen as special cases of `extractList`:

```
relist(flesh, skeleton) is equivalent to
extractList(flesh, PartitioningByEnd(skeleton))
```

```
split(x, f) is equivalent to
extractList(x, split(seq_along(f), f))
```

It is good practise to use `extractList` only for cases not covered by `relist` or `split`. Whenever possible, using `relist` or `split` is preferred as they will always perform more efficiently. In addition their names carry meaning and are familiar to most R users/developers so they'll make your code easier to read/understand.

Note that the transformation performed by `relist` or `split` is always reversible (via `unlist` and `unsplit`, respectively), but not the transformation performed by `extractList` (in general).

The `regroup` function splits the elements of `unlist(x)` into a list according to the grouping `g`. Each element of `unlist(x)` inherits its group from its parent element of `x`. `regroup` is different from `relist` and `split`, because `x` is already grouped, and the goal is to combine groups.

## Value

The `relist` methods behave like `utils::relist` except that they return a [List](#) object. If `skeleton` has names, then they are propagated to the returned value.

`extractList` returns a list-like object parallel to `i` and with the same "shape" as `i` (i.e. same element lengths). If `i` has names, then they are propagated to the returned value.

All these functions return a list-like object where the list elements have the same class as `x`. [relistToClass](#) gives the exact class of the returned object.

## Author(s)

Hervé Pagès

## See Also

- The [relistToClass](#) function and [split](#) methods defined in the [S4Vectors](#) package.
- The [unlist](#) and [relist](#) functions in the [base](#) and [utils](#) packages, respectively.
- The [split](#) and [unsplit](#) functions in the [base](#) package.
- [PartitioningByEnd](#) objects. These objects are used inside [CompressedList](#) derivatives to keep track of the *partitioning* of the single vector-like object made of all the list elements concatenated together.
- [Vector](#), [List](#), [Rle](#), and [DataFrame](#) objects implemented in the [S4Vectors](#) package.
- [IntegerRanges](#) objects.

**Examples**

```
## On an Rle object:
x <- Rle(101:105, 6:2)
i <- IRanges(6:10, 16:12, names=letters[1:5])
extractList(x, i)

## On a DataFrame object:
df <- DataFrame(X=x, Y=LETTERS[1:20])
extractList(df, i)
```

---

extractListFragments *Extract list fragments from a list-like object*

---

**Description**

Utilities for extracting *list fragments* from a list-like object.

**Usage**

```
extractListFragments(x, aranges, use.mcols=FALSE,
                    msg.if.incompatible=INCOMPATIBLE_ARANGES_MSG)

equisplit(x, nchunk, chunksize, use.mcols=FALSE)
```

**Arguments**

|                     |  |
|---------------------|--|
| x                   | The list-like object from which to extract the list fragments.<br>Can be any <a href="#">List</a> derivative for extractListFragments. Can also be an ordinary list if extractListFragments is called with use.mcols=TRUE.<br>Can be any <a href="#">List</a> derivative that supports relist() for equisplit.   |
| aranges             | An <a href="#">IntegerRanges</a> derivative containing the <i>absolute ranges</i> (i.e. the ranges along unlist(x)) of the list fragments to extract.<br>The ranges in aranges must be compatible with the <i>cumulated length</i> of all the list elements in x, that is, start(aranges) and end(aranges) must be >= 1 and <= sum(elementNROWS(x)), respectively.<br>Also please note that only <a href="#">IntegerRanges</a> objects that are disjoint and sorted are supported at the moment. |
| use.mcols           | Whether to propagate the metadata columns on x (if any) or not.<br>Must be TRUE or FALSE (the default). If set to FALSE, instead of having the metadata columns propagated from x, the object returned by extractListFragments has metadata columns revmap and revmap2, and the object returned by equisplit has metadata column revmap. Note that this is the default.  |
| msg.if.incompatible | The error message to use if aranges is not compatible with the <i>cumulated length</i> of all the list elements in x.  |

|           |  |
|-----------|--|
| nchunk    | The number of chunks. Must be a single positive integer.                                 |
| chunksize | The size of the chunks (last chunk might be smaller). Must be a single positive integer. |

### Details

A *list fragment* of list-like object *x* is a window in one of its list elements.

`extractListFragments` is a low-level utility that extracts list fragments from list-like object *x* according to the absolute ranges in `aranges`.

`equisplit` fragments and splits list-like object *x* into a specified number of partitions with equal (total) width. This is useful for instance to ensure balanced loading of workers in parallel evaluation. For example, if *x* is a `GRanges` object, each partition is also a `GRanges` object and the set of all partitions is returned as a `GRangesList` object.

### Value

An object of the same class as *x* for `extractListFragments`.

An object of class `relistToClass(x)` for `equisplit`.

### Author(s)

Hervé Pagès

### See Also

- `IRanges` and `IRangesList` objects.
- `Partitioning` objects.
- `IntegerList` objects.
- `breakInChunks` from breaking a vector-like object in chunks.
- `GRanges` and `GRangesList` objects defined in the `GenomicRanges` package.
- `List` objects defined in the `S4Vectors` package.
- `intra-range-methods` and `inter-range-methods` for *intra range* and *inter range* transformations.

### Examples

```
## -----
## A. extractListFragments()
## -----

x <- IntegerList(a=101:109, b=5:-5)
x

aranges <- IRanges(start=c(2, 4, 8, 17, 17), end=c(3, 6, 14, 16, 19))
aranges
extractListFragments(x, aranges)

x2 <- IRanges(c(1, 101, 1001, 10001), width=c(10, 5, 0, 12),
```

```

        names=letters[1:4])
mcols(x2)$label <- LETTERS[1:4]
x2

aranges <- IRanges(start=13, end=20)
extractListFragments(x2, aranges)
extractListFragments(x2, aranges, use.mcols=TRUE)

aranges2 <- PartitioningByWidth(c(3, 9, 13, 0, 2))
extractListFragments(x2, aranges2)
extractListFragments(x2, aranges2, use.mcols=TRUE)

x2b <- as(x2, "IntegerList")
extractListFragments(x2b, aranges2)

x2c <- as.list(x2b)
extractListFragments(x2c, aranges2, use.mcols=TRUE)

## -----
## B. equisplit()
## -----

## equisplit() first calls breakInChunks() internally to create a
## PartitioningByWidth object that contains the absolute ranges of the
## chunks, then calls extractListFragments() on it 'x' to extract the
## fragments of 'x' that correspond to these absolute ranges. Finally
## the IRanges object returned by extractListFragments() is split into
## an IRangesList object where each list element corresponds to a chunk.
equisplit(x2, nchunk=2)
equisplit(x2, nchunk=2, use.mcols=TRUE)

equisplit(x2, chunksize=5)

library(GenomicRanges)
gr <- GRanges(c("chr1", "chr2"), IRanges(1, c(100, 1e5)))
equisplit(gr, nchunk=2)
equisplit(gr, nchunk=1000)

## -----
## C. ADVANCED extractListFragments() EXAMPLES
## -----

## == D1. Fragment list-like object into length 1 fragments ==

## First we construct a Partitioning object where all the partitions
## have a width of 1:
x2_cumlen <- nobj(PartitioningByWidth(x2)) # Equivalent to
                                           # length(unlist(x2)) except
                                           # that it doesn't unlist 'x2'
                                           # so is much more efficient.
aranges1 <- PartitioningByEnd(seq_len(x2_cumlen))
aranges1

```

```

## Then we use it to fragment 'x2':
extractListFragments(x2, aranges1)
extractListFragments(x2b, aranges1)
extractListFragments(x2c, aranges1, use.mcols=TRUE)

## == D2. Fragment a Partitioning object ==

partitioning2 <- PartitioningByEnd(x2b) # same as PartitioningByEnd(x2)
extractListFragments(partitioning2, aranges2)

## Note that when the 1st arg is a Partitioning derivative, then
## swapping the 1st and 2nd elements in the call to extractListFragments()
## doesn't change the returned partitioning:
extractListFragments(aranges2, partitioning2)

## -----
## D. SANITY CHECKS
## -----

## If 'aranges' is 'PartitioningByEnd(x)' or 'PartitioningByWidth(x)'
## and 'x' has no zero-length list elements, then
## 'extractListFragments(x, aranges, use.mcols=TRUE)' is a no-op.
check_no_ops <- function(x) {
  aranges <- PartitioningByEnd(x)
  stopifnot(identical(
    extractListFragments(x, aranges, use.mcols=TRUE), x
  ))
  aranges <- PartitioningByWidth(x)
  stopifnot(identical(
    extractListFragments(x, aranges, use.mcols=TRUE), x
  ))
}

check_no_ops(x2[lengths(x2) != 0])
check_no_ops(x2b[lengths(x2b) != 0])
check_no_ops(x2c[lengths(x2c) != 0])
check_no_ops(gr)

```

---

findOverlaps-methods *Finding overlapping ranges*

---

## Description

Various methods for finding/counting interval overlaps between two "range-based" objects: a query and a subject.

NOTE: This man page describes the methods that operate on [IntegerRanges](#) and [IntegerRanges-List](#) derivatives. See `?`findOverlaps, GenomicRanges, GenomicRanges-method`` in the **GenomicRanges** package for methods that operate on [GenomicRanges](#) or [GRangesList](#) objects.



**Usage**

```

findOverlaps(query, subject, maxgap=-1L, minoverlap=0L,
             type=c("any", "start", "end", "within", "equal"),
             select=c("all", "first", "last", "arbitrary"),
             ...)

countOverlaps(query, subject, maxgap=-1L, minoverlap=0L,
              type=c("any", "start", "end", "within", "equal"),
              ...)

overlapsAny(query, subject, maxgap=-1L, minoverlap=0L,
            type=c("any", "start", "end", "within", "equal"),
            ...)
query %over% subject
query %within% subject
query %outside% subject

subsetByOverlaps(x, ranges, maxgap=-1L, minoverlap=0L,
                 type=c("any", "start", "end", "within", "equal"),
                 invert=FALSE,
                 ...)

overlapsRanges(query, subject, hits=NULL, ...)

poverlaps(query, subject, maxgap = 0L, minoverlap = 1L,
           type = c("any", "start", "end", "within", "equal"),
           ...)

mergeByOverlaps(query, subject, ...)

findOverlapPairs(query, subject, ...)

```

**Arguments**

query, subject, x, ranges

Each of them can be an [IntegerRanges](#) (e.g. [IRanges](#), [Views](#)) or [IntegerRangesList](#) (e.g. [IRangesList](#), [ViewsList](#)) derivative. In addition, if subject or ranges is an [IntegerRanges](#) object, query or x can be an integer vector to be converted to length-one ranges.

If query (or x) is an [IntegerRangesList](#) object, then subject (or ranges) must also be an [IntegerRangesList](#) object.

If both arguments are list-like objects with names, each list element from the 2nd argument is paired with the list element from the 1st argument with the matching name, if any. Otherwise, list elements are paired by position. The overlap is then computed between the pairs as described below.

If subject is omitted, query is queried against itself. In this case, and only this case, the `drop.self` and `drop.redundant` arguments are allowed. By default, the result will contain hits for each range against itself, and if there is a hit from

|            |  |
|------------|--|
|            | <p>A to B, there is also a hit for B to A. If <code>drop.self</code> is TRUE, all self matches are dropped. If <code>drop.redundant</code> is TRUE, only one of A-&gt;B and B-&gt;A is returned.</p>   |
| maxgap     | <p>A single integer <math>\geq -1</math>.</p> <p>If type is set to "any", maxgap is interpreted as the maximum <i>gap</i> that is allowed between 2 ranges for the ranges to be considered as overlapping. The <i>gap</i> between 2 ranges is the number of positions that separate them. The <i>gap</i> between 2 adjacent ranges is 0. By convention when one range has its start or end strictly inside the other (i.e. non-disjoint ranges), the <i>gap</i> is considered to be -1.</p> <p>If type is set to anything else, maxgap has a special meaning that depends on the particular type. See type below for more information.</p>   |
| minoverlap | <p>A single non-negative integer.</p> <p>Only ranges with a minimum of minoverlap overlapping positions are considered to be overlapping.</p> <p>When type is "any", at least one of maxgap and minoverlap must be set to its default value.</p>   |
| type       | <p>By default, any overlap is accepted. By specifying the type parameter, one can select for specific types of overlap. The types correspond to operations in Allen's Interval Algebra (see references). If type is start or end, the intervals are required to have matching starts or ends, respectively. Specifying equal as the type returns the intersection of the start and end matches. If type is within, the query interval must be wholly contained within the subject interval. Note that all matches must additionally satisfy the minoverlap constraint described above.</p> <p>The maxgap parameter has special meaning with the special overlap types. For start, end, and equal, it specifies the maximum difference in the starts, ends or both, respectively. For within, it is the maximum amount by which the subject may be wider than the query. If maxgap is set to -1 (the default), it's replaced internally by 0.</p>                             |
| select     | <p>If query is an <a href="#">IntegerRanges</a> derivative: When select is "all" (the default), the results are returned as a <a href="#">Hits</a> object. Otherwise the returned value is an integer vector <i>parallel</i> 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.</p> <p>If query is an <a href="#">IntegerRangesList</a> derivative: When select is "all" (the default), the results are returned as a <a href="#">HitsList</a> object. Otherwise the returned value depends on the drop argument. When <code>select != "all" &amp;&amp; !drop</code>, an <a href="#">IntegerList</a> is returned, where each element of the result corresponds to a space in query. When <code>select != "all" &amp;&amp; drop</code>, an integer vector is returned containing indices that are offset to align with the unlisted query.</p> |
| invert     | <p>If TRUE, keep only the ranges in x that do <i>not</i> overlap ranges.</p>   |
| hits       | <p>The <a href="#">Hits</a> or <a href="#">HitsList</a> object returned by <code>findOverlaps</code>, or NULL. If NULL then hits is computed by calling <code>findOverlaps(query, subject, ...)</code> internally (the extra arguments passed to <code>overlapsRanges</code> are passed to <code>findOverlaps</code>).</p>   |
| ...        | <p>Further arguments to be passed to or from other methods:</p>  |

- `drop`: Supported only when `query` is an `IntegerRangesList` derivative. `FALSE` by default. See `select` argument above for the details.
- `drop.self`, `drop.redundant`: When `subject` is omitted, the `drop.self` and `drop.redundant` arguments (both `FALSE` by default) are allowed. See `query` and `subject` arguments above for the details.

## Details

A common type of query that arises when working with intervals is finding which intervals in one set overlap those in another.

The simplest approach is to call the `findOverlaps` function on a `IntegerRanges` or other object with range information (aka "range-based object").

## Value

For `findOverlaps`: see `select` argument above.

For `countOverlaps`: the overlap hit count for each range in `query` using the specified `findOverlaps` parameters. For `IntegerRangesList` objects, it returns an `IntegerList` object.

`overlapsAny` finds the ranges in `query` that overlap any of the ranges in `subject`. For `IntegerRanges` derivatives, it returns a logical vector of length equal to the number of ranges in `query`. For `IntegerRangesList` derivatives, it returns a `LogicalList` object where each element of the result corresponds to a space in `query`.

`%over%` and `%within%` are convenience wrappers for the 2 most common use cases. Currently defined as ``%over%` <- function(query, subject) overlapsAny(query, subject)` and ``%within%` <- function(query, subject) overlapsAny(query, subject, type="within")`. `%outside%` is simply the inverse of `%over%`.

`subsetByOverlaps` returns the subset of `x` that has an overlap hit with a range in `ranges` using the specified `findOverlaps` parameters.

When `hits` is a `Hits` (or `HitsList`) object, `overlapsRanges(query, subject, hits)` returns a `IntegerRanges` (or `IntegerRangesList`) object of the *same shape* as `hits` holding the regions of intersection between the overlapping ranges in objects `query` and `subject`, which should be the same `query` and `subject` used in the call to `findOverlaps` that generated `hits`. *Same shape* means same length when `hits` is a `Hits` object, and same length and same `elementNROWS` when `hits` is a `HitsList` object.

`poverlaps` compares `query` and `subject` in parallel (like e.g., `pmin`) and returns a logical vector indicating whether each pair of ranges overlaps. Integer vectors are treated as width-one ranges.

`mergeByOverlaps` computes the overlap between `query` and `subject` according to the arguments in `...`. It then extracts the corresponding hits from each object and returns a `DataFrame` containing one column for the `query` and one for the `subject`, as well as any `mcols` that were present on either object. The `query` and `subject` columns are named by quoting and deparsing the corresponding argument.

`findOverlapPairs` is like `mergeByOverlaps`, except it returns a formal `Pairs` object that provides useful downstream conveniences, such as finding the intersection of the overlapping ranges with `pintersect`.

**Author(s)**

Michael Lawrence and Hervé Pagès

**References**

Allen's Interval Algebra: James F. Allen: Maintaining knowledge about temporal intervals. In: Communications of the ACM. 26/11/1983. ACM Press. S. 832-843, ISSN 0001-0782

**See Also**

- [Hits](#) and [HitsList](#) objects in the **S4Vectors** package for representing a set of hits between 2 vector-like or list-like objects.
- [findOverlaps](#), [GenomicRanges](#), [GenomicRanges-method](#) in the **GenomicRanges** package for methods that operate on [GRanges](#) or [GRangesList](#) objects.
- The [NCList](#) class and constructor.
- The [IntegerRanges](#), [Views](#), [IntegerRangesList](#), and [ViewsList](#) classes.
- The [IntegerList](#) and [LogicalList](#) classes.

**Examples**

```
## -----
## findOverlaps()
## -----

query <- IRanges(c(1, 4, 9), c(5, 7, 10))
subject <- IRanges(c(2, 2, 10), c(2, 3, 12))

findOverlaps(query, subject)

## at most one hit per query
findOverlaps(query, subject, select="first")
findOverlaps(query, subject, select="last")
findOverlaps(query, subject, select="arbitrary")

## including adjacent ranges in the result
findOverlaps(query, subject, maxgap=0L)

query <- IRanges(c(1, 4, 9), c(5, 7, 10))
subject <- IRanges(c(2, 2), c(5, 4))

## one IRanges object with itself
findOverlaps(query)

## single points as query
subject <- IRanges(c(1, 6, 13), c(4, 9, 14))
findOverlaps(c(3L, 7L, 10L), subject, select="first")

## special overlap types
query <- IRanges(c(1, 5, 3, 4), width=c(2, 2, 4, 6))
subject <- IRanges(c(1, 3, 5, 6), width=c(4, 4, 5, 4))
```

```

findOverlaps(query, subject, type="start")
findOverlaps(query, subject, type="start", maxgap=1L)
findOverlaps(query, subject, type="end", select="first")
ov <- findOverlaps(query, subject, type="within", maxgap=1L)
ov

## Using pairs to find intersection of overlapping ranges
hits <- findOverlaps(query, subject)
p <- Pairs(query, subject, hits=hits)
pintersect(p)

## Shortcut
p <- findOverlapPairs(query, subject)
pintersect(p)

## -----
## overlapsAny()
## -----

overlapsAny(query, subject, type="start")
overlapsAny(query, subject, type="end")
query %over% subject # same as overlapsAny(query, subject)
query %within% subject # same as overlapsAny(query, subject,
#                               type="within")

## -----
## overlapsRanges()
## -----

## Extract the regions of intersection between the overlapping ranges:
overlapsRanges(query, subject, ov)

## -----
## Using IntegerRangesList objects
## -----

query <- IRanges(c(1, 4, 9), c(5, 7, 10))
qpartition <- factor(c("a","a","b"))
qlist <- split(query, qpartition)

subject <- IRanges(c(2, 2, 10), c(2, 3, 12))
spartition <- factor(c("a","a","b"))
slist <- split(subject, spartition)

## at most one hit per query
findOverlaps(qlist, slist, select="first")
findOverlaps(qlist, slist, select="last")
findOverlaps(qlist, slist, select="arbitrary")

query <- IRanges(c(1, 5, 3, 4), width=c(2, 2, 4, 6))
qpartition <- factor(c("a","a","b","b"))
qlist <- split(query, qpartition)

```

```

subject <- IRanges(c(1, 3, 5, 6), width=c(4, 4, 5, 4))
spartition <- factor(c("a","a","b","b"))
slist <- split(subject, spartition)

overlapsAny(qlist, slist, type="start")
overlapsAny(qlist, slist, type="end")
qlist

subsetByOverlaps(qlist, slist)
countOverlaps(qlist, slist)

```

---

Grouping-class

*Grouping objects*


---

### Description

We call *grouping* an arbitrary mapping from a collection of NO objects to a collection of NG groups, or, more formally, a bipartite graph between integer sets [1, NO] and [1, NG]. Objects mapped to a given group are said to belong to, or to be assigned to, or to be in that group. Additionally, the objects in each group are ordered. So for example the 2 following groupings are considered different:

```

Grouping 1: NG = 3, NO = 5
      group  objects
      1 : 4, 2
      2 :
      3 : 4

```

```

Grouping 2: NG = 3, NO = 5
      group  objects
      1 : 2, 4
      2 :
      3 : 4

```

There are no restriction on the mapping e.g. any object can be mapped to 0, 1, or more groups, and can be mapped twice to the same group. Also some or all the groups can be empty.

The Grouping class is a virtual class that formalizes the most general kind of grouping. More specific groupings (e.g. *many-to-one groupings* or *block-groupings*) are formalized via specific Grouping subclasses.

This man page documents the core Grouping API, and 3 important Grouping subclasses: Many-ToOneGrouping, GroupingRanges, and Partitioning (the last one deriving from the 2 first).

### The core Grouping API

Let's give a formal description of the core Grouping API:

Groups  $G_i$  are indexed from 1 to NG ( $1 \leq i \leq NG$ ).

Objects  $O_j$  are indexed from 1 to NO ( $1 \leq j \leq \text{NO}$ ).

Given that empty groups are allowed, NG can be greater than NO.

If  $x$  is a Grouping object:

`length(x)`: Returns the number of groups (NG).

`names(x)`: Returns the names of the groups.

`nobj(x)`: Returns the number of objects (NO).

Going from groups to objects:

`x[[i]]`: Returns the indices of the objects (the  $j$ 's) that belong to  $G_i$ . This provides the mapping from groups to objects.

`grouplengths(x, i=NULL)`: Returns the number of objects in  $G_i$ . Works in a vectorized fashion (unlike `x[[i]]`). `grouplengths(x)` is equivalent to `grouplengths(x, seq_len(length(x)))`.

If  $i$  is not NULL, `grouplengths(x, i)` is equivalent to `sapply(i, function(ii) length(x[[ii]]))`.

Note to developers: Given that `length`, `names` and `[[` are expected to work on any Grouping object, those objects can be seen as [List](#) objects. More precisely, the Grouping class actually extends the [IntegerList](#) class. In particular, many other "list" operations like `as.list`, `elementNROWS`, and `unlist`, etc... should work out-of-the-box on any Grouping object.

### ManyToOneGrouping objects

The ManyToOneGrouping class is a virtual subclass of Grouping for representing *many-to-one groupings*, that is, groupings where each object in the original collection of objects belongs to exactly one group.

The grouping of an empty collection of objects in an arbitrary number of (necessarily empty) groups is a valid ManyToOneGrouping object.

Note that, for a ManyToOneGrouping object, if NG is 0 then NO must also be 0.

The ManyToOneGrouping API extends the core Grouping API by adding a couple more operations for going from groups to objects:

`members(x, i)`: Equivalent to `x[[i]]` if  $i$  is a single integer. Otherwise, if  $i$  is an integer vector of arbitrary length, it's equivalent to `sort(unlist(sapply(i, function(ii) x[[ii]]))`.

`vmembers(x, L)`: A version of `members` that works in a vectorized fashion with respect to the  $L$  argument ( $L$  must be a list of integer vectors). Returns `lapply(L, function(i) members(x, i))`.

And also by adding operations for going from objects to groups:

`togroup(x, j=NULL)`: Returns the index  $i$  of the group that  $O_j$  belongs to. This provides the mapping from objects to groups (many-to-one mapping). Works in a vectorized fashion. `togroup(x)` is equivalent to `togroup(x, seq_len(nobj(x)))`: both return the entire mapping in an integer vector of length NO. If  $j$  is not NULL, `togroup(x, j)` is equivalent to `y <- togroup(x); y[j]`.

`togrouplength(x, j=NULL)`: Returns the number of objects that belong to the same group as  $O_j$  (including  $O_j$  itself). Equivalent to `grouplengths(x, togroup(x, j))`.

One important property of any ManyToOneGrouping object  $x$  is that `unlist(as.list(x))` is always a permutation of `seq_len(nobj(x))`. This is a direct consequence of the fact that every object in the grouping belongs to one group and only one.

## 2 ManyToOneGrouping concrete subclasses: H2LGrouping, Dups and SimpleManyToOneGrouping

[DOCUMENT ME]

Constructors:

H2LGrouping(high2low=integer()): [DOCUMENT ME]

Dups(high2low=integer()): [DOCUMENT ME]

ManyToOneGrouping(..., compress=TRUE): Collect ... into a ManyToOneGrouping. The arguments will be coerced to integer vectors and combined into a list, unless there is a single list argument, which is taken to be an integer list. The resulting integer list should have a structure analogous to that of Grouping itself: each element represents a group in terms of the subscripts of the members. If compress is TRUE, the representation uses a CompressedList, otherwise a SimpleList.

### ManyToManyGrouping objects

The ManyToManyGrouping class is a virtual subclass of Grouping for representing *many-to-many groupings*, that is, groupings where each object in the original collection of objects belongs to any number of groups.

Constructors:

ManyToManyGrouping(x, compress=TRUE): Collect ... into a ManyToManyGrouping. The arguments will be coerced to integer vectors and combined into a list, unless there is a single list argument, which is taken to be an integer list. The resulting integer list should have a structure analogous to that of Grouping itself: each element represents a group in terms of the subscripts of the members. If compress is TRUE, the representation uses a CompressedList, otherwise a SimpleList.

### GroupingRanges objects

The GroupingRanges class is a virtual subclass of Grouping for representing *block-groupings*, that is, groupings where each group is a block of adjacent elements in the original collection of objects. GroupingRanges objects support the IntegerRanges API (e.g. [start](#), [end](#), [width](#), etc...) in addition to the Grouping API. See [?IntegerRanges](#) for a description of the [IntegerRanges](#) API.

### Partitioning objects

The Partitioning class is a virtual subclass of GroupingRanges for representing *block-groupings* where the blocks fully cover the original collection of objects and don't overlap. Since this makes them *many-to-one groupings*, the Partitioning class is also a subclass of ManyToOneGrouping. An additional constraint of Partitioning objects is that the blocks must be ordered by ascending position with respect to the original collection of objects.

The Partitioning virtual class itself has 3 concrete subclasses: PartitioningByEnd (only stores the end of the groups, allowing fast mapping from groups to objects), and PartitioningByWidth (only stores the width of the groups), and PartitioningMap which contains PartitioningByEnd and two additional slots to re-order and re-list the object to a related mapping.

Constructors:



`PartitioningByEnd(x=integer(), NG=NULL, names=NULL)`: `x` must be either a list-like object or a sorted integer vector. `NG` must be either `NULL` or a single integer. `names` must be either `NULL` or a character vector of length `NG` (if supplied) or `length(x)` (if `NG` is not supplied).

Returns the following `PartitioningByEnd` object `y`:

- If `x` is a list-like object, then the returned object `y` has the same length as `x` and is such that `width(y)` is identical to `elementNROWS(x)`.
- If `x` is an integer vector and `NG` is not supplied, then `x` must be sorted (checked) and contain non-NA non-negative values (NOT checked). The returned object `y` has the same length as `x` and is such that `end(y)` is identical to `x`.
- If `x` is an integer vector and `NG` is supplied, then `x` must be sorted (checked) and contain values  $\geq 1$  and  $\leq NG$  (checked). The returned object `y` is of length `NG` and is such that `togroup(y)` is identical to `x`.

If the `names` argument is supplied, it is used to name the partitions.

`PartitioningByWidth(x=integer(), NG=NULL, names=NULL)`: `x` must be either a list-like object or an integer vector. `NG` must be either `NULL` or a single integer. `names` must be either `NULL` or a character vector of length `NG` (if supplied) or `length(x)` (if `NG` is not supplied).

Returns the following `PartitioningByWidth` object `y`:

- If `x` is a list-like object, then the returned object `y` has the same length as `x` and is such that `width(y)` is identical to `elementNROWS(x)`.
- If `x` is an integer vector and `NG` is not supplied, then `x` must contain non-NA non-negative values (NOT checked). The returned object `y` has the same length as `x` and is such that `width(y)` is identical to `x`.
- If `x` is an integer vector and `NG` is supplied, then `x` must be sorted (checked) and contain values  $\geq 1$  and  $\leq NG$  (checked). The returned object `y` is of length `NG` and is such that `togroup(y)` is identical to `x`.

If the `names` argument is supplied, it is used to name the partitions.

`PartitioningMap(x=integer(), mapOrder=integer())`: `x` is a list-like object or a sorted integer vector used to construct a `PartitioningByEnd` object. `mapOrder` numeric vector of the mapped order.

Returns a `PartitioningMap` object.

Note that these constructors don't recycle their `names` argument (to remain consistent with what `names<-`` does on standard vectors).

### Coercions to Grouping objects

These types can be coerced to different derivatives of Grouping objects:

**factor** Analogous to calling `split` with the `factor`. Returns a `ManyToOneGrouping` if there are no NAs, otherwise a `ManyToManyGrouping`. If a `factor` is explicitly converted to a `ManytoOneGrouping`, then any NAs are placed in the last group.

**vector** A vector is effectively treated as a `factor`, but more efficiently. The order of the groups is not defined.

**FactorList** Same as the `factor` coercion, except using the interaction of every `factor` in the list. The interaction has an NA wherever any of the elements has one. Every element must have the same length.

**DataFrame** Effectively converted via a FactorList by coercing each column to a factor.

**grouping** Equivalent Grouping representation of the base R `grouping` object.

**Hits** Returns roughly the same object as `as(x, "List")`, except it is a ManyToManyGrouping, i.e., it knows the number of right nodes.

### Author(s)

Hervé Pagès, Michael Lawrence

### See Also

[IntegerList-class](#), [IntegerRanges-class](#), [IRanges-class](#), [successiveIRanges](#), [cumsum](#), [diff](#)

### Examples

```
showClass("Grouping") # shows (some of) the known subclasses

## -----
## A. H2LGrouping OBJECTS
## -----
high2low <- c(NA, NA, 2, 2, NA, NA, NA, 6, NA, 1, 2, NA, 6, NA, NA, 2)
h2l <- H2LGrouping(high2low)
h2l

## The core Grouping API:
length(h2l)
nobj(h2l) # same as 'length(h2l)' for H2LGrouping objects
h2l[[1]]
h2l[[2]]
h2l[[3]]
h2l[[4]]
h2l[[5]]
grouplengths(h2l) # same as 'unname(sapply(h2l, length))'
grouplengths(h2l, 5:2)
members(h2l, 5:2) # all the members are put together and sorted
togroup(h2l)
togroup(h2l, 5:2)
togrouplength(h2l) # same as 'grouplengths(h2l, togroup(h2l))'
togrouplength(h2l, 5:2)

## The List API:
as.list(h2l)
sapply(h2l, length)

## -----
## B. Dups OBJECTS
## -----
dups1 <- as(h2l, "Dups")
dups1
duplicated(dups1) # same as 'duplicated(ttogroup(dups1))'

### The purpose of a Dups object is to describe the groups of duplicated
```

```

### elements in a vector-like object:
x <- c(2, 77, 4, 4, 7, 2, 8, 8, 4, 99)
x_high2low <- high2low(x)
x_high2low # same length as 'x'
dups2 <- Dups(x_high2low)
dups2
togroup(dups2)
duplicated(dups2)
togrouplength(dups2) # frequency for each element
table(x)

## -----
## C. Partitioning OBJECTS
## -----

pbe1 <- PartitioningByEnd(c(4, 7, 7, 8, 15), names=LETTERS[1:5])
pbe1 # the 3rd partition is empty

## The core Grouping API:
length(pbe1)
nobj(pbe1)
pbe1[[1]]
pbe1[[2]]
pbe1[[3]]
grouplengths(pbe1) # same as 'unname(sapply(pbe1, length))'
# and 'width(pbe1)'

togroup(pbe1)
togrouplength(pbe1) # same as 'grouplengths(pbe1, togroup(pbe1))'
names(pbe1)

## The IntegerRanges core API:
start(pbe1)
end(pbe1)
width(pbe1)

## The List API:
as.list(pbe1)
sapply(pbe1, length)

## Replacing the names:
names(pbe1)[3] <- "empty partition"
pbe1

## Coercion to an IRanges object:
as(pbe1, "IRanges")

## Other examples:
PartitioningByEnd(c(0, 0, 19), names=LETTERS[1:3])
PartitioningByEnd() # no partition
PartitioningByEnd(integer(9)) # all partitions are empty
x <- c(1L, 5L, 5L, 6L, 8L)
pbe2 <- PartitioningByEnd(x, NG=10L)
stopifnot(identical(togroup(pbe2), x))
pbw2 <- PartitioningByWidth(x, NG=10L)

```

```

stopifnot(identical(togroup(pbw2), x))

## -----
## D. RELATIONSHIP BETWEEN Partitioning OBJECTS AND successiveIRanges()
## -----
mywidths <- c(4, 3, 0, 1, 7)

## The 3 following calls produce the same ranges:
ir <- successiveIRanges(mywidths) # IRanges instance.
pbe <- PartitioningByEnd(cumsum(mywidths)) # PartitioningByEnd instance.
pbw <- PartitioningByWidth(mywidths) # PartitioningByWidth instance.
stopifnot(identical(as(ir, "PartitioningByEnd"), pbe))
stopifnot(identical(as(ir, "PartitioningByWidth"), pbw))

```

---

Hits-class-leftovers *Examples of basic manipulation of Hits objects*

---

## Description

IMPORTANT NOTE - 4/29/2014: This man page is being refactored. Most of the things that used to be documented here have been moved to the man page for [Hits](#) objects located in the **S4Vectors** package.

## Details

The `as.data.frame` method coerces a `Hits` object to a two column data frame with one row for each hit, where the value in the first column is the index of an element in the query and the value in the second column is the index of an element in the subject.

## Coercion

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

`as.list(x)`: Coerces `x` to a list of integers, grouping the the right node hits for each left node.

`as(x, "List")`: Analogous to `as.list(x)`.

`as(x, "Grouping")`: Returns roughly the same object as `as(x, "List")`, except it is a `Many-ToManyGrouping`, i.e., it knows the number of right nodes.

## See Also

The [Hits](#) class defined and documented in the **S4Vectors** package.

**Examples**

```

query <- IRanges(c(1, 4, 9), c(5, 7, 10))
subject <- IRanges(c(2, 2, 10), c(2, 3, 12))
hits <- findOverlaps(query, subject)

as.matrix(hits)
as.data.frame(hits)

as.table(hits) # hits per query
as.table(t(hits)) # hits per subject

## Turn a Hits object into an IntegerList object with one list element
## per element in the original query.
as(hits, "IntegerList")
as(hits, "List") # same as as(hits, "IntegerList")

## Turn a Hits object into a PartitioningByEnd object that describes
## the grouping of hits by query.
as(hits, "PartitioningByEnd")
as(hits, "Partitioning") # same as as(hits, "PartitioningByEnd")

## -----
## remapHits()
## -----

hits2 <- remapHits(hits,
                  Rnodes.remapping=factor(c("e", "e", "d"), letters[1:5]))
hits2

hits3 <- remapHits(hits,
                  Rnodes.remapping=c(5, 5, 4), new.nRnode=5)
hits3
stopifnot(identical(hits2, hits3))

```

---

IntegerRanges-class    *IntegerRanges objects*

---

**Description**

The IntegerRanges *virtual* class is a general container for storing ranges on the space of integers.

**Details**

TODO

---

 IntegerRangesList-class

*IntegerRangesList objects*


---

### Description

The `IntegerRangesList` *virtual* class is a general container for storing a list of `IntegerRanges` objects. Most users are probably more interested in the `IRangesList` container, an `IntegerRangesList` derivative for storing a list of `IRanges` objects.

### Details

The place of `IntegerRangesList` in the *Vector class hierarchy*:



Note that the *Vector class hierarchy* has many more classes. In particular `Vector`, `List`, `RangesList`, and `IntegerRangesList` have other subclasses not shown here.

### Accessors

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

All of these accessors collapse over the spaces:

`start(x)`, `start(x) <- value`: Get or set the starts of the ranges. When setting the starts, `value` can be an integer vector of length `sum(elementNROWS(x))` or an `IntegerList` object of length `length(x)` and names `names(x)`.

`end(x)`, `end(x) <- value`: Get or set the ends of the ranges. When setting the ends, `value` can be an integer vector of length `sum(elementNROWS(x))` or an `IntegerList` object of length `length(x)` and names `names(x)`.

`width(x)`, `width(x) <- value`: Get or set the widths of the ranges. When setting the widths, `value` can be an integer vector of length `sum(elementNROWS(x))` or an `IntegerList` object of length `length(x)` and names `names(x)`.

`space(x)`: Gets the spaces of the ranges as a character vector. This is equivalent to `names(x)`, except each name is repeated according to the length of its element.

### Coercion

In the code snippet below, `x` is an `IntegerRangesList` object.

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

In the following code snippet, `from` is something other than a `IntegerRangesList`:

```
as(from, "IntegerRangesList"): When from is a IntegerRanges, analogous to as.list on a
  vector.
```

### Arithmetic Operations

Any arithmetic operation, such as `x + y`, `x * y`, etc, where `x` is a `IntegerRangesList`, is performed identically on each element. Currently, `IntegerRanges` supports only the `*` operator, which zooms the ranges by a numeric factor.

### Author(s)

M. Lawrence & H. Pagès

### See Also

- [IRangesList](#) objects.
- [IntegerRanges](#) and [IRanges](#) objects.

### Examples

```
## -----
## Basic manipulation
## -----

range1 <- IRanges(start=c(1, 2, 3), end=c(5, 2, 8))
range2 <- IRanges(start=c(15, 45, 20, 1), end=c(15, 100, 80, 5))
named <- IRangesList(one = range1, two = range2)
length(named) # 2
start(named) # same as start(c(range1, range2))
```

```

names(named) # "one" and "two"
named[[1]] # range1
unnamed <- IRangesList(range1, range2)
names(unnamed) # NULL

# edit the width of the ranges in the list
edited <- named
width(edited) <- rep(c(3,2), elementNROWS(named))
edited

# same as list(range1, range2)
as.list(IRangesList(range1, range2))

# coerce to data.frame
as.data.frame(named)

IRangesList(range1, range2)

## zoom in 2X
collection <- IRangesList(one = range1, range2)
collection * 2

```

---

inter-range-methods    *Inter range transformations of an IntegerRanges, Views, IntegerRangesList, or MaskCollection object*

---

## Description

Range-based transformations are grouped in 2 categories:

1. *Intra range transformations* (e.g. `shift()`) transform each range individually (and independently of the other ranges). They return an object *parallel* to the input object, that is, where the *i*-th range corresponds to the *i*-th range in the input. Those transformations are described in the [intra-range-methods](#) man page (see `?`intra-range-methods``).
2. *Inter range transformations* (e.g. `reduce()`) transform all the ranges together as a set to produce a new set of ranges. They return an object that is generally *NOT* parallel to the input object. Those transformations are described below.

## Usage

```

## range()
## -----
## S4 method for signature 'IntegerRanges'
range(x, ..., with.revmap=FALSE, na.rm=FALSE)

## S4 method for signature 'IntegerRangesList'
range(x, ..., with.revmap=FALSE, na.rm=FALSE)

## reduce()

```



```

## -----
reduce(x, drop.empty.ranges=FALSE, ...)

## S4 method for signature 'IntegerRanges'
reduce(x, drop.empty.ranges=FALSE, min.gapwidth=1L,
       with.revmap=FALSE, with.inframe.attrib=FALSE)

## S4 method for signature 'Views'
reduce(x, drop.empty.ranges=FALSE, min.gapwidth=1L,
       with.revmap=FALSE, with.inframe.attrib=FALSE)

## S4 method for signature 'IntegerRangesList'
reduce(x, drop.empty.ranges=FALSE, min.gapwidth=1L,
       with.revmap=FALSE, with.inframe.attrib=FALSE)

## gaps()
## -----
gaps(x, start=NA, end=NA, ...)

## disjoint(), isDisjoint(), and disjointBins()
## -----
disjoin(x, ...)

## S4 method for signature 'IntegerRanges'
disjoin(x, with.revmap=FALSE)
## S4 method for signature 'IntegerRangesList'
disjoin(x, with.revmap=FALSE)

isDisjoint(x, ...)
disjointBins(x, ...)

```

### Arguments

|                     |   |
|---------------------|---|
| x                   | A <a href="#">IntegerRanges</a> or <a href="#">IntegerRangesList</a> object for range, disjoin, isDisjoint, and disjointBins.   |
|                     | A <a href="#">IntegerRanges</a> , <a href="#">Views</a> , or <a href="#">IntegerRangesList</a> object for reduce and gaps.  |
| ...                 | For range, additional <a href="#">IntegerRanges</a> or <a href="#">IntegerRangesList</a> object to consider.  |
| na.rm               | Ignored.  |
| drop.empty.ranges   | TRUE or FALSE. Should empty ranges be dropped?  |
| min.gapwidth        | Ranges separated by a gap of at least min.gapwidth positions are not merged.  |
| with.revmap         | TRUE or FALSE. Should the mapping from output to input ranges be stored in the returned object? If yes, then it is stored as metadata column revmap of type <a href="#">IntegerList</a> . |
| with.inframe.attrib | TRUE or FALSE. For internal use.  |

- start, end
- If `x` is a [IntegerRanges](#) or [Views](#) object: A single integer or NA. Use these arguments to specify the interval of reference i.e. which interval the returned gaps should be relative to.
  - If `x` is a [IntegerRangesList](#) object: Integer vectors containing the coordinate bounds for each [IntegerRangesList](#) top-level element.

## Details

Unless specified otherwise, when `x` is a [IntegerRangesList](#) object, any transformation described here is equivalent to applying the transformation to each [IntegerRangesList](#) top-level element separately.

### reduce:

reduce first orders the ranges in `x` from left to right, then merges the overlapping or adjacent ones.

### range:

range first concatenates `x` and the objects in `...` together. If the [IRanges](#) object resulting from this concatenation contains at least 1 range, then range returns an [IRanges](#) instance with a single range, from the minimum start to the maximum end of the concatenated object. Otherwise (i.e. if the concatenated object contains no range), `IRanges()` is returned (i.e. an [IRanges](#) instance of length 0).

When passing more than 1 [IntegerRangesList](#) object to `range()`, they are first merged into a single [IntegerRangesList](#) object: by name if all objects have names, otherwise, if they are all of the same length, by position. Else, an exception is thrown.

### gaps:

gaps returns the "normal" [IRanges](#) object representing the set of integers that remain after the set of integers represented by `x` has been removed from the interval specified by the start and end arguments.

If `x` is a [Views](#) object, then `start=NA` and `end=NA` are interpreted as `start=1` and `end=length(subject(x))`, respectively, so, if `start` and `end` are not specified, then gaps are extracted with respect to the entire subject.

### isDisjoint:

An [IntegerRanges](#) object `x` is considered to be "disjoint" if its ranges are non-overlapping. `isDisjoint` tests whether the object is "disjoint" or not.

Note that a "normal" [IntegerRanges](#) object is always "disjoint" but the opposite is not true. See `?isNormal` for more information about normal [IntegerRanges](#) objects.

About empty ranges. `isDisjoint` handles empty ranges (a.k.a. zero-width ranges) as follow: single empty range `A` is considered to overlap with single range `B` iff it's contained in `B` without being on the edge of `B` (in which case it would be ambiguous whether `A` is contained in or adjacent to `B`). More precisely, single empty range `A` is considered to overlap with single range `B` iff

$$\text{start}(B) < \text{start}(A) \text{ and } \text{end}(A) < \text{end}(B)$$

Because `A` is an empty range it verifies `end(A) = start(A) - 1` so the above is equivalent to:

$$\text{start}(B) < \text{start}(A) \leq \text{end}(B)$$

and also equivalent to:

$$\text{start}(B) \leq \text{end}(A) < \text{end}(B)$$

Finally, it is also equivalent to:

```
pcompare(A, B) == 2
```

See [?`IPosRanges-comparison`](#) for the meaning of the codes returned by the `pcompare` function.

#### **disjoin:**

`disjoin` returns a disjoint object, by finding the union of the end points in `x`. In other words, the result consists of a range for every interval, of maximal length, over which the set of overlapping ranges in `x` is the same and at least of size 1.

#### **disjointBins:**

`disjointBins` segregates `x` into a set of bins so that the ranges in each bin are disjoint. Lower-indexed bins are filled first. The method returns an integer vector indicating the bin index for each range.

### **Value**

If `x` is an [IntegerRanges](#) object:

- `range`, `reduce`, `gaps`, and `disjoin` return an [IRanges](#) instance.
- `isDisjoint` returns TRUE or FALSE.
- `disjointBins` returns an integer vector *parallel* to `x`, that is, where the *i*-th element corresponds to the *i*-th element in `x`.

If `x` is a [Views](#) object: `reduce` and `gaps` return a [Views](#) object on the same subject as `x` but with modified views.

If `x` is a [IntegerRangesList](#) object:

- `range`, `reduce`, `gaps`, and `disjoin` return a [IntegerRangesList](#) object *parallel* to `x`.
- `isDisjoint` returns a logical vector *parallel* to `x`.
- `disjointBins` returns an [IntegerList](#) object *parallel* to `x`.

### **Author(s)**

H. Pagès, M. Lawrence, and P. Aboyoun

### **See Also**

- [intra-range-methods](#) for intra range transformations.
- The [IntegerRanges](#), [Views](#), [IntegerRangesList](#), and [MaskCollection](#) classes.
- The [inter-range-methods](#) man page in the **GenomicRanges** package for *inter range transformations* of genomic ranges.
- [setops-methods](#) for set operations on [IRanges](#) objects.
- [endoapply](#) in the **S4Vectors** package.

**Examples**

```

## -----
## range()
## -----

## On an IntegerRanges object:
x <- IRanges(start=c(-2, 6, 9, -4, 1, 0, -6, 3, 10),
             width=c( 5, 0, 6,  1, 4, 3,  2, 0,  3))
range(x)

## On an IntegerRangesList object (XVector package required):
range1 <- IRanges(start=c(1, 2, 3), end=c(5, 2, 8))
range2 <- IRanges(start=c(15, 45, 20, 1), end=c(15, 100, 80, 5))
range3 <- IRanges(start=c(-2, 6, 7), width=c(8, 0, 0)) # with empty ranges
collection <- IRangesList(one=range1, range2, range3)
if (require(XVector)) {
  range(collection)
}

irl1 <- IRangesList(a=IRanges(c(1, 2),c(4, 3)), b=IRanges(c(4, 6),c(10, 7)))
irl2 <- IRangesList(c=IRanges(c(0, 2),c(4, 5)), a=IRanges(c(4, 5),c(6, 7)))
range(irl1, irl2) # matched by names
names(irl2) <- NULL
range(irl1, irl2) # now by position

## -----
## reduce()
## -----

## On an IntegerRanges object:
reduce(x)
y <- reduce(x, with.revmap=TRUE)
mcols(y)$revmap # an IntegerList

reduce(x, drop.empty.ranges=TRUE)
y <- reduce(x, drop.empty.ranges=TRUE, with.revmap=TRUE)
mcols(y)$revmap

## Use the mapping from reduced to original ranges to split the DataFrame
## of original metadata columns by reduced range:
ir0 <- IRanges(c(11:13, 2, 7:6), width=3)
mcols(ir0) <- DataFrame(id=letters[1:6], score=1:6)
ir <- reduce(ir0, with.revmap=TRUE)
ir
revmap <- mcols(ir)$revmap
revmap
relist(mcols(ir0)[unlist(revmap), ], revmap) # a SplitDataFrameList

## On an IntegerRangesList object. These 4 are the same:
res1 <- reduce(collection)
res2 <- IRangesList(one=reduce(range1), reduce(range2), reduce(range3))
res3 <- do.call(IRangesList, lapply(collection, reduce))

```

```

res4 <- endoapply(collection, reduce)

stopifnot(identical(res2, res1))
stopifnot(identical(res3, res1))
stopifnot(identical(res4, res1))

reduce(collection, drop.empty.ranges=TRUE)

## -----
## gaps()
## -----

## On an IntegerRanges object:
x0 <- IRanges(start=c(-2, 6, 9, -4, 1, 0, -6, 10),
              width=c( 5, 0, 6,  1, 4, 3,  2,  3))
gaps(x0)
gaps(x0, start=-6, end=20)

## On a Views object:
subject <- Rle(1:-3, 6:2)
v <- Views(subject, start=c(8, 3), end=c(14, 4))
gaps(v)

## On an IntegerRangesList object. These 4 are the same:
res1 <- gaps(collection)
res2 <- IRangesList(one=gaps(range1), gaps(range2), gaps(range3))
res3 <- do.call(IRangesList, lapply(collection, gaps))
res4 <- endoapply(collection, gaps)

stopifnot(identical(res2, res1))
stopifnot(identical(res3, res1))
stopifnot(identical(res4, res1))

## On a MaskCollection object:
mask1 <- Mask(mask.width=29, start=c(11, 25, 28), width=c(5, 2, 2))
mask2 <- Mask(mask.width=29, start=c(3, 10, 27), width=c(5, 8, 1))
mask3 <- Mask(mask.width=29, start=c(7, 12), width=c(2, 4))
mymasks <- append(append(mask1, mask2), mask3)
mymasks
gaps(mymasks)

## -----
## disjoint()
## -----

## On an IntegerRanges object:
ir <- IRanges(c(1, 1, 4, 10), c(6, 3, 8, 10))
disjoin(ir) # IRanges(c(1, 4, 7, 10), c(3, 6, 8, 10))
disjoin(ir, with.revmap=TRUE)

## On an IntegerRangesList object:
disjoin(collection)
disjoin(collection, with.revmap=TRUE)

```

```

## -----
## isDisjoint()
## -----

## On an IntegerRanges object:
isDisjoint(IRanges(c(2,5,1), c(3,7,3))) # FALSE
isDisjoint(IRanges(c(2,9,5), c(3,9,6))) # TRUE
isDisjoint(IRanges(1, 5)) # TRUE

## Handling of empty ranges:
x <- IRanges(c(11, 16, 11, -2, 11), c(15, 29, 10, 10, 10))
stopifnot(isDisjoint(x))

## Sliding an empty range along a non-empty range:
sapply(11:17,
       function(i) pcompare(IRanges(i, width=0), IRanges(12, 15)))

sapply(11:17,
       function(i) isDisjoint(c(IRanges(i, width=0), IRanges(12, 15))))

## On an IntegerRangesList object:
isDisjoint(collection)

## -----
## disjointBins()
## -----

## On an IntegerRanges object:
disjointBins(IRanges(1, 5)) # 1L
disjointBins(IRanges(c(3, 1, 10), c(5, 12, 13))) # c(2L, 1L, 2L)

## On an IntegerRangesList object:
disjointBins(collection)

```

---

intra-range-methods    *Intra range transformations of an IRanges, IPos, Views, RangesList, or MaskCollection object*

---

## Description

Range-based transformations are grouped in 2 categories:

1. *Intra range transformations* (e.g. `shift()`) transform each range individually (and independently of the other ranges). They return an object *parallel* to the input object, that is, where the *i*-th range corresponds to the *i*-th range in the input. Those transformations are described below.
2. *Inter range transformations* (e.g. `reduce()`) transform all the ranges together as a set to produce a new set of ranges. They return an object that is generally *NOT* parallel to the input object. Those transformations are described in the [inter-range-methods](#) man page (see `?`inter-range-methods``).

Except for `threebands()`, all the transformations described in this man page are *endomorphisms* that operate on a single "range-based" object, that is, they transform the ranges contained in the input object and return them in an object of the *same class* as the input object.

## Usage

```

shift(x, shift=0L, use.names=TRUE)

narrow(x, start=NA, end=NA, width=NA, use.names=TRUE)

resize(x, width, fix="start", use.names=TRUE, ...)

flank(x, width, start=TRUE, both=FALSE, use.names=TRUE, ...)

promoters(x, upstream=2000, downstream=200, use.names=TRUE, ...)
terminators(x, upstream=2000, downstream=200, use.names=TRUE, ...)

reflect(x, bounds, use.names=TRUE)

restrict(x, start=NA, end=NA, keep.all.ranges=FALSE, use.names=TRUE)

threebands(x, start=NA, end=NA, width=NA)

```

## Arguments

|                         |  |
|-------------------------|--|
| <code>x</code>          | An <a href="#">IRanges</a> , <a href="#">IPos</a> , <a href="#">Views</a> , <a href="#">RangesList</a> , or <a href="#">MaskCollection</a> object.   |
| <code>shift</code>      | An integer vector containing the shift information. Recycled as necessary so that each element corresponds to a range in <code>x</code> .<br>Can also be a list-like object <i>parallel</i> to <code>x</code> if <code>x</code> is a <a href="#">RangesList</a> object.  |
| <code>use.names</code>  | TRUE or FALSE. Should names be preserved?  |
| <code>start, end</code> | If <code>x</code> is an <a href="#">IRanges</a> , <a href="#">IPos</a> or <a href="#">Views</a> object: A vector of integers for all functions except for <code>flank</code> . For <code>restrict</code> , the supplied <code>start</code> and <code>end</code> arguments must be vectors of integers, eventually with NAs, that specify the restriction interval(s). Recycled as necessary so that each element corresponds to a range in <code>x</code> . Same thing for <code>narrow</code> and <code>threebands</code> , except that here <code>start</code> and <code>end</code> must contain coordinates relative to the ranges in <code>x</code> . See the Details section below. For <code>flank</code> , <code>start</code> is a logical indicating whether <code>x</code> should be flanked at the start (TRUE) or the end (FALSE). Recycled as necessary so that each element corresponds to a range in <code>x</code> .<br>Can also be list-like objects <i>parallel</i> to <code>x</code> if <code>x</code> is a <a href="#">RangesList</a> object. |
| <code>width</code>      | If <code>x</code> is an <a href="#">IRanges</a> , <a href="#">IPos</a> or <a href="#">Views</a> object: For <code>narrow</code> and <code>threebands</code> , a vector of integers, eventually with NAs. See the SEW (Start/End/Width) interface for the details ( <code>?solveUserSEW</code> ). For <code>resize</code> and <code>flank</code> , the width of the resized or flanking regions. Note that if <code>both</code> is TRUE, this is effectively doubled. Recycled as necessary so that each element corresponds to a range in <code>x</code> .<br>Can also be a list-like object <i>parallel</i> to <code>x</code> if <code>x</code> is a <a href="#">RangesList</a> object.   |

|                                   |  |
|-----------------------------------|--|
| <code>fix</code>                  | If <code>x</code> is an <a href="#">IRanges</a> , <a href="#">IPos</a> or <a href="#">Views</a> object: A character vector or character-Rle of length 1 or <code>length(x)</code> containing the values "start", "end", and "center" denoting what to use as an anchor for each element in <code>x</code> .<br>Can also be a list-like object <i>parallel</i> to <code>x</code> if <code>x</code> is a <a href="#">RangesList</a> object.  |
| <code>...</code>                  | Additional arguments for methods.  |
| <code>both</code>                 | If TRUE, extends the flanking region width positions <i>into</i> the range. The resulting range thus straddles the end point, with width positions on either side.   |
| <code>upstream, downstream</code> | Vectors of non-NA non-negative integers. Recycled as necessary so that each element corresponds to a range in <code>x</code> . Can also be list-like objects <i>parallel</i> to <code>x</code> if <code>x</code> is a <a href="#">RangesList</a> object.<br><code>upstream</code> defines the number of nucleotides toward the 5' end and <code>downstream</code> defines the number toward the 3' end, relative to the transcription start site. Promoter regions are formed by merging the upstream and downstream ranges. Default values for the upstream and downstream arguments of <code>promoters()</code> were chosen based on our current understanding of gene regulation. On average, promoter regions in the mammalian genome are 5000 bp upstream and downstream of the transcription start site. Note that the same default values are used in <code>terminators()</code> at the moment. However this could be revisited if the case is made to use values that reflect more closely the biology of terminator regions in mammalian genomes. |
| <code>bounds</code>               | An <a href="#">IRanges</a> object to serve as the reference bounds for the reflection, see below.  |
| <code>keep.all.ranges</code>      | TRUE or FALSE. Should ranges that don't overlap with the restriction interval(s) be kept? Note that "don't overlap" means that they end strictly before <code>start - 1</code> or start strictly after <code>end + 1</code> . Ranges that end at <code>start - 1</code> or start at <code>end + 1</code> are always kept and their width is set to zero in the returned <a href="#">IRanges</a> object.  |

## Details

Unless specified otherwise, when `x` is a [RangesList](#) object, any transformation described here is equivalent to applying the transformation to each list element in `x`.

### shift:

`shift` shifts all the ranges in `x` by the amount specified by the `shift` argument.

### narrow:

`narrow` narrows the ranges in `x` i.e. each range in the returned [IntegerRanges](#) object is a sub-range of the corresponding range in `x`. The supplied start/end/width values are solved by a call to `solveUserSEW(width(x), start=start, end=end, width=width)` and therefore must be compliant with the rules of the SEW (Start/End/Width) interface (see [?solveUserSEW](#) for the details). Then each subrange is derived from the original range according to the solved start/end/width values for this range. Note that those solved values are interpreted relatively to the original range.

### resize:

`resize` resizes the ranges to the specified width where either the start, end, or center is used as an anchor.



**flank:**

`flank` generates flanking ranges for each range in `x`. If `start` is `TRUE` for a given range, the flanking occurs at the start, otherwise the end. The widths of the flanks are given by the `width` parameter. The widths can be negative, in which case the flanking region is reversed so that it represents a prefix or suffix of the range in `x`. The `flank` operation is illustrated below for a call of the form `flank(x, 3, TRUE)`, where `x` indicates a range in `x` and `-` indicates the resulting flanking region:

```
---xxxxxxx
```

If `start` were `FALSE`:

```
xxxxxxx---
```

For negative width, i.e. `flank(x, -3, FALSE)`, where `*` indicates the overlap between `x` and the result:

```
xxxx***
```

If both is `TRUE`, then, for all ranges in `x`, the flanking regions are extended *into* (or out of, if width is negative) the range, so that the result straddles the given endpoint and has twice the width given by `width`. This is illustrated below for `flank(x, 3, both=TRUE)`:

```
---**xxxxx
```

**promoters and terminators:**

`promoters` generates promoter ranges for each range in `x` relative to the transcription start site (TSS), where TSS is `start(x)`. The promoter range is expanded around the TSS according to the `upstream` and `downstream` arguments. `upstream` represents the number of nucleotides in the 5' direction and `downstream` the number in the 3' direction. The full range is defined as,  $(start(x) - upstream)$  to  $(start(x) + downstream - 1)$ . For documentation for using `promoters` on a `GRanges` object see `?promoters, GenomicRanges-method` in the **GenomicRanges** package.

`terminators` is similar to `promoters` except that the generated ranges are relative to the transcription end sites (TES) returned by `end(x)`.

**reflect:**

`reflect` "reflects" or reverses each range in `x` relative to the corresponding range in `bounds`, which is recycled as necessary. Reflection preserves the width of a range, but shifts it such the distance from the left bound to the start of the range becomes the distance from the end of the range to the right bound. This is illustrated below, where `x` represents a range in `x` and `[ and ]` indicate the bounds:

```
[. .xxx. . . . .]
becomes
[. . . . .xxx. . .]
```

**restrict:**

`restrict` restricts the ranges in `x` to the interval(s) specified by the `start` and `end` arguments.

**threebands:**

`threebands` extends the capability of `narrow` by returning the 3 ranges objects associated to the narrowing operation. The returned value `y` is a list of 3 ranges objects named "left", "middle"

and "right". The middle component is obtained by calling `narrow` with the same arguments (except that names are dropped). The left and right components are also instances of the same class as `x` and they contain what has been removed on the left and right sides (respectively) of the original ranges during the narrowing.

Note that original object `x` can be reconstructed from the left and right bands with `punion(y$left, y$right, fill.gap=TRUE)`.

### Author(s)

H. Pagès, M. Lawrence, and P. Aboyoun

### See Also

- [inter-range-methods](#) for inter range transformations.
- The [IRanges](#), [IPos](#), [Views](#), [RangesList](#), and [MaskCollection](#) classes.
- The [intra-range-methods](#) man page in the **GenomicRanges** package for *intra range transformations* of genomic ranges.
- [setops-methods](#) for set operations on [IRanges](#) objects.
- [endoapply](#) in the **S4Vectors** package.

### Examples

```
## -----
## shift()
## -----

## On an IRanges object:
ir1 <- successiveIRanges(c(19, 5, 0, 8, 5))
ir1
shift(ir1, shift=-3)

## On an IRangesList object:
range1 <- IRanges(start=c(1, 2, 3), end=c(5, 2, 8))
range2 <- IRanges(start=c(15, 45, 20, 1), end=c(15, 100, 80, 5))
range3 <- IRanges(start=c(-2, 6, 7), width=c(8, 0, 0)) # with empty ranges
collection <- IRangesList(one=range1, range2, range3)
shift(collection, shift=5) # same as endoapply(collection, shift, shift=5)

## Sanity check:
res1 <- shift(collection, shift=5)
res2 <- endoapply(collection, shift, shift=5)
stopifnot(identical(res1, res2))

## -----
## narrow()
## -----

## On an IRanges object:
ir2 <- ir1[width(ir1) != 0]
narrow(ir2, start=4, end=-2)
```

```

narrow(ir2, start=-4, end=-2)
narrow(ir2, end=5, width=3)
narrow(ir2, start=c(3, 4, 2, 3), end=c(12, 5, 7, 4))

## On an IRangesList object:
narrow(collection[-3], start=2)
narrow(collection[-3], end=-2)

## On a MaskCollection object:
mask1 <- Mask(mask.width=29, start=c(11, 25, 28), width=c(5, 2, 2))
mask2 <- Mask(mask.width=29, start=c(3, 10, 27), width=c(5, 8, 1))
mask3 <- Mask(mask.width=29, start=c(7, 12), width=c(2, 4))
mymasks <- append(append(mask1, mask2), mask3)
mymasks
narrow(mymasks, start=8)

## -----
## resize()
## -----

## On an IRanges object:
resize(ir2, 200)
resize(ir2, 2, fix="end")

## On an IRangesList object:
resize(collection, width=200)

## -----
## flank()
## -----

## On an IRanges object:
ir3 <- IRanges(start=c(2,5,1), end=c(3,7,3))
flank(ir3, 2)
flank(ir3, 2, start=FALSE)
flank(ir3, 2, start=c(FALSE, TRUE, FALSE))
flank(ir3, c(2, -2, 2))
flank(ir3, 2, both = TRUE)
flank(ir3, 2, start=FALSE, both=TRUE)
flank(ir3, -2, start=FALSE, both=TRUE)

## On an IRangesList object:
flank(collection, width=10)

## -----
## promoters()
## -----

## On an IRanges object:
ir4 <- IRanges(start=10001:10004, end=12000)
promoters(ir4, upstream=800, downstream=0)
promoters(ir4, upstream=0, downstream=50)
promoters(ir4, upstream=800, downstream=50)

```

```

promoters(ir4, upstream=0, downstream=1) # TSS

## On an IRangesList object:
promoters(collection, upstream=5, downstream=2)

## -----
## reflect()
## -----

## On an IRanges object:
bounds <- IRanges(start=c(0, 5, 3), end=c(10, 6, 9))
reflect(ir3, bounds)

## reflect() does not yet support IRangesList objects!

## -----
## restrict()
## -----

## On an IRanges object:
restrict(ir1, start=12, end=34)
restrict(ir1, start=20)
restrict(ir1, start=21)
restrict(ir1, start=21, keep.all.ranges=TRUE)

## On an IRangesList object:
restrict(collection, start=2, end=8)
restrict(collection, start=2, end=8, keep.all.ranges=TRUE)

## -----
## threebands()
## -----

## On an IRanges object:
z <- threebands(ir2, start=4, end=-2)
ir2b <- punion(z$left, z$right, fill.gap=TRUE)
stopifnot(identical(ir2, ir2b))
threebands(ir2, start=-5)

## threebands() does not support IRangesList objects.

```

---

IPos-class

*IPos objects*


---

## Description

The IPos class is a container for storing a set of *integer positions*. It exists in 2 flavors: UnstitchedIPos and StitchedIPos. Each flavor uses a particular internal representation:

- In an UnstitchedIPos instance the positions are stored as an integer vector.

- In a `StitchedIPos` instance the positions are stored as an `IRanges` object where each range represents a run of *consecutive positions* (i.e. a run of positions that are adjacent and in *ascending order*). This storage is particularly memory-efficient when the vector of positions contains long runs of consecutive positions.

Because integer positions can be seen as integer ranges of width 1, the `IPos` class extends the `IntegerRanges` virtual class.

## Usage

```
IPos(pos=integer(0), names=NULL, ..., stitch=NA) # constructor function
```

## Arguments

|                     |  |
|---------------------|--|
| <code>pos</code>    | An integer or numeric vector, or an <code>IRanges</code> object (or other <code>IntegerRanges</code> derivative). If <code>pos</code> is anything else, <code>IPos()</code> will first try to coerce it to an <code>IRanges</code> object with <code>as(pos, "IRanges")</code> .<br>When <code>pos</code> is an <code>IRanges</code> object (or other <code>IntegerRanges</code> derivative), each range in it is interpreted as a run of consecutive positions.   |
| <code>names</code>  | A character vector or <code>NULL</code> .  |
| <code>...</code>    | Metadata columns to set on the <code>IPos</code> object. All the metadata columns must be vector-like objects of the same length as the object to construct.   |
| <code>stitch</code> | <code>TRUE</code> , <code>FALSE</code> , or <code>NA</code> (the default).<br>Controls which internal representation should be used: <code>StitchedIPos</code> (when <code>stitch</code> is <code>TRUE</code> ) or <code>UnstitchedIPos</code> (when <code>stitch</code> is <code>FALSE</code> ).<br>When <code>stitch</code> is <code>NA</code> (the default), which internal representation will be used depends on the type of <code>pos</code> : <code>UnstitchedIPos</code> if <code>pos</code> is an integer or numeric vector, and <code>StitchedIPos</code> otherwise. |

## Details

Even though an `IRanges` object can be used for storing integer positions, using an `IPos` object is more efficient. In particular the memory footprint of an `UnstitchedIPos` object is half that of an `IRanges` object.

OTOH the memory footprint of a `StitchedIPos` object can vary a lot but will never be worse than that of an `IRanges` object. However it will reduce dramatically if the vector of positions contains long runs of consecutive positions. In the worst case scenario (i.e. when the object contains no consecutive positions) its memory footprint will be the same as that of an `IRanges` object.

Like for any `Vector` derivative, the length of an `IPos` object cannot exceed `.Machine$integer.max` (i.e.  $2^{31}$  on most platforms). `IPos()` will return an error if `pos` contains too many positions.

## Value

An `UnstitchedIPos` or `StitchedIPos` object. If the input object `pos` is itself an `IPos` derivative, its metadata columns are propagated.

## Accessors

**Getters:** IPos objects support the same set of getters as other [IntegerRanges](#) derivatives (i.e. `length()`, `start()`, `end()`, `names()`, `mcols()`, etc...), plus the `pos()` getter which is equivalent to `start()` and `end()`. See [?IntegerRanges](#) for the list of getters supported by [IntegerRanges](#) derivatives.

**Setters:** IPos derivatives support the `names()`, `mcols()` and `metadata()` setters only.

In particular there is no `pos()` setter for IPos derivatives at the moment (although one might be added in the future).

## Coercion

From `UnstitchedIPos` to `StitchedIPos` and vice-versa: coercion back and forth between `UnstitchedIPos` and `StitchedIPos` is supported via `as(x, "StitchedIPos")` and `as(x, "UnstitchedIPos")`. This is the most efficient and recommended way to switch between the 2 internal representations. Note that this switch can have dramatic consequences on memory usage so is for advanced users only. End users should almost never need to do this switch when following a typical workflow.

From [IntegerRanges](#) to `UnstitchedIPos`, `StitchedIPos`, or `IPos`: An [IntegerRanges](#) derivative `x` in which all the ranges have a width of 1 can be coerced to an `UnstitchedIPos` or `StitchedIPos` object with `as(x, "UnstitchedIPos")` or `as(x, "StitchedIPos")`, respectively. For convenience `as(x, "IPos")` is supported and is equivalent to `as(x, "UnstitchedIPos")`.

From `IPos` to [IRanges](#): An `IPos` derivative `x` can be coerced to an [IRanges](#) object with `as(x, "IRanges")`. However be aware that if `x` is a `StitchedIPos` instance, the memory footprint of the resulting object can be thousands times (or more) than that of `x`! See "MEMORY USAGE" in the Examples section below.

From `IPos` to ordinary R objects: Like with any other [IntegerRanges](#) derivative, `as.character()`, `as.factor()`, and `as.data.frame()` work on an `IPos` derivative `x`. Note however that `as.data.frame(x)` returns a data frame with a `pos` column (containing `pos(x)`) instead of the `start`, `end`, and `width` columns that one gets with other [IntegerRanges](#) derivatives.

## Subsetting

An `IPos` derivative can be subsetted exactly like an [IRanges](#) object.

## Concatenation

`IPos` derivatives can be concatenated with `c()` or `append()`. See [?c](#) in the [S4Vectors](#) package for more information about concatenating Vector derivatives.

## Splitting and Relisting

Like with an [IRanges](#) object, `split()` and `relist()` work on an `IPos` derivative.

## Author(s)

Hervé Pagès; based on ideas borrowed from Georg Stricker <georg.stricker@in.tum.de> and Julien Gagneur <gagneur@in.tum.de>

**See Also**

- The [GPos](#) class in the **GenomicRanges** package for representing a set of *genomic positions* (i.e. genomic ranges of width 1, a.k.a. *genomic loci*).
- The [IRanges](#) class for storing a set of *integer ranges* of arbitrary width.
- [IPosRanges-comparison](#) for comparing and ordering integer ranges and/or positions.
- [findOverlaps-methods](#) for finding overlapping integer ranges and/or positions.
- [intra-range-methods](#) and [inter-range-methods](#) for *intra range* and *inter range* transformations.
- [coverage-methods](#) for computing the coverage of a set of ranges and/or positions.
- [nearest-methods](#) for finding the nearest integer range/position neighbor.

**Examples**

```
showClass("IPos") # shows the known subclasses

## -----
## BASIC EXAMPLES
## -----

## Example 1:
ipos1a <- IPos(c(44:53, 5:10, 2:5))
ipos1a # unstitched

length(ipos1a)
pos(ipos1a) # same as 'start(ipos1a)' and 'end(ipos1a)'
as.character(ipos1a)
as.data.frame(ipos1a)
as(ipos1a, "IRanges")
as.data.frame(as(ipos1a, "IRanges"))
ipos1a[9:17]

ipos1b <- IPos(c(44:53, 5:10, 2:5), stitch=TRUE)
ipos1b # stitched

## 'ipos1a' and 'ipos1b' are semantically equivalent, only their
## internal representations differ:
all(ipos1a == ipos1b)

ipos1c <- IPos(c("44-53", "5-10", "2-5"))
ipos1c # stitched

identical(ipos1b, ipos1c)

## Example 2:
my_pos <- IRanges(c(1, 6, 12, 17), c(5, 10, 16, 20))
ipos2 <- IPos(my_pos)
ipos2 # stitched

## Example 3:
ipos3A <- ipos3B <- IPos(c("1-15000", "15400-88700"))
npos <- length(ipos3A)
```

```

mcols(ipos3A)$sample <- Rle("sA")
sA_counts <- sample(10, npos, replace=TRUE)
mcols(ipos3A)$counts <- sA_counts

mcols(ipos3B)$sample <- Rle("sB")
sB_counts <- sample(10, npos, replace=TRUE)
mcols(ipos3B)$counts <- sB_counts

ipos3 <- c(ipos3A, ipos3B)
ipos3

## -----
## MEMORY USAGE
## -----

## Coercion to IRanges works on a StitchedIPos object...
ipos4 <- IPos(c("1-125000", "135000-575000"))
ir4 <- as(ipos4, "IRanges")
ir4
## ... but is generally not a good idea:
object.size(ipos4)
object.size(ir4) # 1652 times bigger than the StitchedIPos object!

## Shuffling the order of the positions impacts memory usage:
ipos4r <- rev(ipos4)
object.size(ipos4r)
ipos4s <- sample(ipos4)
object.size(ipos4s)

## If one anticipates a lot of shuffling of the positions,
## then an UnstitchedIPos object should be used instead:
ipos4b <- as(ipos4, "UnstitchedIPos")
object.size(ipos4b) # initial size is bigger than stitched version
object.size(rev(ipos4b)) # size didn't change
object.size(sample(ipos4b)) # size didn't change

## AN IMPORTANT NOTE: In the worst situations, IPos still performs
## as good as an IRanges object.
object.size(as(ipos4r, "IRanges")) # same size as 'ipos4r'
object.size(as(ipos4s, "IRanges")) # same size as 'ipos4s'

## Best case scenario is when the object is strictly sorted (i.e.
## positions are in strict ascending order).
## This can be checked with:
is.unsorted(ipos4, strict=TRUE) # 'ipos4' is strictly sorted

## -----
## USING MEMORY-EFFICIENT METADATA COLUMNS
## -----

## In order to keep memory usage as low as possible, it is recommended
## to use a memory-efficient representation of the metadata columns that
## we want to set on the object. Rle's are particularly well suited for

```



```

## this, especially if the metadata columns contain long runs of
## identical values. This is the case for example if we want to use an
## IPos object to represent the coverage of sequencing reads along a
## chromosome.

## Example 5:
library(pasillaBamSubset)
library(Rsamtools) # for the BamFile() constructor function
bamfile1 <- BamFile(untreated1_chr4())
bamfile2 <- BamFile(untreated3_chr4())
ipos5 <- IPos(IRanges(1, seqlengths(bamfile1)[["chr4"]]))
library(GenomicAlignments) # for "coverage" method for BamFile objects
cvg1 <- coverage(bamfile1)$chr4
cvg2 <- coverage(bamfile2)$chr4
mcols(ipos5) <- DataFrame(cvg1, cvg2)
ipos5

object.size(ipos5) # lightweight

## Keep only the positions where coverage is at least 10 in one of the
## 2 samples:
ipos5[mcols(ipos5)$cvg1 >= 10 | mcols(ipos5)$cvg2 >= 10]

```

---

IPosRanges-class

*IPosRanges objects*


---

## Description

The IPosRanges *virtual* class is a general container for storing a vector of ranges of integer positions.

## Details

An IPosRanges object is a vector-like object where each element describes a "range of integer positions".

A "range of integer values" is a finite set of consecutive integer values. Each range can be fully described with exactly 2 integer values which can be arbitrarily picked up among the 3 following values: its "start" i.e. its smallest (or first, or leftmost) value; its "end" i.e. its greatest (or last, or rightmost) value; and its "width" i.e. the number of integer values in the range. For example the set of integer values that are greater than or equal to -20 and less than or equal to 400 is the range that starts at -20 and has a width of 421. In other words, a range is a closed, one-dimensional interval with integer end points and on the domain of integers.

The starting point (or "start") of a range can be any integer (see start below) but its "width" must be a non-negative integer (see width below). The ending point (or "end") of a range is equal to its "start" plus its "width" minus one (see end below). An "empty" range is a range that contains no value i.e. a range that has a null width. Depending on the context, it can be interpreted either as just the empty *set* of integers or, more precisely, as the position *between* its "end" and its "start" (note that for an empty range, the "end" equals the "start" minus one).

The length of an IPosRanges object is the number of ranges in it, not the number of integer values in its ranges.

An IPosRanges object is considered empty iff all its ranges are empty.

IPosRanges objects have a vector-like semantic i.e. they only support single subscript subsetting (unlike, for example, standard R data frames which can be subsetted by row and by column).

The IPosRanges class itself is a virtual class. The following classes derive directly from it: [IRanges](#), [IPos](#), [NCList](#), and [GroupingRanges](#).

## Methods

In the code snippets below, `x`, `y` and `object` are IPosRanges objects. Not all the functions described below will necessarily work with all kinds of IPosRanges derivatives but they should work at least for [IRanges](#) objects.

Note that many more operations on IPosRanges objects are described in other man pages of the **IRanges** package. See for example the man page for *intra range transformations* (e.g. `shift()`, see `?`intra-range-methods``), or the man page for *inter range transformations* (e.g. `reduce()`, see `?`inter-range-methods``), or the man page for *findOverlaps methods* (see `?`findOverlaps-methods``), or the man page for [IntegerRangesList](#) objects where the `split` method for [IntegerRanges](#) derivatives is documented.

`length(x)`: The number of ranges in `x`.

`start(x)`: The start values of the ranges. This is an integer vector of the same length as `x`.

`width(x)`: The number of integer values in each range. This is a vector of non-negative integers of the same length as `x`.

`end(x)`:  $\text{start}(x) + \text{width}(x) - 1L$

`mid(x)`: returns the midpoint of the range,  $\text{start}(x) + \text{floor}((\text{width}(x) - 1)/2)$ .

`names(x)`: NULL or a character vector of the same length as `x`.

`tile(x, n, width, ...)`: Splits each range in `x` into subranges as specified by `n` (number of ranges) or `width`. Only one of `n` or `width` can be specified. The return value is a [IRangesList](#) the same length as `x`. IPosRanges with a width less than the `width` argument are returned unchanged.

`slidingWindows(x, width, step=1L)`: Generates sliding windows within each range of `x`, of width `width`, and starting every `step` positions. The return value is a [IRangesList](#) the same length as `x`. IPosRanges with a width less than the `width` argument are returned unchanged. If the sliding windows do not exactly cover `x`, the last window is partial.

`isEmpty(x)`: Return a logical value indicating whether `x` is empty or not.

`as.matrix(x, ...)`: Convert `x` into a 2-column integer matrix containing `start(x)` and `width(x)`. Extra arguments (...) are ignored.

`as.data.frame(x, row.names=NULL, optional=FALSE)`: Convert `x` into a standard R data frame object. `row.names` must be NULL or a character vector giving the row names for the data frame, and `optional` is ignored. See `?as.data.frame` for more information about these arguments.

`x[[i]]`: Return integer vector `start(x[i]):end(x[i])` denoted by `i`. Subscript `i` can be a single integer or a character string.

- `x[i]`: Return a new IPosRanges object (of the same type as `x`) made of the selected ranges. `i` can be a numeric vector, a logical vector, NULL or missing. If `x` is a [NormalIRanges](#) object and `i` a positive numeric subscript (i.e. a numeric vector of positive values), then `i` must be strictly increasing.
- `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 IPosRanges elements 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.
- `c(x, ..., ignore.mcols=FALSE)`: Concatenate IPosRanges object `x` and the IPosRanges objects in `...` together. See `?c` in the [S4Vectors](#) package for more information about concatenating Vector derivatives.
- `x * y`: The arithmetic operation `x * y` is for centered zooming. It symmetrically scales the width of `x` by  $1/y$ , where `y` is a numeric vector that is recycled as necessary. For example, `x * 2` results in ranges with half their previous width but with approximately the same midpoint. The ranges have been “zoomed in”. If `y` is negative, it is equivalent to `x * (1/abs(y))`. Thus, `x * -2` would double the widths in `x`. In other words, `x` has been “zoomed out”.
- `x + y`: Expands the ranges in `x` on either side by the corresponding value in the numeric vector `y`.
- `show(x)`: By default the `show` method displays 5 head and 5 tail lines. The number of lines can be altered by setting the global options `showHeadLines` and `showTailLines`. If the object length is less than the sum of the options, the full object is displayed. These options affect display of [IRanges](#), [IPos](#), [Hits](#), [GRanges](#), [GPos](#), [GAlignments](#), [XStringSet](#) objects, and more...

## Normality

An IPosRanges object `x` is implicitly representing an arbitrary finite set of integers (that are not necessarily consecutive). This set is the set obtained by taking the union of all the values in all the ranges in `x`. This representation is clearly not unique: many different IPosRanges objects can be used to represent the same set of integers. However one and only one of them is guaranteed to be *normal*.

By definition an IPosRanges object is said to be *normal* when its ranges are: (a) not empty (i.e. they have a non-null width); (b) not overlapping; (c) ordered from left to right; (d) not even adjacent (i.e. there must be a non empty gap between 2 consecutive ranges).

Here is a simple algorithm to determine whether `x` is *normal*: (1) if `length(x) == 0`, then `x` is normal; (2) if `length(x) == 1`, then `x` is normal iff `width(x) >= 1`; (3) if `length(x) >= 2`, then `x` is normal iff:

$$\text{start}(x)[i] \leq \text{end}(x)[i] < \text{start}(x)[i+1] \leq \text{end}(x)[i+1]$$

for every  $1 \leq i < \text{length}(x)$ .

The obvious advantage of using a *normal* IPosRanges object to represent a given finite set of integers is that it is the smallest in terms of number of ranges and therefore in terms of storage space. Also the fact that we impose its ranges to be ordered from left to right makes it unique for this representation.

A special container ([NormalIRanges](#)) is provided for holding a *normal* [IRanges](#) object: a [NormalIRanges](#) object is just an [IRanges](#) object that is guaranteed to be *normal*.

Here are some methods related to the notion of *normal* IPosRanges:

`isNormal(x)`: Return TRUE or FALSE indicating whether `x` is *normal* or not.

`whichFirstNotNormal(x)`: Return NA if `x` is *normal*, or the smallest valid indice `i` in `x` for which `x[1:i]` is not *normal*.

### Author(s)

H. Pagès and M. Lawrence

### See Also

- The [IRanges](#) class, a concrete `IPosRanges` direct subclass for storing a set of *integer ranges*.
- The [IPos](#) class, an `IPosRanges` direct subclass for representing a set of *integer positions* (i.e. *integer ranges* of width 1).
- [IPosRanges-comparison](#) for comparing and ordering ranges.
- [findOverlaps-methods](#) for finding/counting overlapping ranges.
- [intra-range-methods](#) and [inter-range-methods](#) for *intra range* and *inter range* transformations of `IntegerRanges` derivatives.
- [coverage-methods](#) for computing the coverage of a set of ranges.
- [setops-methods](#) for set operations on ranges.
- [nearest-methods](#) for finding the nearest range neighbor.

### Examples

```
## -----
## Basic manipulation
## -----
x <- IRanges(start=c(2:-1, 13:15), width=c(0:3, 2:0))
x
length(x)
start(x)
width(x)
end(x)
isEmpty(x)
as.matrix(x)
as.data.frame(x)

## Subsetting:
x[4:2]           # 3 ranges
x[-1]           # 6 ranges
x[FALSE]        # 0 range
x0 <- x[width(x) == 0] # 2 ranges
isEmpty(x0)

## Use the replacement methods to resize the ranges:
width(x) <- width(x) * 2 + 1
x
end(x) <- start(x)           # equivalent to width(x) <- 0
x
width(x) <- c(2, 0, 4)
```

```

x
start(x)[3] <- end(x)[3] - 2 # resize the 3rd range
x

## Name the elements:
names(x)
names(x) <- c("range1", "range2")
x
x[is.na(names(x))] # 5 ranges
x[!is.na(names(x))] # 2 ranges

ir <- IRanges(c(1,5), c(3,10))
ir*1 # no change
ir*c(1,2) # zoom second range by 2X
ir*-2 # zoom out 2X

```

---

IPosRanges-comparison *Comparing and ordering ranges*

---

## Description

Methods for comparing and/or ordering the ranges in [IPosRanges](#) derivatives (e.g. [IRanges](#), [IPos](#), or [NCList](#) objects).

## Usage

```

## match() & selfmatch()
## -----

## S4 method for signature 'IPosRanges,IPosRanges'
match(x, table, nomatch=NA_integer_, incomparables=NULL,
      method=c("auto", "quick", "hash"))

## S4 method for signature 'IPosRanges'
selfmatch(x, method=c("auto", "quick", "hash"))

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

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

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

## Generalized parallel comparison of 2 IPosRanges derivatives
## -----

```

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

rangeComparisonCodeToLetter(code)
```

### Arguments

|               |  |
|---------------|--|
| x, table, y   | IPosRanges derivatives e.g. IRanges, IPos, or NCList objects.  |
| nomatch       | The value to be returned in the case when no match is found. It is coerced to an integer.  |
| incomparables | Not supported.   |
| method        | For match and selfmatch: Use a Quicksort-based (method="quick") or a hash-based (method="hash") algorithm. The latter tends to give better performance, except maybe for some pathological input that we've not encountered so far. When method="auto" is specified, the most efficient algorithm will be used, that is, the hash-based algorithm if $\text{length}(x) \leq 2^{29}$ , otherwise the Quicksort-based algorithm.<br>For order: The method argument is ignored. |
| na.rm         | Ignored.   |
| strictly      | Logical indicating if the check should be for <i>strictly</i> increasing values.   |
| ...           | One or more IPosRanges derivatives. The 2nd and following objects are used to break ties.  |
| na.last       | Ignored.   |
| decreasing    | TRUE or FALSE.   |
| code          | A vector of codes as returned by pcompare.   |

### Details

Two ranges of an IPosRanges derivative are considered equal iff they share the same start and width. duplicated() and unique() on an IPosRanges derivative are conforming to this.

Note that with this definition, 2 empty ranges are generally not equal (they need to share the same start to be considered equal). This means that, when it comes to comparing ranges, an empty range is interpreted as a position between its end and start. For example, a typical usecase is comparison of insertion points defined along a string (like a DNA sequence) and represented as empty ranges.

The "natural order" for the elements of an IPosRanges derivative is to order them (a) first by start and (b) then by width. This way, the space of integer ranges is totally ordered.

pcompare(), ==, !=, <=, >=, < and > on IPosRanges derivatives behave accordingly to this "natural order".

is.unsorted(), order(), sort(), rank() on IPosRanges derivatives also behave accordingly to this "natural order".

Finally, note that some *inter range transformations* like reduce or disjoint also use this "natural order" implicitly when operating on IPosRanges derivatives.

`pcompare(x, y)`: Performs element-wise (aka "parallel") comparison of 2 [IPosRanges](#) objects of `x` and `y`, that is, returns an integer vector where the `i`-th element is a code describing how `x[i]` is qualitatively positioned with respect to `y[i]`.

Here is a summary of the 13 predefined codes (and their letter equivalents) and their meanings:

|  |   |
|--|---|
| -6 a: <code>x[i]: .0000.....</code><br><code>y[i]: .....0000.</code>     | 6 m: <code>x[i]: .....0000.</code><br><code>y[i]: .0000.....</code>     |
| -5 b: <code>x[i]: ..0000.....</code><br><code>y[i]: .....0000..</code>   | 5 l: <code>x[i]: .....0000..</code><br><code>y[i]: ..0000.....</code>   |
| -4 c: <code>x[i]: ...0000.....</code><br><code>y[i]: .....0000...</code> | 4 k: <code>x[i]: .....0000...</code><br><code>y[i]: ...0000.....</code> |
| -3 d: <code>x[i]: ...000000...</code><br><code>y[i]: .....0000...</code> | 3 j: <code>x[i]: .....0000...</code><br><code>y[i]: ...000000...</code> |
| -2 e: <code>x[i]: ..00000000..</code><br><code>y[i]: ....0000....</code> | 2 i: <code>x[i]: ....0000....</code><br><code>y[i]: ..00000000..</code> |
| -1 f: <code>x[i]: ...0000.....</code><br><code>y[i]: ...000000...</code> | 1 h: <code>x[i]: ...000000...</code><br><code>y[i]: ...0000.....</code> |
| 0 g: <code>x[i]: ...000000...</code><br><code>y[i]: ...000000...</code>  |   |

Note that this way of comparing ranges is a refinement over the standard ranges comparison defined by the `==`, `!=`, `<=`, `>=`, `<` and `>` operators. In particular a code that is `< 0`, `= 0`, or `> 0`, corresponds to `x[i] < y[i]`, `x[i] == y[i]`, or `x[i] > y[i]`, respectively.

The `pcompare` method for [IPosRanges](#) derivatives is guaranteed to return predefined codes only but methods for other objects (e.g. for [GenomicRanges](#) objects) can return non-predefined codes. Like for the predefined codes, the sign of any non-predefined code must tell whether `x[i]` is less than, or greater than `y[i]`.

`rangeComparisonCodeToLetter(x)`: Translate the codes returned by `pcompare`. The 13 predefined codes are translated as follow: -6 -> a; -5 -> b; -4 -> c; -3 -> d; -2 -> e; -1 -> f; 0 -> g; 1 -> h; 2 -> i; 3 -> j; 4 -> k; 5 -> l; 6 -> m. Any non-predefined code is translated to X. The translated codes are returned in a factor with 14 levels: a, b, ..., l, m, X.

`match(x, table, nomatch=NA_integer_, method=c("auto", "quick", "hash"))`: 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 range in `x`.

`selfmatch(x, method=c("auto", "quick", "hash"))`: Equivalent to, but more efficient than, `match(x, x, method=method)`.

`duplicated(x, fromLast=FALSE, method=c("auto", "quick", "hash"))`: Determines which elements of `x` are equal to elements with smaller subscripts, and returns a logical vector indicating which elements are duplicates. `duplicated(x)` is equivalent to, but more efficient than, `duplicated(as.data.frame(x))` on an [IPosRanges](#) derivative. See [duplicated](#) in the **base** package for more details.

`unique(x, fromLast=FALSE, method=c("auto", "quick", "hash"))`: Removes duplicate ranges from `x`. `unique(x)` is equivalent to, but more efficient than, `unique(as.data.frame(x))` on an [IPosRanges](#) derivative. 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 ranges in `table`. Returns a logical vector of length equal to the number of ranges in `x`.

`findMatches(x, table, method=c("auto", "quick", "hash"))`: An enhanced version of `match` that returns all the matches in a [Hits](#) object.

`countMatches(x, table, method=c("auto", "quick", "hash"))`: 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 (an [IPosRanges](#) derivative) into ascending order, breaking ties by further arguments (also [IPosRanges](#) derivatives).

`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 ranges in `x`. See [rank](#) in the **base** package for more details.

### Author(s)

Hervé Pagès

### See Also

- The [IPosRanges](#) class.
- [Vector-comparison](#) in the **S4Vectors** package for general information about comparing, ordering, and tabulating vector-like objects.
- [GenomicRanges-comparison](#) in the **GenomicRanges** package for comparing and ordering genomic ranges.
- [findOverlaps](#) for finding overlapping ranges.
- [intra-range-methods](#) and [inter-range-methods](#) for *intra range* and *inter range* transformations.
- [setops-methods](#) for set operations on [IRanges](#) objects.

### Examples

```
## -----
## A. ELEMENT-WISE (AKA "PARALLEL") COMPARISON OF 2 IPosRanges
##   DERIVATIVES
## -----
x0 <- IRanges(1:11, width=4)
x0
y0 <- IRanges(6, 9)
pcompare(x0, y0)
pcompare(IRanges(4:6, width=6), y0)
pcompare(IRanges(6:8, width=2), y0)
pcompare(x0, y0) < 0 # equivalent to 'x0 < y0'
pcompare(x0, y0) == 0 # equivalent to 'x0 == y0'
pcompare(x0, y0) > 0 # equivalent to 'x0 > y0'

rangeComparisonCodeToLetter(-10:10)
```



```

rangeComparisonCodeToLetter(pcompare(x0, y0))

## Handling of zero-width ranges (a.k.a. empty ranges):
x1 <- IRanges(11:17, width=0)
x1
pcompare(x1, x1[4])
pcompare(x1, IRanges(12, 15))

## Note that x1[2] and x1[6] are empty ranges on the edge of non-empty
## range IRanges(12, 15). Even though -1 and 3 could also be considered
## valid codes for describing these configurations, pcompare()
## considers x1[2] and x1[6] to be *adjacent* to IRanges(12, 15), and
## thus returns codes -5 and 5:
pcompare(x1[2], IRanges(12, 15)) # -5
pcompare(x1[6], IRanges(12, 15)) # 5

x2 <- IRanges(start=c(20L, 8L, 20L, 22L, 25L, 20L, 22L, 22L),
              width=c( 4L, 0L, 11L, 5L, 0L, 9L, 5L, 0L))
x2

which(width(x2) == 0) # 3 empty ranges
x2[2] == x2[2] # TRUE
x2[2] == x2[5] # FALSE
x2 == x2[4]
x2 >= x2[3]

## -----
## B. match(), selfmatch(), %in%, duplicated(), unique()
## -----
table <- x2[c(2:4, 7:8)]
match(x2, table)

x2 %in% table

duplicated(x2)
unique(x2)

## -----
## C. findMatches(), countMatches()
## -----
findMatches(x2, table)
countMatches(x2, table)

x2_levels <- unique(x2)
countMatches(x2_levels, x2)

## -----
## D. order() AND RELATED METHODS
## -----
is.unsorted(x2)
order(x2)
sort(x2)
rank(x2, ties.method="first")

```

---

|                   |                          |
|-------------------|--------------------------|
| IRanges internals | <i>IRanges internals</i> |
|-------------------|--------------------------|

---

### Description

Objects, classes and methods defined in the **IRanges** package that are not intended to be used directly.

---

|               |  |
|---------------|--|
| IRanges-class | <i>IRanges and NormalIRanges objects</i> |
|---------------|--|

---

### Description

The IRanges class is a simple implementation of the [IntegerRanges](#) container where 2 integer vectors of the same length are used to store the start and width values. See the [IntegerRanges](#) virtual class for a formal definition of [IntegerRanges](#) objects and for their methods (all of them should work for IRanges objects).

Some subclasses of the IRanges class are: [NormalIRanges](#), [Views](#), etc...

A [NormalIRanges](#) object is just an IRanges object that is guaranteed to be "normal". See the Normality section in the man page for [IntegerRanges](#) objects for the definition and properties of "normal" [IntegerRanges](#) objects.

### Constructor

See [?IRanges-constructor](#).

### Coercion

`ranges(x, use.names=FALSE, use.mcols=FALSE)`: Squeeze the ranges out of [IntegerRanges](#) object `x` and return them in an IRanges object *parallel* to `x` (i.e. same length as `x`).

`as(from, "IRanges")`: Creates an IRanges instance from an [IntegerRanges](#) derivative, or from a logical or integer vector. When `from` is a logical vector, the resulting IRanges object contains the indices for the runs of TRUE values. When `from` is an integer vector, the elements are either singletons or "increase by 1" sequences.

`as(from, "NormalIRanges")`: Creates a [NormalIRanges](#) instance from a logical or integer vector. When `from` is an integer vector, the elements must be strictly increasing.

### Concatenation

`c(x, ..., ignore.mcols=FALSE)`: Concatenate IRanges object `x` and the IRanges objects in `...` together. See [?c](#) in the **S4Vectors** package for more information about concatenating Vector derivatives.

**Methods for NormalIRanges objects**

`max(x)`: The maximum value in the finite set of integers represented by `x`.

`min(x)`: The minimum value in the finite set of integers represented by `x`.

**Author(s)**

Hervé Pagès

**See Also**

- The [GRanges](#) class in the **GenomicRanges** package for storing a set of *genomic ranges*.
- The [IPos](#) class for representing a set of *integer positions* (i.e. *integer ranges* of width 1).
- [IPosRanges-comparison](#) for comparing and ordering integer ranges and/or positions.
- [IRanges-utils](#) for some utility functions for creating or modifying IRanges objects.
- [findOverlaps-methods](#) for finding overlapping integer ranges and/or positions.
- [intra-range-methods](#) and [inter-range-methods](#) for *intra range* and *inter range* transformations.
- [coverage-methods](#) for computing the coverage of a set of ranges and/or positions.
- [setops-methods](#) for set operations on IRanges objects.
- [nearest-methods](#) for finding the nearest integer range/position neighbor.

**Examples**

```
showClass("IRanges") # shows the known subclasses

## -----
## A. MANIPULATING IRanges OBJECTS
## -----
## All the methods defined for IntegerRanges objects work on IRanges
## objects.
## See ?IntegerRanges for some examples.
## Also see ?`IRanges-utils` and ?`setops-methods` for additional
## operations on IRanges objects.

## Concatenating IRanges objects
ir1 <- IRanges(c(1, 10, 20), width=5)
mcols(ir1) <- DataFrame(score=runif(3))
ir2 <- IRanges(c(101, 110, 120), width=10)
mcols(ir2) <- DataFrame(score=runif(3))
ir3 <- IRanges(c(1001, 1010, 1020), width=20)
mcols(ir3) <- DataFrame(value=runif(3))
some.iranges <- c(ir1, ir2)
## all.iranges <- c(ir1, ir2, ir3) ## This will raise an error
all.iranges <- c(ir1, ir2, ir3, ignore.mcols=TRUE)
stopifnot(is.null(mcols(all.iranges)))

## -----
## B. A NOTE ABOUT PERFORMANCE
## -----
```

```

## Using an IRanges object for storing a big set of ranges is more
## efficient than using a standard R data frame:
N <- 2000000L # nb of ranges
W <- 180L     # width of each range
start <- 1L
end <- 50000000L
set.seed(777)
range_starts <- sort(sample(end-W+1L, N))
range_widths <- rep.int(W, N)
## Instantiation is faster
system.time(x <- IRanges(start=range_starts, width=range_widths))
system.time(y <- data.frame(start=range_starts, width=range_widths))
## Subsetting is faster
system.time(x16 <- x[c(TRUE, rep.int(FALSE, 15))])
system.time(y16 <- y[c(TRUE, rep.int(FALSE, 15)), ])
## Internal representation is more compact
object.size(x16)
object.size(y16)

```

---

IRanges-constructor     *The IRanges constructor and supporting functions*

---

## Description

The IRanges function is a constructor that can be used to create IRanges instances.

solveUserSEW is a low-level utility function for solving a set of user-supplied start/end/width triplets.

## Usage

```

## IRanges constructor:
IRanges(start=NULL, end=NULL, width=NULL, names=NULL, ...)

## Supporting functions (not for the end user):
solveUserSEW(refwidths, start=NA, end=NA, width=NA,
             rep.refwidths=FALSE,
             translate.negative.coord=TRUE,
             allow.nonnarrowing=FALSE)

```

## Arguments

|                   |  |
|-------------------|--|
| start, end, width | For IRanges: NULL or vector of integers.<br>For solveUserSEW: vector of integers (eventually with NAs).  |
| names             | A character vector or NULL.  |
| ...               | Metadata columns to set on the IRanges object. All the metadata columns must be vector-like objects of the same length as the object to construct. |

|   |   |
|---|---|
| <code>refwidths</code>                                    | Vector of non-NA non-negative integers containing the reference widths.   |
| <code>rep.refwidths</code>                                | TRUE or FALSE. Use of <code>rep.refwidths=TRUE</code> is supported only when <code>refwidths</code> is of length 1. |
| <code>translate.negative.coord, allow.nonnarrowing</code> | TRUE or FALSE.  |

### IRanges constructor

Return the IRanges object containing the ranges specified by `start`, `end` and `width`. Input falls into one of two categories:

**Category 1** `start`, `end` and `width` are numeric vectors (or NULLs). If necessary they are recycled to the length of the longest (NULL arguments are filled with NAs). After this recycling, each row in the 3-column matrix obtained by binding those 3 vectors together is "solved" i.e. NAs are treated as unknown in the equation  $end = start + width - 1$ . Finally, the solved matrix is returned as an IRanges instance.

**Category 2** The `start` argument is a logical vector or logical Rle object and `IRanges(start)` produces the same result as `as(start, "IRanges")`. Note that, in that case, the returned IRanges instance is guaranteed to be normal.

Note that the `names` argument is never recycled (to remain consistent with what ``names<-`` does on standard vectors).

### Supporting functions

`solveUserSEW(refwidths, start=NA, end=NA, width=NA, rep.refwidths=FALSE, translate.negative.coord=TRUE)`

Use of `rep.refwidths=TRUE` is supported only when `refwidths` is of length 1. If `rep.refwidths=FALSE` (the default) then `start`, `end` and `width` are recycled to the length of `refwidths` (it's an error if one of them is longer than `refwidths`, or is of zero length while `refwidths` is not). If `rep.refwidths=TRUE` then `refwidths` is first replicated `L` times where `L` is the length of the longest of `start`, `end` and `width`. After this replication, `start`, `end` and `width` are recycled to the new length of `refwidths` (`L`) (it's an error if one of them is of zero length while `L` is != 0).

From now, `refwidths`, `start`, `end` and `width` are integer vectors of equal lengths. Each row in the 3-column matrix obtained by binding those 3 vectors together must contain at least one NA (otherwise an error is returned). Then each row is "solved" i.e. the 2 following transformations are performed (`i` is the indice of the row): (1) if `translate.negative.coord` is TRUE then a negative value of `start[i]` or `end[i]` is considered to be a `-refwidths[i]`-based coordinate so `refwidths[i]+1` is added to it to make it 1-based; (2) the NAs in the row are treated as unknowns which values are deduced from the known values in the row and from `refwidths[i]`.

The exact rules for (2) are the following. Rule (2a): if the row contains at least 2 NAs, then `width[i]` must be one of them (otherwise an error is returned), and if `start[i]` is one of them it is replaced by 1, and if `end[i]` is one of them it is replaced by `refwidths[i]`, and finally `width[i]` is replaced by `end[i] - start[i] + 1`. Rule (2b): if the row contains only 1 NA, then it is replaced by the solution of the `width[i] == end[i] - start[i] + 1` equation.

Finally, the set of solved rows is returned as an IRanges object of the same length as `refwidths` (after replication if `rep.refwidths=TRUE`).

Note that an error is raised if either (1) the set of user-supplied start/end/width values is invalid or (2) `allow.nonnarrowing` is `FALSE` and the ranges represented by the solved start/end/width values are not narrowing the ranges represented by the user-supplied start/end/width values.

### Author(s)

Hervé Pagès

### See Also

- [IRanges-class](#) for the IRanges class.
- [narrow](#)

### Examples

```
## -----
## A. USING THE IRanges() CONSTRUCTOR
## -----
IRanges(start=11, end=rep.int(20, 5))
IRanges(start=11, width=rep.int(20, 5))
IRanges(-2, 20) # only one range
IRanges(start=c(2, 0, NA), end=c(NA, NA, 14), width=11:0)
IRanges() # IRanges instance of length zero
IRanges(names=character())

## With ranges specified as strings:
IRanges(c("11-20", "15-14", "-4--2"))

## With logical input:
x <- IRanges(c(FALSE, TRUE, TRUE, FALSE, TRUE)) # logical vector input
isNormal(x) # TRUE
x <- IRanges(Rle(1:30) %>= 5 <= 2) # logical Rle input
isNormal(x) # TRUE

## -----
## B. USING solveUserSEW()
## -----
refwidths <- c(5:3, 6:7)
refwidths

solveUserSEW(refwidths)
solveUserSEW(refwidths, start=4)
solveUserSEW(refwidths, end=3, width=2)
solveUserSEW(refwidths, start=-3)
solveUserSEW(refwidths, start=-3, width=2)
solveUserSEW(refwidths, end=-4)

## The start/end/width arguments are recycled:
solveUserSEW(refwidths, start=c(3, -4, NA), end=c(-2, NA))

## Using 'rep.refwidths=TRUE':
```

```
solveUserSEW(10, start=-(1:6), rep.refwidths=TRUE)
solveUserSEW(10, end=-(1:6), width=3, rep.refwidths=TRUE)
```

---

IRanges-utils

*IRanges utility functions*


---

## Description

Utility functions for creating or modifying [IRanges](#) objects.

## Usage

```
## Create an IRanges instance:
successiveIRanges(width, gapwidth=0, from=1)
breakInChunks(totalsize, nchunk, chunksize)

## Turn a logical vector into a set of ranges:
whichAsIRanges(x)

## Coercion:
asNormalIRanges(x, force=TRUE)
```

## Arguments

|           |   |
|-----------|---|
| width     | A vector of non-negative integers (with no NAs) specifying the widths of the ranges to create.  |
| gapwidth  | A single integer or an integer vector with one less element than the width vector specifying the widths of the gaps separating one range from the next one. |
| from      | A single integer specifying the starting position of the first range.   |
| totalsize | A single non-negative integer. The total size of the object to break.   |
| nchunk    | A single positive integer. The number of chunks.  |
| chunksize | A single positive integer. The size of the chunks (last chunk might be smaller).  |
| x         | A logical vector for whichAsIRanges.<br>An <a href="#">IRanges</a> object for asNormalIRanges.  |
| force     | TRUE or FALSE. Should x be turned into a <a href="#">NormalIRanges</a> object even if isNormal(x) is FALSE?   |

## Details

successiveIRanges returns an [IRanges](#) instance containing the ranges that have the widths specified in the width vector and are separated by the gaps specified in gapwidth. The first range starts at position from. When gapwidth=0 and from=1 (the defaults), the returned IRanges can be seen as a partitioning of the 1:sum(width) interval. See [?Partitioning](#) for more details on this.

breakInChunks returns a [PartitioningByEnd](#) object describing the "chunks" that result from breaking a vector-like object of length totalsize in the chunks described by nchunk or chunksize.

whichAsIRanges returns an [IRanges](#) instance containing all of the ranges where x is TRUE.

If force=TRUE (the default), then asNormalIRanges will turn x into a [NormalIRanges](#) instance by reordering and reducing the set of ranges if necessary (i.e. only if isNormal(x) is FALSE, otherwise the set of ranges will be untouched). If force=FALSE, then asNormalIRanges will turn x into a [NormalIRanges](#) instance only if isNormal(x) is TRUE, otherwise it will raise an error. Note that when force=FALSE, the returned object is guaranteed to contain exactly the same set of ranges than x. as(x, "NormalIRanges") is equivalent to asNormalIRanges(x, force=TRUE).

### Author(s)

Hervé Pagès

### See Also

- [IRanges](#) objects.
- [Partitioning](#) objects.
- [equisplit](#) for splitting a list-like object into a specified number of partitions.
- [intra-range-methods](#) and [inter-range-methods](#) for intra range and inter range transformations.
- [setops-methods](#) for performing set operations on [IRanges](#) objects.
- [solveUserSEW](#)
- [successiveViews](#)

### Examples

```
vec <- as.integer(c(19, 5, 0, 8, 5))

successiveIRanges(vec)

breakInChunks(600999, chunksize=50000) # chunks of size 50000 (last
                                         # chunk is smaller)

whichAsIRanges(vec >= 5)

x <- IRanges(start=c(-2L, 6L, 9L, -4L, 1L, 0L, -6L, 10L),
             width=c( 5L, 0L, 6L,  1L, 4L, 3L,  2L,  3L))
asNormalIRanges(x) # 3 non-empty ranges ordered from left to right and
                  # separated by gaps of width >= 1.

## More on normality:
example(`IRanges-class`)
isNormal(x16) # FALSE
if (interactive())
  x16 <- asNormalIRanges(x16) # Error!
whichFirstNotNormal(x16) # 57
isNormal(x16[1:56]) # TRUE
xx <- asNormalIRanges(x16[1:56])
class(xx)
max(xx)
min(xx)
```



---

IRangesList-class      *List of IRanges and NormalIRanges*

---

### Description

[IRangesList](#) and [NormalIRangesList](#) objects for storing [IRanges](#) and [NormalIRanges](#) objects respectively.

### Constructor

`IRangesList(..., compress=TRUE)`: The ... argument accepts either a comma-separated list of [IRanges](#) objects, or a single [LogicalList](#) / [logicalRleList](#) object, or 2 elements named `start` and `end` each of them being either a list of integer vectors or an [IntegerList](#) object. When [IRanges](#) objects are supplied, each of them becomes an element in the new [IRangesList](#), in the same order, which is analogous to the `list` constructor. If `compress`, the internal storage of the data is compressed.

### Coercion

In the code snippets below, `from` is a *list-like* object.

`as(from, "SimpleIRangesList")`: Coerces `from`, to a [SimpleIRangesList](#), requiring that all [IntegerRanges](#) elements are coerced to internal [IRanges](#) elements. This is a convenient way to ensure that all [IntegerRanges](#) have been imported into R (and that there is no unwanted overhead when accessing them).

`as(from, "CompressedIRangesList")`: Coerces `from`, to a [CompressedIRangesList](#), requiring that all [IntegerRanges](#) elements are coerced to internal [IRanges](#) elements. This is a convenient way to ensure that all [IntegerRanges](#) have been imported into R (and that there is no unwanted overhead when accessing them).

`as(from, "SimpleNormalIRangesList")`: Coerces `from`, to a [SimpleNormalIRangesList](#), requiring that all [IntegerRanges](#) elements are coerced to internal [NormalIRanges](#) elements.

`as(from, "CompressedNormalIRangesList")`: Coerces `from`, to a [CompressedNormalIRangesList](#), requiring that all [IntegerRanges](#) elements are coerced to internal [NormalIRanges](#) elements.

In the code snippet below, `x` is an [IRangesList](#) object.

`unlist(x)`: Unlists `x`, an [IRangesList](#), by concatenating all of the ranges into a single [IRanges](#) instance. If the length of `x` is zero, an empty [IRanges](#) is returned.

### Methods for NormalIRangesList objects

`max(x)`: An integer vector containing the maximum values of each of the elements of `x`.

`min(x)`: An integer vector containing the minimum values of each of the elements of `x`.

### Author(s)

Michael Lawrence and Hervé Pagès

**See Also**

- [IntegerRangesList](#), the parent of this class, for more functionality.
- [intra-range-methods](#) and [inter-range-methods](#) for *intra range* and *inter range* transformations.
- [setops-methods](#) for set operations on IRangesList objects.

**Examples**

```

range1 <- IRanges(start=c(1,2,3), end=c(5,2,8))
range2 <- IRanges(start=c(15,45,20,1), end=c(15,100,80,5))
named <- IRangesList(one = range1, two = range2)
length(named) # 2
names(named) # "one" and "two"
named[[1]] # range1
unnamed <- IRangesList(range1, range2)
names(unnamed) # NULL

x <- IRangesList(start=list(c(1,2,3), c(15,45,20,1)),
                 end=list(c(5,2,8), c(15,100,80,5)))
as.list(x)

```

---

MaskCollection-class    *MaskCollection objects*

---

**Description**

The MaskCollection class is a container for storing a collection of masks that can be used to mask regions in a sequence.

**Details**

In the context of the Biostrings package, a mask is a set of regions in a sequence that need to be excluded from some computation. For example, when calling [alphabetFrequency](#) or [matchPattern](#) on a chromosome sequence, you might want to exclude some regions like the centromere or the repeat regions. This can be achieved by putting one or several masks on the sequence before calling [alphabetFrequency](#) on it.

A MaskCollection object is a vector-like object that represents such set of masks. Like standard R vectors, it has a "length" which is the number of masks contained in it. But unlike standard R vectors, it also has a "width" which determines the length of the sequences it can be "put on". For example, a MaskCollection object of width 20000 can only be put on an [XString](#) object of 20000 letters.

Each mask in a MaskCollection object *x* is just a finite set of integers that are  $\geq 1$  and  $\leq \text{width}(x)$ . When "put on" a sequence, these integers indicate the positions of the letters to mask. Internally, each mask is represented by a [NormalIRanges](#) object.

**Basic accessor methods**

In the code snippets below, *x* is a MaskCollection object.

`length(x)`: The number of masks in *x*.

`width(x)`: The common width of all the masks in *x*. This determines the length of the sequences that *x* can be "put on".

`active(x)`: A logical vector of the same length as *x* where each element indicates whether the corresponding mask is active or not.

`names(x)`: NULL or a character vector of the same length as *x*.

`desc(x)`: NULL or a character vector of the same length as *x*.

`nir_list(x)`: A list of the same length as *x*, where each element is a [NormalIRanges](#) object representing a mask in *x*.

**Constructor**

`Mask(mask.width, start=NULL, end=NULL, width=NULL)`: Return a single mask (i.e. a MaskCollection object of length 1) of width `mask.width` (a single integer  $\geq 1$ ) and masking the ranges of positions specified by `start`, `end` and `width`. See the [IRanges](#) constructor (`?IRanges`) for how `start`, `end` and `width` can be specified. Note that the returned mask is active and unnamed.

**Other methods**

In the code snippets below, *x* is a MaskCollection object.

`isEmpty(x)`: Return a logical vector of the same length as *x*, indicating, for each mask in *x*, whether it's empty or not.

`max(x)`: The greatest (or last, or rightmost) masked position for each mask. This is a numeric vector of the same length as *x*.

`min(x)`: The smallest (or first, or leftmost) masked position for each mask. This is a numeric vector of the same length as *x*.

`maskedwidth(x)`: The number of masked position for each mask. This is an integer vector of the same length as *x* where all values are  $\geq 0$  and  $\leq \text{width}(x)$ .

`maskedratio(x)`: `maskedwidth(x) / width(x)`

**Subsetting and appending**

In the code snippets below, *x* and *values* are MaskCollection objects.

`x[i]`: Return a new MaskCollection object made of the selected masks. Subscript *i* can be a numeric, logical or character vector.

`x[[i, exact=TRUE]]`: Extract the mask selected by *i* as a [NormalIRanges](#) object. Subscript *i* can be a single integer or a character string.

`append(x, values, after=length(x))`: Add masks in *values* to *x*.

**Other methods**

In the code snippets below, x is a MaskCollection object.

`collapse(x)`: Return a MaskCollection object of length 1 obtained by collapsing all the active masks in x.

**Author(s)**

Hervé Pagès

**See Also**

[NormalIRanges-class](#), [read.Mask](#), [MaskedXString-class](#), [reverse](#), [alphabetFrequency](#), [matchPattern](#)

**Examples**

```
## Making a MaskCollection object:
mask1 <- Mask(mask.width=29, start=c(11, 25, 28), width=c(5, 2, 2))
mask2 <- Mask(mask.width=29, start=c(3, 10, 27), width=c(5, 8, 1))
mask3 <- Mask(mask.width=29, start=c(7, 12), width=c(2, 4))
mymasks <- append(append(mask1, mask2), mask3)
mymasks
length(mymasks)
width(mymasks)
collapse(mymasks)

## Names and descriptions:
names(mymasks) <- c("A", "B", "C") # names should be short and unique...
mymasks
mymasks[c("C", "A")] # ...to make subsetting by names easier
desc(mymasks) <- c("you can be", "more verbose", "here")
mymasks[-2]

## Activate/deactivate masks:
active(mymasks)["B"] <- FALSE
mymasks
collapse(mymasks)
active(mymasks) <- FALSE # deactivate all masks
mymasks
active(mymasks)[-1] <- TRUE # reactivate all masks except mask 1
active(mymasks) <- !active(mymasks) # toggle all masks

## Other advanced operations:
mymasks[[2]]
length(mymasks[[2]])
mymasks[[2]][-3]
append(mymasks[-2], gaps(mymasks[2]))
```

---

`multisplit`*Split elements belonging to multiple groups*

---

**Description**

This is like `split`, except elements can belong to multiple groups, in which case they are repeated to appear in multiple elements of the return value.

**Usage**

```
multisplit(x, f)
```

**Arguments**

|                |   |
|----------------|---|
| <code>x</code> | The object to split, like a vector.   |
| <code>f</code> | A list-like object of vectors, the same length as <code>x</code> , where each element indicates the groups to which each element of <code>x</code> belongs. |

**Value**

A list-like object, with an element for each unique value in the unlisted `f`, containing the elements in `x` where the corresponding element in `f` contained that value. Just try it.

**Author(s)**

Michael Lawrence

**Examples**

```
multisplit(1:3, list(letters[1:2], letters[2:3], letters[2:4]))
```

---

`NList-class`*Nested Containment List objects*

---

**Description**

The `NList` class is a container for storing the Nested Containment List representation of a `IntegerRanges` object. Preprocessing a `IntegerRanges` object as a Nested Containment List allows efficient overlap-based operations like `findOverlaps`.

The `NLists` class is a container for storing a collection of `NList` objects. An `NLists` object is typically the result of preprocessing each list element of a `IntegerRangesList` object as a Nested Containment List. Like with `NList`, the `NLists` object can then be used for efficient overlap-based operations.

To preprocess a `IntegerRanges` or `IntegerRangesList` object, simply call the `NList` or `NLists` constructor function on it.

**Usage**

```
NCList(x, circle.length=NA_integer_)
NCLists(x, circle.length=NA_integer_)
```

**Arguments**

**x** The [IntegerRanges](#) or [IntegerRangesList](#) object to preprocess.

**circle.length** Use only if the space (or spaces if **x** is a [IntegerRangesList](#) object) on top of which the ranges in **x** are defined needs (need) to be considered circular. If that's the case, then use **circle.length** to specify the length(s) of the circular space(s).  
 For [NCList](#), **circle.length** must be a single positive integer (or NA if the space is linear).  
 For [NCLists](#), it must be an integer vector parallel to **x** (i.e. same length) and with positive or NA values (NAs indicate linear spaces).

**Details**

The [GenomicRanges](#) package also defines the [GNCList](#) constructor and class for preprocessing and representing a vector of genomic ranges as a data structure based on Nested Containment Lists.

Some important differences between the new [findOverlaps](#)/[countOverlaps](#) implementation based on Nested Containment Lists (BioC >= 3.1) and the old implementation based on Interval Trees (BioC < 3.1):

- With the new implementation, the hits returned by [findOverlaps](#) are not *fully* ordered (i.e. ordered by [queryHits](#) and [subjectHits](#)) anymore, but only *partially* ordered (i.e. ordered by [queryHits](#) only). Other than that, and except for the 2 particular situations mentioned below, the 2 implementations produce the same output. However, the new implementation is faster and more memory efficient.
- With the new implementation, either the query or the subject can be preprocessed with [NCList](#) for a [IntegerRanges](#) object (replacement for [IntervalTree](#)), [NCLists](#) for a [IntegerRangesList](#) object (replacement for [IntervalForest](#)), and [GNCList](#) for a [GenomicRanges](#) object (replacement for [GIntervalTree](#)). However, for a one-time use, it is NOT advised to explicitly preprocess the input. This is because [findOverlaps](#) or [countOverlaps](#) will take care of it and do a better job at it (by preprocessing only what's needed when it's needed, and releasing memory as they go).
- With the new implementation, [countOverlaps](#) on [IntegerRanges](#) or [GenomicRanges](#) objects doesn't call [findOverlaps](#) in order to collect all the hits in a growing [Hits](#) object and count them only at the end. Instead, the counting happens at the C level and the hits are not kept. This reduces memory usage considerably when there is a lot of hits.
- When `minoverlap=0`, zero-width ranges are now interpreted as insertion points and considered to overlap with ranges that contain them. With the old algorithm, zero-width ranges were always ignored. This is the 1st situation where the new and old implementations produce different outputs.
- When using `select="arbitrary"`, the new implementation will generally not select the same hits as the old implementation. This is the 2nd situation where the new and old implementations produce different outputs.

- The new implementation supports preprocessing of a [GenomicRanges](#) object with ranges defined on circular sequences (e.g. on the mitochondrial chromosome). See [GNCList](#) in the [GenomicRanges](#) package for some examples.
- Objects preprocessed with `NCList`, `NCLists`, and [GNCList](#) are serializable (with `save`) for later use. Not a typical thing to do though, because preprocessing is very cheap (i.e. very fast and memory efficient).

### Value

An `NCList` object for the `NCList` constructor and an `NCLists` object for the `NCLists` constructor.

### Author(s)

Hervé Pagès

### References

Alexander V. Alekseyenko and Christopher J. Lee – Nested Containment List (NCList): a new algorithm for accelerating interval query of genome alignment and interval databases. *Bioinformatics* (2007) 23 (11): 1386-1393. doi: 10.1093/bioinformatics/btl647

### See Also

- The [GNCList](#) constructor and class defined in the [GenomicRanges](#) package.
- [findOverlaps](#) for finding/counting interval overlaps between two *range-based* objects.
- [IntegerRanges](#) and [IntegerRangesList](#) objects.

### Examples

```
## The example below is for illustration purpose only and does NOT
## reflect typical usage. This is because, for a one-time use, it is
## NOT advised to explicitly preprocess the input for findOverlaps()
## or countOverlaps(). These functions will take care of it and do a
## better job at it (by preprocessing only what's needed when it's
## needed, and release memory as they go).

query <- IRanges(c(1, 4, 9), c(5, 7, 10))
subject <- IRanges(c(2, 2, 10), c(2, 3, 12))

## Either the query or the subject of findOverlaps() can be preprocessed:

ppsubject <- NCList(subject)
hits1 <- findOverlaps(query, ppsubject)
hits1

ppquery <- NCList(query)
hits2 <- findOverlaps(ppquery, subject)
hits2

## Note that 'hits1' and 'hits2' contain the same hits but not in the
```

```
## same order.
stopifnot(identical(sort(hits1), sort(hits2)))
```

---

nearest-methods

*Finding the nearest range/position neighbor*


---

## Description

The `nearest()`, `precede()`, `follow()`, `distance()` and `distanceToNearest()` methods for [IntegerRanges](#) derivatives (e.g. [IRanges](#) objects).

## Usage

```
## S4 method for signature 'IntegerRanges,IntegerRanges_OR_missing'
nearest(x, subject, select=c("arbitrary", "all"))

## S4 method for signature 'IntegerRanges,IntegerRanges_OR_missing'
precede(x, subject, select=c("first", "all"))

## S4 method for signature 'IntegerRanges,IntegerRanges_OR_missing'
follow(x, subject, select=c("last", "all"))

## S4 method for signature 'IntegerRanges,IntegerRanges'
distance(x, y)
## S4 method for signature 'Pairs,missing'
distance(x, y)

## S4 method for signature 'IntegerRanges,IntegerRanges_OR_missing'
distanceToNearest(x, subject, select=c("arbitrary", "all"))
```

## Arguments

|                      |  |
|----------------------|--|
| <code>x</code>       | The query <a href="#">IntegerRanges</a> derivative, or (for <code>distance()</code> ) a <a href="#">Pairs</a> object containing both the query (first) and subject (second).   |
| <code>subject</code> | The subject <a href="#">IntegerRanges</a> object, within which the nearest neighbors are found. Can be missing, in which case <code>x</code> is also the subject.  |
| <code>select</code>  | Logic for handling ties. By default, all the methods select a single interval (arbitrary for <code>nearest</code> , the first by order in <code>subject</code> for <code>precede</code> , and the last for <code>follow</code> ). To get all matchings, as a <a href="#">Hits</a> object, use <code>"all"</code> . |
| <code>y</code>       | For the <code>distance</code> method, a <a href="#">IntegerRanges</a> derivative. 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>hits</code>    | The hits between <code>x</code> and <code>subject</code>   |
| <code>...</code>     | Additional arguments for methods   |



## Details

- `nearest(x, subject, select=c("arbitrary", "all"))`: The conventional nearest neighbor finder. Returns an integer vector containing the index of the nearest neighbor range in `subject` for each range in `x`. If there is no nearest neighbor (if `subject` is empty), NA's are returned.

Here is roughly how it proceeds, for a range `xi` in `x`:

1. Find the ranges in `subject` that overlap `xi`. If a single range `si` in `subject` overlaps `xi`, `si` is returned as the nearest neighbor of `xi`. If there are multiple overlaps, one of the overlapping ranges is chosen arbitrarily.
  2. If no ranges in `subject` overlap with `xi`, then the range in `subject` with the shortest distance from its end to the start `xi` or its start to the end of `xi` is returned.
- `precede(x, subject, select=c("first", "all"))`: For each range in `x`, `precede` returns the index of the interval in `subject` that is directly preceded by the query range. Overlapping ranges are excluded. NA is returned when there are no qualifying ranges in `subject`.
  - `follow(x, subject, select=c("last", "all"))`: The opposite of `precede`, this function returns the index of the range in `subject` that a query range in `x` directly follows. Overlapping ranges are excluded. NA is returned when there are no qualifying ranges in `subject`.
  - `distance(x, y)`: Returns the distance for each range in `x` to the range in `y`.

The distance method differs from others documented on this page in that it is symmetric; `y` cannot be missing. If `x` and `y` are not the same length, the shortest will be recycled to match the length of the longest. The `select` argument is not available for `distance` because comparisons are made in a pair-wise fashion. The return value is the length of the longest of `x` and `y`.

The distance calculation changed in BioC 2.12 to accommodate zero-width ranges in a consistent and intuitive manner. The new distance can be explained by a *block* model where a range is represented by a series of blocks of size 1. Blocks are adjacent to each other and there is no gap between them. A visual representation of `IRanges(4, 7)` would be

```
+-----+-----+-----+-----+
  4       5       6       7
```

The distance between two consecutive blocks is 0L (prior to Bioconductor 2.12 it was 1L). The new distance calculation now returns the size of the gap between two ranges.

This change to `distance` affects the notion of overlaps in that we no longer say:

`x` and `y` overlap  $\Leftrightarrow$  `distance(x, y) == 0`

Instead we say

`x` and `y` overlap  $\Rightarrow$  `distance(x, y) == 0`

or

`x` and `y` overlap or are adjacent  $\Leftrightarrow$  `distance(x, y) == 0`

- `distanceToNearest(x, subject, select=c("arbitrary", "all"))`: Returns the distance for each range in `x` to its nearest neighbor in `subject`.
- `selectNearest(hits, x, subject)`: Selects the hits that have the minimum distance within those for each query range. Ties are possible and can be broken with `breakTies`.

**Value**

For `nearest()`, `precede()` and `follow()`, an integer vector of indices in `subject`, or a [Hits](#) object if `select="all"`.

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

For `distanceToNearest()`, a [Hits](#) object with a metadata column reporting the distance between the pair. Access the distance metadata column with the `mcols()` accessor.

For `selectNearest()`, a [Hits](#) object, sorted by query.

**Author(s)**

M. Lawrence

**See Also**

- [Hits](#) objects implemented in the **S4Vectors** package.
- [findOverlaps](#) for finding just the overlapping ranges.
- The [IntegerRanges](#) class.
- [nearest-methods](#) in the **GenomicRanges** package for the `nearest()`, `precede()`, `follow()`, `distance()`, and `distanceToNearest()` methods for [GenomicRanges](#) objects.

**Examples**

```
## -----
## precede() and follow()
## -----
query <- IRanges(c(1, 3, 9), c(3, 7, 10))
subject <- IRanges(c(3, 2, 10), c(3, 13, 12))

precede(query, subject)      # c(3L, 3L, NA)
precede(IRanges(), subject) # integer()
precede(query, IRanges())   # rep(NA_integer_, 3)
precede(query)              # c(3L, 3L, NA)

follow(query, subject)      # c(NA, NA, 1L)
follow(IRanges(), subject) # integer()
follow(query, IRanges())   # rep(NA_integer_, 3)
follow(query)               # c(NA, NA, 2L)

## -----
## nearest()
## -----
query <- IRanges(c(1, 3, 9), c(2, 7, 10))
subject <- IRanges(c(3, 5, 12), c(3, 6, 12))

nearest(query, subject) # c(1L, 1L, 3L)
nearest(query)         # c(2L, 1L, 2L)

## -----
## distance()
```

```
## -----
## adjacent
distance(IRanges(1,5), IRanges(6,10)) # 0L
## overlap
distance(IRanges(1,5), IRanges(3,7)) # 0L
## zero-width
sapply(-3:3, function(i) distance(shift(IRanges(4,3), i), IRanges(4,3)))
```

---

range-squeezers

*Squeeze the ranges out of a range-based object*


---

## Description

S4 generic functions for squeezing the ranges out of a range-based object.

These are analog to range squeezers `granges` and `grglist` defined in the **GenomicRanges** package, except that `ranges` returns the ranges in an `IRanges` object (instead of a `GRanges` object for `granges`), and `rglist` returns them in an `IRangesList` object (instead of a `GRangesList` object for `grglist`).

## Usage

```
ranges(x, use.names=TRUE, use.mcols=FALSE, ...)
rglist(x, use.names=TRUE, use.mcols=FALSE, ...)
```

## Arguments

|                        |  |
|------------------------|--|
| <code>x</code>         | An object containing ranges e.g. a <code>IntegerRanges</code> , <code>GenomicRanges</code> , <code>RangedSummarizedExperiment</code> , <code>GAlignments</code> , <code>GAlignmentPairs</code> , or <code>GAlignmentsList</code> object, or a <code>Pairs</code> object containing ranges. |
| <code>use.names</code> | TRUE (the default) or FALSE. Whether or not the names on <code>x</code> (accessible with <code>names(x)</code> ) should be propagated to the returned object.  |
| <code>use.mcols</code> | TRUE or FALSE (the default). Whether or not the metadata columns on <code>x</code> (accessible with <code>mcols(x)</code> ) should be propagated to the returned object.   |
| <code>...</code>       | Additional arguments, for use in specific methods.   |

## Details

Various packages (e.g. **IRanges**, **GenomicRanges**, **SummarizedExperiment**, **GenomicAlignments**, etc...) define and document various range squeezing methods for various types of objects.

Note that these functions can be seen as *object getters* or as functions performing coercion.

For some objects (e.g. `GAlignments` and `GAlignmentPairs` objects defined in the **GenomicAlignments** package), `as(x, "IRanges")` and `as(x, "IRangesList")`, are equivalent to `ranges(x, use.names=TRUE, use.mcols=TRUE)` and `rglist(x, use.names=TRUE, use.mcols=TRUE)`, respectively.

**Value**

An [IRanges](#) object for ranges.

An [IRangesList](#) object for `rplist`.

If `x` is a vector-like object (e.g. [GAlignments](#)), 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 `use.names` is `TRUE`, then the names on `x` (if any) are propagated to the returned object. If `use.mcols` is `TRUE`, then the metadata columns on `x` (if any) are propagated to the returned object.

**Author(s)**

H. Pagès

**See Also**

- [IRanges](#) and [IRangesList](#) objects.
- [RangedSummarizedExperiment](#) objects in the **SummarizedExperiment** packages.
- [GAlignments](#), [GAlignmentPairs](#), and [GAlignmentsList](#) objects in the **GenomicAlignments** package.

**Examples**

```
## See ?GAlignments in the GenomicAlignments package for examples of
## "ranges" and "rplist" methods.
```

---

RangedSelection-class *Selection of ranges and columns*

---

**Description**

A `RangedSelection` represents a query against a table of interval data in terms of ranges and column names. The ranges select any table row with an overlapping interval. Note that the intervals are always returned, even if no columns are selected.

**Details**

Traditionally, tabular data structures have supported the `subset` function, which allows one to select a subset of the rows and columns from the table. In that case, the rows and columns are specified by two separate arguments. As querying interval data sources, especially those external to R, such as binary indexed files and databases, is increasingly common, there is a need to encapsulate the row and column specifications into a single data structure, mostly for the sake of interface cleanliness. The `RangedSelection` class fills that role.

**Constructor**

`RangedSelection(ranges=IRangesList(), colnames = character())`: Constructors a `RangedSelection` with the given ranges and colnames.

**Coercion**

`as(from, "RangedSelection")`: Coerces from to a RangedSelection object. Typically, from is a [IntegerRangesList](#), the ranges of which become the ranges in the new RangedSelection.

**Accessors**

In the code snippets below, x is always a RangedSelection.

`ranges(x)`, `ranges(x) <- value`: Gets or sets the ranges, a [IntegerRangesList](#), that select rows with overlapping intervals.

`colnames(x)`, `colnames(x) <- value`: Gets the names, a character vector, indicating the columns.

**Author(s)**

Michael Lawrence

**Examples**

```
r1 <- IRangesList(chr1 = IRanges(c(1, 5), c(3, 6)))

RangedSelection(r1)
as(r1, "RangedSelection") # same as above

RangedSelection(r1, "score")
```

---

|           |                                |
|-----------|--------------------------------|
| read.Mask | <i>Read a mask from a file</i> |
|-----------|--------------------------------|

---

**Description**

`read.agpMask` and `read.gapMask` extract the AGAPS mask from an NCBI "agp" file or a UCSC "gap" file, respectively.

`read.liftMask` extracts the AGAPS mask from a UCSC "lift" file (i.e. a file containing offsets of contigs within sequences).

`read.rmMask` extracts the RM mask from a RepeatMasker .out file.

`read.trfMask` extracts the TRF mask from a Tandem Repeats Finder .bed file.

**Usage**

```
read.agpMask(file, seqname="?", mask.width=NA, gap.types=NULL, use.gap.types=FALSE)
read.gapMask(file, seqname="?", mask.width=NA, gap.types=NULL, use.gap.types=FALSE)
read.liftMask(file, seqname="?", mask.width=NA)
read.rmMask(file, seqname="?", mask.width=NA, use.IDs=FALSE)
read.trfMask(file, seqname="?", mask.width=NA)
```



```

mask11 <- read.agpMask(file1, seqname="chrY", mask.width=chrY_length,
                      gap.types=c("centromere", "heterochromatin"))
mask11[[1]]

## -----
## B. Extract a mask of assembly gaps ("AGAPS" mask) with read.liftMask()
## -----
## Note: The hg18liftAll.lft file was obtained by downloading,
## extracting and renaming the liftAll.zip file from
##
## http://hgdownload.cse.ucsc.edu/goldenPath/hg18/bigZips/
## liftAll.zip          03-Feb-2006 11:35 5.5K
##
## on May 8, 2008.

file2 <- system.file("extdata", "hg18liftAll.lft", package="IRanges")
mask2 <- read.liftMask(file2, seqname="chr1")
mask2
if (interactive()) {
  ## contigs 7 and 8 for chrY are adjacent
  read.liftMask(file2, seqname="chrY")

  ## displays the sequence names found in the file
  read.liftMask(file2)

  ## specify an unknown sequence name
  read.liftMask(file2, seqname="chrZ", mask.width=300)
}

## -----
## C. Extract a RepeatMasker ("RM") or Tandem Repeats Finder ("TRF")
## mask with read.rmMask() or read.trfMask()
## -----
## Note: The ce2chrM.fa.out and ce2chrM.bed files were obtained by
## downloading, extracting and renaming the chromOut.zip and
## chromTrf.zip files from
##
## http://hgdownload.cse.ucsc.edu/goldenPath/ce2/bigZips/
## chromOut.zip          21-Apr-2004 09:05 2.6M
## chromTrf.zip          21-Apr-2004 09:07 182K
##
## on May 7, 2008.

## Before you can extract a mask with read.rmMask() or read.trfMask(), you
## need to know the length of the sequence that you're going to put the
## mask on:
if (interactive()) {
  library(BSgenome.Celegans.UCSC.ce2)
  chrM_length <- seqlengths(Celegans)[["chrM"]]

  ## Read the RepeatMasker .out file for chrM in ce2:
  file3 <- system.file("extdata", "ce2chrM.fa.out", package="IRanges")
  RMmask <- read.rmMask(file3, seqname="chrM", mask.width=chrM_length)
}

```

```

RMmask

## Read the Tandem Repeats Finder .bed file for chrM in ce2:
file4 <- system.file("extdata", "ce2chrM.bed", package="IRanges")
TRFmask <- read.trfMask(file4, seqname="chrM", mask.width=chrM_length)
TRFmask
desc(TRFmask) <- paste(desc(TRFmask), "[period<=12]")
TRFmask

## Put the 2 masks on chrM:
chrM <- Celegans$chrM
masks(chrM) <- RMmask # this would drop all current masks, if any
masks(chrM) <- append(masks(chrM), TRFmask)
chrM
}

```

---

reverse

*reverse*


---

## Description

A generic function for reversing vector-like or list-like objects. This man page describes methods for reversing a character vector, a [Views](#) object, or a [MaskCollection](#) object. Note that `reverse` is similar to but not the same as [rev](#).

## Usage

```
reverse(x, ...)
```

## Arguments

|                  |   |
|------------------|---|
| <code>x</code>   | A vector-like or list-like object.                    |
| <code>...</code> | Additional arguments to be passed to or from methods. |

## Details

On a character vector or a [Views](#) object, `reverse` reverses each element individually, without modifying the top-level order of the elements. More precisely, each individual string of a character vector is reversed.

## Value

An object of the same class and length as the original object.



**See Also**

- [rev](#) in base R.
- [revElements](#) in the **S4Vectors** package to reverse all or some of the list elements of a list-like object.
- [Views](#) objects.
- [MaskCollection](#) objects.
- [reverse-methods](#) in the **XVector** package.

**Examples**

```
## On a character vector:
reverse(c("Hi!", "How are you?"))
rev(c("Hi!", "How are you?"))

## On a Views object:
v <- successiveViews(Rle(c(-0.5, 12.3, 4.88), 4:2), 1:4)
v
reverse(v)
rev(v)

## On a MaskCollection object:
mask1 <- Mask(mask.width=29, start=c(11, 25, 28), width=c(5, 2, 2))
mask2 <- Mask(mask.width=29, start=c(3, 10, 27), width=c(5, 8, 1))
mask3 <- Mask(mask.width=29, start=c(7, 12), width=c(2, 4))
mymasks <- append(append(mask1, mask2), mask3)
reverse(mymasks)
```

---

Rle-class-leftovers     *Rle objects (old man page)*

---

**Description**

IMPORTANT NOTE - 7/3/2014: This man page is being refactored. Most of the things that used to be documented here have been moved to the man page for [Rle](#) objects located in the **S4Vectors** package.

**Coercion**

In the code snippets below, `from` is an [Rle](#) object:

`as(from, "IRanges")`: Creates an [IRanges](#) instance from a logical [Rle](#). Note that this instance is guaranteed to be normal.

`as(from, "NormalIRanges")`: Creates a [NormalIRanges](#) instance from a logical [Rle](#).

## General Methods

In the code snippets below, `x` is an Rle object:

`split(x, f, drop=FALSE)`: Splits `x` according to `f` to create a [CompressedRleList](#) 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`.

`findRange(x, vec)`: Returns an [IRanges](#) object representing the ranges in Rle `vec` that are referenced by the indices in the integer vector `x`.

`splitRanges(x)`: Returns a [CompressedIRangesList](#) object that contains the ranges for each of the unique run values.

## See Also

The [Rle](#) class defined and documented in the [S4Vectors](#) package.

## Examples

```
x <- Rle(10:1, 1:10)
x
```

---

RleViews-class

*The RleViews class*

---

## Description

The RleViews class is the basic container for storing a set of views (start/end locations) on the same Rle object.

## Details

An RleViews object contains a set of views (start/end locations) on the same [Rle](#) object called "the subject vector" or simply "the subject". Each view is defined by its start and end locations: both are integers such that `start <= end`. An RleViews object is in fact a particular case of a [Views](#) object (the RleViews class contains the [Views](#) class) so it can be manipulated in a similar manner: see [?Views](#) for more information. Note that two views can overlap and that a view can be "out of limits" i.e. it can start before the first element of the subject or/and end after its last element.

## Author(s)

P. Aboyoun

## See Also

[Views-class](#), [Rle-class](#), [view-summarization-methods](#)

**Examples**

```

subject <- Rle(rep(c(3L, 2L, 18L, 0L), c(3,2,1,5)))
myViews <- Views(subject, 3:0, 5:8)
myViews
subject(myViews)
length(myViews)
start(myViews)
end(myViews)
width(myViews)
myViews[[2]]

set.seed(0)
vec <- Rle(sample(0:2, 20, replace = TRUE))
vec
Views(vec, vec > 0)

```

---

RleViewsList-class      *List of RleViews*


---

**Description**

An extension of [ViewsList](#) that holds only [RleViews](#) objects. Useful for storing coverage vectors over a set of spaces (e.g. chromosomes), each of which requires a separate [RleViews](#) object.

**Details**

For more information on methods available for RleViewsList objects consult the man pages for [ViewsList-class](#) and [view-summarization-methods](#).

**Constructor**

`RleViewsList(..., rleList, rangesList)`: Either ... or the rleList/rangesList couplet provide the RleViews for the list. If ... is provided, each of these arguments must be RleViews objects. Alternatively, rleList and rangesList accept Rle and IntegerRanges objects respectively that are meshed together for form the RleViewsList.

`Views(subject, start=NULL, end=NULL, width=NULL, names=NULL)`: Same as `RleViewsList(rleList = subject, rangesList = start)`.

**Coercion**

In the code snippet below, from is an RleViewsList object:

`as(from, "IRangesList")`: Creates an IRangesList object containing the view locations in from.

**Author(s)**

P. Aboyoun

**See Also**

[ViewsList-class](#), [view-summarization-methods](#)

**Examples**

```
## Rle objects
subject1 <- Rle(c(3L,2L,18L,0L), c(3,2,1,5))
set.seed(0)
subject2 <- Rle(c(0L,5L,2L,0L,3L), c(8,5,2,7,4))

## Views
rleViews1 <- Views(subject1, 3:0, 5:8)
rleViews2 <- Views(subject2, subject2 > 0)

## RleList and IntegerRangesList objects
rleList <- RleList(subject1, subject2)
rangesList <- IRangesList(IRanges(3:0, 5:8), IRanges(subject2 > 0))

## methods for construction
method1 <- RleViewsList(rleViews1, rleViews2)
method2 <- RleViewsList(rleList = rleList, rangesList = rangesList)
identical(method1, method2)

## calculation over the views
viewSums(method1)
```

---

seqapply

*2 methods that should be documented somewhere else*

---

**Description**

unsplit method for [List](#) object and split<- method for [Vector](#) object.

**Usage**

```
## S4 method for signature 'List'
unsplit(value, f, drop = FALSE)
## S4 replacement method for signature 'Vector'
split(x, f, drop = FALSE, ...) <- value
```

**Arguments**

|       |   |
|-------|---|
| value | The <a href="#">List</a> object to unsplit.           |
| f     | A factor or list of factors                           |
| drop  | Whether to drop empty elements from the returned list |
| x     | Like X  |
| ...   | Extra arguments to pass to FUN                        |

**Details**

unsplit unlists value, where the order of the returned vector is as if value were originally created by splitting that vector on the factor f.

split(x, f, drop = FALSE) <- value: Virtually splits x by the factor f, replaces the elements of the resulting list with the elements from the list value, and restores x to its original form. Note that this works for any Vector, even though split itself is not universally supported.

**Author(s)**

Michael Lawrence

---

setops-methods

*Set operations on IntegerRanges and IntegerRangesList objects*

---

**Description**

Performs set operations on [IntegerRanges](#) and [IntegerRangesList](#) objects.

**Usage**

```
## Vector-wise set operations
## -----

## S4 method for signature 'IntegerRanges,IntegerRanges'
union(x, y)
## S4 method for signature 'Pairs,missing'
union(x, y, ...)

## S4 method for signature 'IntegerRanges,IntegerRanges'
intersect(x, y)
## S4 method for signature 'Pairs,missing'
intersect(x, y, ...)

## S4 method for signature 'IntegerRanges,IntegerRanges'
setdiff(x, y)
## S4 method for signature 'Pairs,missing'
setdiff(x, y, ...)

## Element-wise (aka "parallel") set operations
## -----

## S4 method for signature 'IntegerRanges,IntegerRanges'
punion(x, y, fill.gap=FALSE)
## S4 method for signature 'Pairs,missing'
punion(x, y, ...)
```

```

## S4 method for signature 'IntegerRanges,IntegerRanges'
pintersect(x, y, resolve.empty=c("none", "max.start", "start.x"))
## S4 method for signature 'Pairs,missing'
pintersect(x, y, ...)

## S4 method for signature 'IntegerRanges,IntegerRanges'
psetdiff(x, y)
## S4 method for signature 'Pairs,missing'
psetdiff(x, y, ...)

## S4 method for signature 'IntegerRanges,IntegerRanges'
pgap(x, y)

```

### Arguments

|                            |   |
|----------------------------|---|
| <code>x, y</code>          | Objects representing ranges.  |
| <code>fill.gap</code>      | Logical indicating whether or not to force a union by using the rule <code>start = min(start(x), start(y))</code> , <code>end = max(end(x), end(y))</code> .  |
| <code>resolve.empty</code> | One of "none", "max.start", or "start.x" denoting how to handle ambiguous empty ranges formed by intersections. "none" - throw an error if an ambiguous empty range is formed, "max.start" - associate the maximum start value with any ambiguous empty range, and "start.x" - associate the start value of x with any ambiguous empty range. (See Details section below for the definition of an ambiguous range.) |
| <code>...</code>           | The methods for <a href="#">Pairs</a> objects pass any extra argument to the internal call to <code>punion(first(x), last(x), ...)</code> , <code>pintersect(first(x), last(x), ...)</code> , etc...  |

### Details

The union, intersect and setdiff methods for [IntegerRanges](#) objects return a "normal" [IntegerRanges](#) object representing the union, intersection and (asymmetric!) difference of the sets of integers represented by `x` and `y`.

`punion`, `pintersect`, `psetdiff` and `pgap` are generic functions that compute the element-wise (aka "parallel") union, intersection, (asymmetric!) difference and gap between each element in `x` and its corresponding element in `y`. Methods for [IntegerRanges](#) objects are defined. For these methods, `x` and `y` must have the same length (i.e. same number of ranges). They return a [IntegerRanges](#) object *parallel* to `x` and `y` i.e. where the `i`-th range corresponds to the `i`-th range in `x` and `y` and represents the union/intersection/difference/gap of/between the corresponding `x[i]` and `y[i]`.

If `x` is a [Pairs](#) object, then `y` should be missing, and the operation is performed between the members of each pair.

By default, `pintersect` will throw an error when an "ambiguous empty range" is formed. An ambiguous empty range can occur three different ways: 1) when corresponding non-empty ranges elements `x` and `y` have an empty intersection, 2) if the position of an empty range element does not fall within the corresponding limits of a non-empty range element, or 3) if two corresponding empty range elements do not have the same position. For example if empty range element `[22,21]` is intersected with non-empty range element `[1,10]`, an error will be produced; but if it is intersected

with the range [22,28], it will produce [22,21]. As mentioned in the Arguments section above, this behavior can be changed using the `resolve.empty` argument.

### Value

On [IntegerRanges](#) objects, `union`, `intersect`, and `setdiff` return an [IRanges](#) instance that is guaranteed to be *normal* (see `isNormal`) but is NOT promoted to [NormalIRanges](#).

On [IntegerRanges](#) objects, `punion`, `pintersect`, `psetdiff`, and `pgap` return an object of the same class and length as their first argument.

### Author(s)

H. Pagès and M. Lawrence

### See Also

- `pintersect` is similar to [narrow](#), except the end points are absolute, not relative. `pintersect` is also similar to [restrict](#), except ranges outside of the restriction become empty and are not discarded.
- [setops-methods](#) in the **GenomicRanges** package for set operations on genomic ranges.
- [findOverlaps-methods](#) for finding/counting overlapping ranges.
- [intra-range-methods](#) and [inter-range-methods](#) for *intra range* and *inter range* transformations.
- [IntegerRanges](#) and [IntegerRangesList](#) objects. In particular, *normality* of an [IntegerRanges](#) object is discussed in the man page for [IntegerRanges](#) objects.
- [mendoapply](#) in the **S4Vectors** package.

### Examples

```
x <- IRanges(c(1, 5, -2, 0, 14), c(10, 9, 3, 11, 17))
subject <- Rle(1:-3, 6:2)
y <- Views(subject, start=c(14, 0, -5, 6, 18), end=c(20, 2, 2, 8, 20))

## Vector-wise operations:
union(x, ranges(y))
union(ranges(y), x)

intersect(x, ranges(y))
intersect(ranges(y), x)

setdiff(x, ranges(y))
setdiff(ranges(y), x)

## Element-wise (aka "parallel") operations:
try(punion(x, ranges(y)))
punion(x[3:5], ranges(y)[3:5])
punion(x, ranges(y), fill.gap=TRUE)
try(pintersect(x, ranges(y)))
pintersect(x[3:4], ranges(y)[3:4])
pintersect(x, ranges(y), resolve.empty="max.start")
```

```

psetdiff(ranges(y), x)
try(psetdiff(x, ranges(y)))
start(x)[4] <- -99
end(y)[4] <- 99
psetdiff(x, ranges(y))
pgap(x, ranges(y))

## On IntegerRangesList objects:
irl1 <- IRangesList(a=IRanges(c(1,2),c(4,3)), b=IRanges(c(4,6),c(10,7)))
irl2 <- IRangesList(c=IRanges(c(0,2),c(4,5)), a=IRanges(c(4,5),c(6,7)))
union(irl1, irl2)
intersect(irl1, irl2)
setdiff(irl1, irl2)

```

---

slice-methods

*Slice a vector-like or list-like object*

---

## Description

`slice` is a generic function that creates views on a vector-like or list-like object that contain the elements that are within the specified bounds.

## Usage

```

slice(x, lower=-Inf, upper=Inf, ...)

## S4 method for signature 'Rle'
slice(x, lower=-Inf, upper=Inf,
      includeLower=TRUE, includeUpper=TRUE, rangesOnly=FALSE)

## S4 method for signature 'RleList'
slice(x, lower=-Inf, upper=Inf,
      includeLower=TRUE, includeUpper=TRUE, rangesOnly=FALSE)

```

## Arguments

|   |   |
|---|---|
| <code>x</code>                          | An <a href="#">Rle</a> or <a href="#">RleList</a> object, or any object coercible to an Rle object. |
| <code>lower, upper</code>               | The lower and upper bounds for the slice.   |
| <code>includeLower, includeUpper</code> | Logical indicating whether or not the specified boundary is open or closed.                         |
| <code>rangesOnly</code>                 | A logical indicating whether or not to drop the original data from the output.                      |
| <code>...</code>                        | Additional arguments to be passed to specific methods.  |

## Details

`slice` is useful for finding areas of absolute maxima (peaks), absolute minima (troughs), or fluctuations within specified limits. One or more view summarization methods can be used on the result of `slice`. See `?link{view-summarization-methods}`



**Value**

The method for [Rle](#) objects returns an [RleViews](#) object if `rangesOnly=FALSE` or an [IRanges](#) object if `rangesOnly=TRUE`.

The method for [RleList](#) objects returns an [RleViewsList](#) object if `rangesOnly=FALSE` or an [IRangesList](#) object if `rangesOnly=TRUE`.

**Author(s)**

P. Aboyoun

**See Also**

- [view-summarization-methods](#) for summarizing the views returned by `slice`.
- [slice-methods](#) in the **XVector** package for more `slice` methods.
- [coverage](#) for computing the coverage across a set of ranges.
- The [Rle](#), [RleList](#), [RleViews](#), and [RleViewsList](#) classes.

**Examples**

```
## Views derived from coverage
x <- IRanges(start=c(1L, 9L, 4L, 1L, 5L, 10L),
             width=c(5L, 6L, 3L, 4L, 3L, 3L))
cvg <- coverage(x)
slice(cvg, lower=2)
slice(cvg, lower=2, rangesOnly=TRUE)
```

---

Vector-class-leftovers

*Vector objects (old man page)*

---

**Description**

IMPORTANT NOTE - 4/29/2014: This man page is being refactored. Most of the things that used to be documented here have been moved to the man page for [Vector](#) objects located in the **S4Vectors** package.

**Evaluation**

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

`with(x, expr)`: Evaluates `expr` within `as.env(x)` via `eval(x)`.

`eval(expr, envir, enclos=parent.frame())`: Evaluates `expr` within `envir`, where `envir` is coerced to an environment with `as.env(envir, enclos)`. The `expr` is first processed with [bquote](#), such that any escaped symbols are directly resolved in the calling frame.

### Convenience wrappers for common subsetting operations

In the code snippets below, `x` is a `Vector` object or regular R vector object. The R vector object methods for `window` are defined in this package and the remaining methods are defined in base R.

`window(x, start=NA, end=NA, width=NA) <- value`: Replace 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)`, or be coercible to `class(x)` or a subclass of `class(x)`. The elements of `value` are repeated to create a `Vector` with the same number of elements as the width of the subsequence window it is replacing.

### Looping

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

`tapply(X, INDEX, FUN = NULL, ..., simplify = TRUE)`: Like the standard `tapply` function defined in the base package, the `tapply` method for `Vector` objects applies a function to each cell of a ragged array, that is to each (non-empty) group of values given by a unique combination of the levels of certain factors.

### Coercion

`as.list(x)`: coerce a `Vector` to a list, where the `i`th element of the result corresponds to `x[i]`.

### See Also

The `Vector` class defined and documented in the `S4Vectors` package.

---

view-summarization-methods

*Summarize views on a vector-like object with numeric values*

---

### Description

`viewApply` applies a function on each view of a `Views` or `ViewsList` object.

`viewMins`, `viewMaxs`, `viewSums`, `viewMeans` calculate respectively the minima, maxima, sums, and means of the views in a `Views` or `ViewsList` object.

### Usage

```
viewApply(X, FUN, ..., simplify = TRUE)
```

```
viewMins(x, na.rm=FALSE)
## S4 method for signature 'Views'
min(x, ..., na.rm = FALSE)
```

```
viewMaxs(x, na.rm=FALSE)
## S4 method for signature 'Views'
```

```

max(x, ..., na.rm = FALSE)

viewSums(x, na.rm=FALSE)
## S4 method for signature 'Views'
sum(x, ..., na.rm = FALSE)

viewMeans(x, na.rm=FALSE)
## S4 method for signature 'Views'
mean(x, ...)

viewWhichMins(x, na.rm=FALSE)
## S4 method for signature 'Views'
which.min(x)

viewWhichMaxs(x, na.rm=FALSE)
## S4 method for signature 'Views'
which.max(x)

viewRangeMins(x, na.rm=FALSE)

viewRangeMaxs(x, na.rm=FALSE)

```

### Arguments

|          |  |
|----------|--|
| X        | A Views object.  |
| FUN      | The function to be applied to each view in X.  |
| ...      | Additional arguments to be passed on.  |
| simplify | A logical value specifying whether or not the result should be simplified to a vector or matrix if possible. |
| x        | An <a href="#">RleViews</a> or <a href="#">RleViewsList</a> object.  |
| na.rm    | Logical indicating whether or not to include missing values in the results.                                  |

### Details

The `viewMins`, `viewMaxs`, `viewSums`, and `viewMeans` functions provide efficient methods for calculating the specified numeric summary by performing the looping in compiled code.

The `viewWhichMins`, `viewWhichMaxs`, `viewRangeMins`, and `viewRangeMaxs` functions provide efficient methods for finding the locations of the minima and maxima.

### Value

For all the functions in this man page (except `viewRangeMins` and `viewRangeMaxs`): A numeric vector of the length of `x` if `x` is an [RleViews](#) object, or a [List](#) object of the length of `x` if it's an [RleViewsList](#) object.

For `viewRangeMins` and `viewRangeMaxs`: An [IRanges](#) object if `x` is an [RleViews](#) object, or an [IRangesList](#) object if it's an [RleViewsList](#) object.

**Note**

For convenience, methods for `min`, `max`, `sum`, `mean`, `which.min` and `which.max` are provided as wrappers around the corresponding `view*` functions (which might be deprecated at some point).

**Author(s)**

P. Aboyoun

**See Also**

- The [slice](#) function for slicing an [Rle](#) or [RleList](#) object.
- [view-summarization-methods](#) in the **XVector** package for more view summarization methods.
- The [RleViews](#) and [RleViewsList](#) classes.
- The [which.min](#) and [colSums](#) functions.

**Examples**

```
## Views derived from coverage
x <- IRanges(start=c(1L, 9L, 4L, 1L, 5L, 10L),
             width=c(5L, 6L, 3L, 4L, 3L, 3L))
cvg <- coverage(x)
cvg_views <- slice(cvg, lower=2)

viewApply(cvg_views, diff)

viewMins(cvg_views)
viewMaxs(cvg_views)

viewSums(cvg_views)
viewMeans(cvg_views)

viewWhichMins(cvg_views)
viewWhichMaxs(cvg_views)

viewRangeMins(cvg_views)
viewRangeMaxs(cvg_views)
```

---

Views-class

*Views objects*

---

**Description**

The Views virtual class is a general container for storing a set of views on an arbitrary [Vector](#) object, called the "subject".

Its primary purpose is to introduce concepts and provide some facilities that can be shared by the concrete classes that derive from it.

Some direct subclasses of the Views class are: [RleViews](#), [XIntegerViews](#) (defined in the XVector package), [XStringViews](#) (defined in the Biostrings package), etc...

**Constructor**

`Views(subject, start=NULL, end=NULL, width=NULL, names=NULL)`: This constructor is a generic function with dispatch on argument `subject`. Specific methods must be defined for the subclasses of the `Views` class. For example a method for `XString` subjects is defined in the `Biostrings` package that returns an `XStringViews` object. There is no default method.

The treatment of the `start`, `end` and `width` arguments is the same as with the `IRanges` constructor, except that, in addition, `Views` allows `start` to be an `IntegerRanges` object. With this feature, `Views(subject, IRanges(my_starts, my_ends, my_widths, my_names))` and `Views(subject, my_starts, my_ends, my_widths, my_names)` are equivalent (except when `my_starts` is itself a `IntegerRanges` object).

**Coercion**

In the code snippets below, `from` is a `Views` object:

`as(from, "IRanges")`: Creates an `IRanges` object containing the view locations in `from`.

**Accessor-like methods**

All the accessor-like methods defined for `IRanges` objects work on `Views` objects. In addition, the following accessors are defined for `Views` objects:

`subject(x)`: Return the subject of the views.

**Subsetting**

`x[i]`: Select the views specified by `i`.

`x[[i]]`: Extracts the view selected by `i` as an object of the same class as `subject(x)`. Subscript `i` can be a single integer or a character string. The result is the subsequence of `subject(x)` defined by `window(subject(x), start=start(x)[i], end=end(x)[i])` or an error if the view is "out of limits" (i.e. `start(x)[i] < 1` or `end(x)[i] > length(subject(x))`).

**Concatenation**

`c(x, ..., ignore.mcols=FALSE)`: Concatenate `Views` objects. They must have the same subject.

**Other methods**

`trim(x, use.names=TRUE)`: Equivalent to `restrict(x, start=1L, end=length(subject(x)), keep.all.ranges=TRUE, use.names=use.names)`.

`subviews(x, start=NA, end=NA, width=NA, use.names=TRUE)`: `start`, `end`, and `width` arguments must be vectors of integers, eventually with `NA`s, that contain coordinates relative to the current ranges. Equivalent to `trim(narrow(x, start=start, end=end, width=width, use.names=use.names))`.

`successiveViews(subject, width, gapwidth=0, from=1)`: Equivalent to `Views(subject, successiveIRanges(width, gapwidth, from))`. See `?successiveIRanges` for a description of the `width`, `gapwidth` and `from` arguments.

**Author(s)**

Hervé Pagès

**See Also**[IRanges-class](#), [Vector-class](#), [IRanges-utils](#), [XVector](#).Some direct subclasses of the Views class: [RleViews-class](#), [XIntegerViews-class](#), [XDoubleViews-class](#), [XStringViews-class](#).[findOverlaps](#).**Examples**

```
showClass("Views") # shows (some of) the known subclasses

## Create a set of 4 views on an XInteger subject of length 10:
subject <- Rle(3:-6)
v1 <- Views(subject, start=4:1, end=4:7)

## Extract the 2nd view:
v1[[2]]

## Some views can be "out of limits"
v2 <- Views(subject, start=4:-1, end=6)
trim(v2)
subviews(v2, end=-2)

## See ?`XIntegerViews-class` in the XVector package for more examples.
```

ViewsList-class

*List of Views***Description**An extension of [List](#) that holds only [Views](#) objects.**Details**

ViewsList is a virtual class. Specialized subclasses like e.g. [RleViewsList](#) are useful for storing coverage vectors over a set of spaces (e.g. chromosomes), each of which requires a separate [RleViews](#) object.

As a [List](#) subclass, ViewsList inherits all the methods available for [List](#) objects. It also presents an API that is very similar to that of [Views](#), where operations are vectorized over the elements and generally return lists.

**Author(s)**

P. Aboyoun and H. Pagès

**See Also**

[List-class](#), [RleViewsList-class](#).  
[findOverlaps](#).

**Examples**

```
showClass("ViewsList")
```

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