

# Package ‘IRanges’

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**Title** Infrastructure for manipulating intervals on sequences

**Description** The package provides efficient low-level and highly reusable S4 classes for storing ranges of integers, RLE vectors (Run-Length Encoding), and, more generally, data that can be organized sequentially (formally defined as Vector objects), as well as views on these Vector objects.

Efficient list-like classes are also provided for storing big collections of instances of the basic classes. All classes in the package use consistent naming and share the same rich and consistent “Vector API” as much as possible.

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AtomicList	<i>Lists of Atomic Vectors in Natural and Rle Form</i>
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## 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, "NumericList"), as(from, "RawList"), 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.

## 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 Basic 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:

**General** is.na, duplicated, unique, match, %in%, table, order, sort

**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

**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 RangesList.

**Specialized Methods**

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

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

**Author(s)**

P. Aboyoun

**See Also**

[List](#) for the applicable methods.

**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

## combining
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)

## group generics
2 * col1
col1 + col1
col1 > 2
sum(col1) # equivalent to (but faster than) 'sapply(col1, sum)'
mean(col1) # equivalent to 'sapply(col1, mean)'
```

---

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](#) objects have a switch that lets the user choose between the `CompressedList` and [SimpleList](#) representation at construction time. For example, a [CompressedCharacterList](#) object can be constructed with `CharacterList(..., compress=TRUE)`.

### 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

- The [List](#) class defined and documented in the **S4Vectors** package for the parent class.
- The [SimpleList](#) class defined and documented in the **S4Vectors** package for an alternative to `CompressedList`.
- The [CompressedIntegerList](#) class for a `CompressedList` subclass example.

## Examples

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

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

## This is controlled by internal helper classNameForDisplay():
classNameForDisplay(x)
```

---

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 'Ranges'
coverage(x, shift=0L, width=NULL, weight=1L,
         method=c("auto", "sort", "hash"))

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

## Arguments

x	A <a href="#">Ranges</a> , <a href="#">Views</a> , or <a href="#">RangesList</a> object. See ?`coverage-methods` in the <b>GenomicRanges</b> package for coverage methods for other objects.
shift	Specifies how much each range in x should be shifted before the coverage is computed. <ul style="list-style-type: none"> <li>• If x is a <a href="#">Ranges</a> or <a href="#">Views</a> object: shift must be an integer or numeric vector parallel to x (will get recycled if necessary) and with no NAs.</li> <li>• If x is a <a href="#">RangesList</a> object: shift 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 <code>as.list</code>. After recycling, each list element <code>shift[[i]]</code> must be an integer or numeric vector parallel to <code>x[[i]]</code> (will get recycled if necessary) and with no NAs.</li> </ul> <p>A positive shift value will shift the corresponding range in x to the right, and a negative value to the left.</p>



width	<p>Specifies the length of the returned coverage vector(s).</p> <ul style="list-style-type: none"> <li>• If <i>x</i> is a <a href="#">Ranges</a> object: <i>width</i> must be NULL (the default), an NA, or a single non-negative integer. After being shifted, the ranges in <i>x</i> are always clipped on the left to keep only their positive portion i.e. their intersection with the [1, +inf) interval. If <i>width</i> is a single non-negative integer, then they're also clipped on the right to keep only their intersection with the [1, <i>width</i>] interval. In that case <i>coverage</i> returns a vector of length <i>width</i>. Otherwise, it returns a vector that extends to the last position in the underlying space covered by the shifted ranges.</li> <li>• If <i>x</i> is a <a href="#">Views</a> object: Same as for a <a href="#">Ranges</a> object, except that, if <i>width</i> is NULL then it's treated as if it was <code>length(subject(x))</code>.</li> <li>• If <i>x</i> is a <a href="#">RangesList</a> object: <i>width</i> must be NULL or an integer vector parallel to <i>x</i> (i.e. with one element per list element in <i>x</i>). If not NULL, the vector must contain NAs or non-negative integers and it will get recycled to the length of <i>x</i> if necessary. If NULL, it is replaced with NA and recycled to the length of <i>x</i>. Finally <i>width</i>[<i>i</i>] is used to compute the coverage vector for <i>x</i>[[<i>i</i>]] and is therefore treated like explained above (when <i>x</i> is a <a href="#">Ranges</a> object).</li> </ul>
weight	<p>Assigns a weight to each range in <i>x</i>.</p> <ul style="list-style-type: none"> <li>• If <i>x</i> is a <a href="#">Ranges</a> or <a href="#">Views</a> object: <i>weight</i> must be an integer or numeric vector parallel to <i>x</i> (will get recycled if necessary).</li> <li>• If <i>x</i> is a <a href="#">RangesList</a> object: <i>weight</i> must be a numeric vector or list-like object of the same length as <i>x</i> (will get recycled if necessary). If it's a numeric vector, it's first turned into a list with <code>as.list</code>. After recycling, each list element <i>weight</i>[[<i>i</i>]] must be an integer or numeric vector parallel to <i>x</i>[[<i>i</i>]] (will get recycled if necessary).</li> </ul> <p>If <i>weight</i> is an integer vector or list-like object of integer vectors, the coverage vector(s) will be returned as integer-<a href="#">Rle</a> object(s). If it's a numeric vector or list-like object of numeric vectors, the coverage vector(s) will be returned as numeric-<a href="#">Rle</a> object(s).</p> <p>Alternatively, <i>weight</i> can also be specified as a single string naming a metadata column in <i>x</i> (i.e. a column in <code>mcols(x)</code>) to be used as the weight vector.</p>
method	<p>If <i>method</i> is set to "sort", then <i>x</i> is sorted previous to the calculation of the coverage. If <i>method</i> is set to hash, then <i>x</i> is hashed directly to a vector of length <i>width</i> without previous sorting.</p> <p>The "hash" method is faster than the "sort" method when <i>x</i> is large (i.e. contains a lot of ranges). When <i>x</i> is small and <i>width</i> is big (e.g. <i>x</i> represents a small set of reads aligned to a big chromosome), then <i>method</i>="sort" is faster and uses less memory than <i>method</i>="hash".</p> <p>Using <i>method</i>="auto" selects the best method based on <code>length(x)</code> and <i>width</i>.</p>
...	Further arguments to be passed to or from other methods.

### Value

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

If `x` is a [RangesList](#) 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. Pages 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`.
- The [Ranges](#), [RangesList](#), [Rle](#), and [RleList](#) classes.

### 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. 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 Ranges 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 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))

## -----
## C. SOME SANITY CHECKS
## -----
dummy.coverage <- function(x, shift=0L, width=NULL)
{
  y <- unlist(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)))

```

```
## -----
## 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))
```

---

DataFrame-utils

*Common operations on DataFrame objects*


---

## Description

Common operations on [DataFrame](#) objects.

## Splitting

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

`split(x, f, drop = FALSE)`: Splits `x` into a [CompressedSplitDataFrameList](#), according to `f`, dropping elements corresponding to unrepresented levels if `drop` is `TRUE`.

`mstack(..., .index.var = "name")`: Stacks the data frames passed as through `...`, using `.index.var` as the index column name. See [stack](#).

## Author(s)

Michael Lawrence

## See Also

[DataTable](#), [Vector](#), and [RangedData](#), which makes heavy use of this class.

**Examples**

```
## split

sw <- DataFrame(swiss)
swsplit <- split(sw, sw[["Education"]])

## rbind

do.call(rbind, as.list(swsplit))

## cbind

cbind(DataFrame(score), DataFrame(counts))
```

---

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`.

`dim(x)`: Get the two element integer vector indicating the number of rows and columns over the entire dataset.

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

`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 `RangesList` 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)`: Coerces `x` to a `data.frame`. See `as.data.frame` on the `List` man page for details (?List).

**Author(s)**

Michael Lawrence

**See Also**

[DataFrame](#), [RangedData](#), which uses a `DataFrameList` to split the data by the spaces.

---

 expand

*The expand method for uncompressing compressed data columns*


---

**Description**

Expand an object with compressed columns such that all compressed values are represented as separate rows.

**Usage**

```
## S4 method for signature 'DataFrame'
expand(x, colnames, keepEmptyRows = FALSE)
```

**Arguments**

x	A <code>DataFrame</code> containing some columns that are compressed (e.g., <code>CompressedCharacterList</code> ), or a <code>Vector</code> with compressed columns in <code>mcols(x)</code> .
colnames	A character or numeric vector containing the names or indices of the compressed columns to expand. The order of expansion is controlled by the column order in this vector. This defaults to all of the recursive (list-like) columns in <code>x</code> (or <code>mcols(x)</code> ).
keepEmptyRows	A logical indicating if rows containing empty values in the specified <code>colnames</code> should be retained or dropped. When <code>TRUE</code> , empty values are set to <code>NA</code> and all rows are kept. When <code>FALSE</code> , rows with empty values in the <code>colnames</code> columns are dropped.

**Value**

A `DataFrame` that has been expanded row-wise to match the dimension of the uncompressed columns.

**Author(s)**

Herve Pages and Marc Carlson

**See Also**

[DataFrame-class](#)

**Examples**

```
aa <- CharacterList("a", paste0("d", 1:2), paste0("b", 1:3), c(), "c")
bb <- CharacterList(paste0("sna", 1:2), "foo", paste0("bar", 1:3), c(), "hica")
df <- DataFrame(aa=aa, bb=bb, cc=11:15)

## expand by all list-like columns (aa, bb), dropping empty rows
expand(df)
```



```

## expand the aa column only, and keep rows adjacent to empty values
expand(df, colnames="aa", keepEmptyRows=TRUE)

## expand the aa column only but do not keep rows
expand(df, colnames="aa", keepEmptyRows=FALSE)

## expand the aa and then the bb column, but
## keeping rows next to empty compressed values
expand(df, colnames=c("aa","bb"), keepEmptyRows=TRUE)

## expand the bb and then the aa column, but don't keep rows adjacent to
## empty values from bb and aa
expand(df, colnames=c("aa","bb"), keepEmptyRows=FALSE)

```

---

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. Note that the **split** methods defined in **S4Vectors** delegate to the splitAsList function defined in **IRanges** and documented below.

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)

## splitAsList()
## -----

splitAsList(x, f, drop=FALSE, ...)

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

extractList(x, i)

```

```
## relistToClass()
## -----
```

```
relistToClass(x)
```

### 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.
f	An atomic vector or a factor (possibly in <a href="#">Rle</a> form).
drop	Logical indicating if levels that do not occur should be dropped (if f is a factor).
i	A list-like object. Unlike for skeleton, the content here matters (see <a href="#">Details</a> section below). Note that i can be a <a href="#">Ranges</a> object (a particular type of list-like object), and, in that case, extractList is particularly fast (this is a common use case).
...	Arguments to pass to methods.

### Details

relist, split, and extractList have in common that they return a list-like value where each list element has the same class as the original vector-like object. Thus they need to be able to select the appropriate [List](#) concrete subclass to use for this returned value. This selection is performed by relistToClass and is based only on the class of the original object.

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 [Ranges](#) object.

relist and split (or splitAsList) 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 the not the transformation performed by extractList (in general).

**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.

`splitAsList` behaves like `base::split` except that the former returns a `List` object instead of an ordinary list.

`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 (except `relistToClass`) 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)**

H. Pages

**See Also**

- The `unlist` and `relist` functions in the **base** and **utils** packages, respectively.
- The `split` and `unsplit` functions in the **base** package.
- The `split` methods defined in the **S4Vectors** package.
- `Vector`, `List`, `Rle`, and `DataFrame` objects in the **S4Vectors** package.
- `Ranges` 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)
```

---

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 `Ranges`, `Views`, `RangesList`, or `ViewsList` objects. See `?`findOverlaps, GenomicRanges, GenomicRanges-method`` in the **GenomicRanges** package for methods that operate on `GenomicRanges` or `GRangesList` objects.

**Usage**

```

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

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

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

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

mergeByOverlaps(query, subject, ...)

## S4 method for signature 'Hits'
ranges(x, query, subject)

```

**Arguments**

query, subject Each of them can be a [Ranges](#), [Views](#), [RangesList](#), [ViewsList](#), or [RangedData](#) object. In addition, if subject is a [Ranges](#) object, query can be an integer vector to be converted to length-one ranges.

If query is a [RangesList](#) or [RangedData](#), subject must be a [RangesList](#) or [RangedData](#). If both lists have names, each element from the subject is paired with the element from the query with the matching name, if any. Otherwise, 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 ignoreSelf and ignoreRedundant arguments are allowed. By default, the result will contain hits for each range against itself, and if there is a hit from A to B, there is also a hit for B to A. If ignoreSelf is TRUE, all self matches are dropped. If ignoreRedundant is TRUE, only one of A->B and B->A is returned.

maxgap, minoverlap

Intervals with a separation of maxgap or less and a minimum of minoverlap overlapping positions, allowing for maxgap, are considered to be overlapping. maxgap should be a scalar, non-negative, integer. minoverlap should be a scalar, positive integer.

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 <code>start</code> or <code>end</code>, the intervals are required to have matching starts or ends, respectively. While this operation seems trivial, the naive implementation using <code>outer</code> would be much less efficient. Specifying <code>equal</code> as the type returns the intersection of the <code>start</code> and <code>end</code> matches. If type is <code>within</code>, the query interval must be wholly contained within the subject interval. Note that all matches must additionally satisfy the <code>minoverlap</code> constraint described above.</p> <p>The <code>maxgap</code> parameter has special meaning with the special overlap types. For <code>start</code>, <code>end</code>, and <code>equal</code>, it specifies the maximum difference in the starts, ends or both, respectively. For <code>within</code>, it is the maximum amount by which the query may be wider than the subject.</p>
select	<p>If query is a <a href="#">Ranges</a> or <a href="#">Views</a> object: When <code>select</code> is "all" (the default), the results are returned as a <a href="#">Hits</a> object. Otherwise the returned value is an integer vector parallel to query (i.e. same length) containing the first, last, or arbitrary overlapping interval in subject, with NA indicating intervals that did not overlap any intervals in subject.</p> <p>If query is a <a href="#">RangesList</a>, <a href="#">ViewsList</a>, or <a href="#">RangedData</a> object: When <code>select</code> is "all" (the default), the results are returned as a <a href="#">HitsList</a> object. Otherwise the returned value depends on the <code>drop</code> 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>
algorithm	<p>Can be "nclist" (the default) or "intervaltree". This argument was added in BioC 3.1 to facilitate the transition between the new <code>findOverlaps/countOverlaps</code> implementation based on Nested Containment Lists and the old implementation based on Interval Trees. See <a href="#">?NCList</a> and <a href="#">?IntervalTree</a> for more information about these implementations.. Note that the old implementation is defunct starting with BioC 3.2. The <code>algorithm</code> argument will be removed in BioC 3.3.</p>
...	<p>Further arguments to be passed to or from other methods:</p> <ul style="list-style-type: none"> <li>• <code>drop</code>: Supported only when query is a <a href="#">RangesList</a>, <a href="#">ViewsList</a>, or <a href="#">RangedData</a> object. FALSE by default. See <code>select</code> argument above for the details.</li> <li>• <code>ignoreSelf</code>, <code>ignoreRedundant</code>: When subject is omitted, the <code>ignoreSelf</code> and <code>ignoreRedundant</code> arguments (both FALSE by default) are allowed. See query and subject arguments above for the details.</li> </ul>
x	<p><a href="#">Hits</a> object returned by <code>findOverlaps</code>.</p>

## 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 [Ranges](#) 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 [RangesList](#) objects, it returns an [IntegerList](#) object.

`overlapsAny` finds the ranges in query that overlap any of the ranges in subject. For [Ranges](#) or [Views](#) objects, it returns a logical vector of length equal to the number of ranges in query. For [RangesList](#), [RangedData](#), or [ViewsList](#) objects, 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 query that has an overlap hit with a range in subject using the specified `findOverlaps` parameters.

`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.

`ranges(x, query, subject)` returns a `Ranges` of the same length as `Hits` object `x` 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 `x`.

**Author(s)**

Michael Lawrence and H. Pages

**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**

- The [Hits](#) and [HitsList](#) classes for representing a set of hits between 2 vector-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 [IntervalTree](#) and [IntervalForest](#) classes and constructors (defunct).
- The [Ranges](#), [Views](#), [RangesList](#), [ViewsList](#), and [RangedData](#) classes.
- The [IntegerList](#) and [LogicalList](#) classes.

**Examples**

```

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

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

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

## overlap even if adjacent only
## (FIXME: the gap between 2 adjacent ranges should be still considered
## 0. So either we have an argument naming problem, or we should modify
## the handling of the 'maxgap' argument so that the user would need to
## specify maxgap=0L to obtain the result below.)
findOverlaps(query, subject, maxgap=1L)

## shortcut
findOverlaps(query, subject)

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

## one Ranges 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")

## alternative 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

## -----
## 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")

```

```

## -----
## "ranges" METHOD FOR Hits OBJECTS
## -----

## extract the regions of intersection between the overlapping ranges
ranges(ov, query, subject)

## -----
## Using RangesList 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)

```

---

GappedRanges-class      *GappedRanges objects*

---

## Description

The GappedRanges class is a vector-like container for storing a set of "gapped ranges".

## Details

A "gapped range" is conceptually the union of 1 or more non-overlapping (and non-empty) ranges ordered from left to right. More precisely, a "gapped range" can be represented by a normal IRanges



object of length  $\geq 1$ . In particular normality here ensures that the individual ranges are non-empty and are separated by non-empty gaps. The start of a "gapped range" is the start of its first range. The end of a "gapped range" is the end of its last range. If we ignore the gaps, then a GappedRanges object can be seen as a [Ranges](#) object.

### Constructor

No constructor function is provided for GappedRanges objects. The coercion methods described below can be used to create GappedRanges objects.

### Coercion

`as(from, "GappedRanges")`: Turns a [CompressedNormalIRangesList](#) or [CompressedIRangesList](#) object into a GappedRanges object.

`as(from, "RangesList")`: Turns a GappedRanges object into a [RangesList](#) object (more precisely the result will be a [CompressedNormalIRangesList](#) object).

### Accessor methods

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

`length(x)`: Returns the number of "gapped ranges" in `x`.

`start(x)`, `end(x)`: Returns an integer vector of length `length(x)` containing the start and end (respectively) of each "gapped range" in `x`. See Details section above for the exact definitions of the start and end of a "gapped range".

`width(x)`: Defined as `end(x) - start(x) + 1L`.

`ngap(x)`: Returns an integer vector of length `length(x)` containing the number of gaps for each "gapped range" in `x`. Equivalent to `elementLengths(x) - 1L`.

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

### Subsetting and related operations

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

`x[i]`: Returns a new GappedRanges object made of the selected "gapped ranges". `i` can be a numeric, character or logical vector, or any of the types supported by the `[]` method for [CompressedNormalIRangesList](#) objects.

`x[[i]]`: Returns the [NormalIRanges](#) object representing the `i`-th element in `x`. Equivalent to `as(from, "RangesList")[[i]]`. `i` can be a single numeric value or a single character string.

`elementType(x)`: Returns the type of `x[[i]]` as a single string (always "NormalIRanges"). Note that the semantic of the `[[` method for GappedRanges objects is different from the semantic of the method for [Ranges](#) objects (the latter returns an integer vector).

`elementLengths(x)`: Semantically equivalent to

```
sapply(seq_len(length(x)), function(i) length(x[[i]]))
```

but much faster. Note that the semantic of the `elementLengths` method for GappedRanges objects is different from the semantic of the method for [Ranges](#) objects (the latter returns the width of the [Ranges](#) object).

**Combining and related operations**

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

`c(x, ...)`: Combine `x` and the `GappedRanges` objects in `...` together. The result is an object of the same class as `x`.

**Author(s)**

H. Pages

**See Also**

[Ranges-class](#), [CompressedNormalIRangesList-class](#)

**Examples**

```
## The 3 following IRanges objects are normal. Each of them will be
## stored as a "gapped range" in the GappedRanges object 'gr'.
ir1 <- IRanges(start=c(11, 21, 23), end=c(15, 21, 30))
ir2 <- IRanges(start=-2, end=15)
ir3 <- IRanges(start=c(-2, 21), end=c(10, 22))
ir1 <- IRangesList(ir1, ir2, ir3)

gr <- as(ir1, "GappedRanges")
gr

length(gr)
start(gr)
end(gr)
width(gr)
ngap(gr)
gr[-1]
gr[ngap(gr) >= 1]
gr[[1]]
as.integer(gr[[1]])
gr[[2]]
as.integer(gr[[2]])
as(gr, "RangesList")
start(as(gr, "RangesList")) # not the same as 'start(gr)'
```

---

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 mappings) are formalized via specific Grouping subclasses.

This man page documents the core Grouping API, and 2 important Grouping subclasses: Many-ToOneGrouping and Partitioning (the latter being a particular case of the former).

### 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 ( $1 \leq j \leq NO$ ).

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.

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

If  $i$  is not NULL, `grouplength(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`, `elementLengths`, and `unlist`, etc... should work out-of-the-box on any Grouping object.

### ManyToOneGrouping objects

The `ManyToOneGrouping` class is a virtual class for representing groupings where every object belongs to one group and only one. The grouping of an empty collection of objects in an arbitrary number of 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 `grouplength(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 and Dups

DOCUMENT ME Constructors:

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

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

### Partitioning objects

The `Partitioning` class is a virtual subclass of `ManyToOneGrouping` for representing *block-groupings* i.e. groupings where each group contains objects that are neighbors in the original collection of objects. More formally, a grouping `x` is a block-grouping iff `togroup(x)` is sorted in increasing order (not necessarily strictly increasing).

A `Partitioning` object can also be seen (and manipulated) as a [Ranges](#) object where all the ranges are adjacent starting at 1 (i.e. it covers the `1:NO` interval with no overlap between the ranges).

Note that a `Partitioning` object is both: a particular type of `ManyToOneGrouping` object and a particular type of [Ranges](#) object. Therefore all the methods that are defined for `ManyToOneGrouping` and [Ranges](#) objects can also be used on a `Partitioning` object. See `?Ranges` for a description of the [Ranges](#) API.

The `Partitioning` virtual class 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 `elementLengths(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 `elementLengths(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).

### Author(s)

H. Pages

### See Also

[IntegerList-class](#), [Ranges-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]]
grouplength(h2l) # same as 'unname(sapply(h2l, length))'
grouplength(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 'grouplength(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]]
grouplength(pbe1) # same as 'unname(sapply(pbe1, length))' and 'width(pbe1)'
togroup(pbe1)
togrouplength(pbe1) # same as 'grouplength(pbe1, togroup(pbe1))'
names(pbe1)

## The Ranges 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))

```

## 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(from, "DataFrame")`: Creates a DataFrame by combining the result of `as.matrix(from)` with `mcols(from)`.

`as.data.frame(x)`: Attempts to coerce the result of `as(from, "DataFrame")` to a data.frame.

`as(x, "List")`: Like `as.list`, above.

## 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, subject.map=factor(c("e", "e", "d"), letters[1:5]))
hits2
hits3 <- remapHits(hits, subject.map=c(5, 5, 4), new.subjectLength=5)
hits3
stopifnot(identical(hits2, hits3))

```

---

HitsList-class

*List of Hits objects*


---

## Description

The HitsList class stores a set of Hits objects. It's typically used to represent the result of `findOverlaps` on two [RangesList](#) objects.

## Details

Roughly the same set of utilities are provided for HitsList as for Hits:

The `as.matrix` method coerces a HitsList in a similar way to Hits, except a column is prepended that indicates which space (or element in the query RangesList) to which the row corresponds.

The `as.table` method flattens or unlists the list, counts the number of hits for each query range and outputs the counts as a table, which has the same shape as from a single Hits object.

To transpose a HitsList `x`, so that the subject and query in each space are interchanged, call `t(x)`. This allows, for example, counting the number of hits for each subject element using `as.table`.

When the HitsList object is the result of a call to `findOverlaps` on two [RangesList](#) objects, the actual regions of intersection between the overlapping ranges can be obtained with the `ranges` accessor.

## Coercion

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

`as.matrix(x)`: calls `as.matrix` on each Hits, combines them row-wise and offsets the indices so that they are aligned with the result of calling `unlist` on the query and subject.

`as.table(x)`: counts the number of hits for each query element in `x` and outputs the counts as a table, which is aligned with the result of calling `unlist` on the query.

`t(x)`: Interchange the query and subject in each space of `x`, returns a transposed HitsList.

### Accessors

`queryHits(x)`: Equivalent to `unname(as.matrix(x)[,1])`.

`subjectHits(x)`: Equivalent to `unname(as.matrix(x)[,2])`.

`space(x)`: gets the character vector naming the space in the query `RangesList` for each hit, or `NULL` if the query did not have any names.

`ranges(x, query, subject)`: returns a `RangesList` holding the intersection of the ranges in the `RangesList` objects `query` and `subject`, which should be the same `subject` and `query` used in the call to `findOverlaps` that generated `x`. Eventually, we might store the `query` and `subject` inside `x`, in which case the arguments would be redundant.

### Note

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

### Author(s)

Michael Lawrence

### See Also

[findOverlaps](#), which generates an instance of this class.

---

inter-range-methods    *Inter range transformations of a Ranges, Views, RangesList, MaskCollection, or RangedData object*

---

### Description

Except for `disjointBins()`, 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.

Range-based endomorphisms are grouped in 2 categories:

1. Intra range transformations like `shift()` that transform each range individually (and independently of the other ranges) and return an object of the *same length* as the input object. Those transformations are described in the [intra-range-methods](#) man page (see `?`intra-range-methods``).
2. Inter range transformations like `reduce()` that transform all the ranges together as a set to produce a new set of ranges and return an object not necessarily of the same length as the input object. Those transformations are described in this man page.

**Usage**

```

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

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

## reduce()
## -----
reduce(x, ...)

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

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

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

## disjoint()
## -----
disjoin(x, ...)

## disjointBins()
## -----
disjointBins(x, ...)

```

**Arguments**

x	A <a href="#">Ranges</a> , <a href="#">Views</a> , <a href="#">RangesList</a> , <a href="#">MaskCollection</a> , or <a href="#">RangedData</a> object.
...	For range, additional Ranges or RangesList to consider.
na.rm	Ignored.
drop.empty.ranges	TRUE or FALSE. Should empty ranges be dropped?

<code>min.gapwidth</code>	Ranges separated by a gap of at least <code>min.gapwidth</code> positions are not merged.
<code>with.revmap</code>	TRUE or FALSE. Should the mapping from reduced to original ranges be stored in the returned object? If yes, then it is stored as metadata column "revmap" of type <a href="#">IntegerList</a> .
<code>with.inframe.attrib</code>	TRUE or FALSE. For internal use.
<code>by</code>	A character vector.
<code>start, end</code>	<ul style="list-style-type: none"> <li>• If <code>x</code> is a <a href="#">Ranges</a> or <a href="#">Views</a> 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.</li> <li>• If <code>x</code> is a <a href="#">RangesList</a> object: Integer vectors containing the coordinate bounds for each <a href="#">RangesList</a> top-level element.</li> </ul>

## Details

Here we start by describing how each transformation operates on a [Ranges](#) object `x`.

`range` first combines `x` and the arguments in `...`. If the combined [IRanges](#) object 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 combined object. Otherwise (i.e. if the combined object contains no range), `IRanges()` is returned (i.e. an [IRanges](#) instance of length 0).

If `x` is a [RangedData](#) object, then `range` returns a [RangesList](#) object resulting from calling `range(ranges(x))`, i.e. the bounds of the ranges in each space.

`reduce` first orders the ranges in `x` from left to right, then merges the overlapping or adjacent ones. If `x` is a [RangedData](#) object, `reduce` merges the ranges in each of the spaces after grouping by the `by` values columns and returns the result as a [RangedData](#) containing the reduced ranges and the `by` value columns.

`gaps` returns the "normal" [Ranges](#) 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.

`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` 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.

When `x` is a [RangesList](#) object, doing any of the transformation above is equivalent to applying the transformation to each [RangesList](#) top-level element separately.

For `range`, if there are additional [RangesList](#) objects in `...`, they are merged into `x` by name, if all objects have names, otherwise, if they are all of the same length, by position. Else, an exception is thrown.

**Author(s)**

H. Pages, M. Lawrence, P. Aboyoun

**See Also**

- [intra-range-methods](#) for intra range transformations.
- The [Ranges](#), [Views](#), [RangesList](#), [MaskCollection](#), and [RangedData](#) classes.
- The [inter-range-methods](#) man page in the GenomicRanges package for methods that operate on [GenomicRanges](#) and other objects.
- [setops-methods](#) for set operations on [IRanges](#) objects.
- [solveUserSEW](#) for the SEW (Start/End/Width) interface.

**Examples**

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

## On a Ranges 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 a RangesList 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

## On a RangedData object:
ranges <- IRanges(c(1,2,3),c(4,5,6))
score <- c(10L, 2L, NA)
rd <- RangedData(ranges, score)
range(rd)
rd2 <- RangedData(IRanges(c(5,2,0), c(6,3,1)))
range(rd, rd2)

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

```

## On a Ranges 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 a RangesList 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)

## On a RangedData object:
rd <- RangedData(
  RangesList(
    chrA=IRanges(start=c(1, 4, 6), width=c(3, 2, 4)),
    chrB=IRanges(start=c(1, 3, 6), width=c(3, 3, 4))),
  score=c(2, 7, 3, 1, 1, 1))
rd
reduce(rd)

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

## On a Ranges 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 a RangesList 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 a Ranges 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))

## On a RangesList object:
disjoin(collection)

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

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

## On a RangesList object:
disjointBins(collection)

```

---

IntervalForest-class *Interval Search Forests*


---

## Description

Efficiently perform overlap queries with a set of interval trees.

**WARNING:** IntervalForest objects are defunct. Please use [NCLists](#) objects instead. See [?NCLists](#) for more information.

## Details

A common type of query that arises when working with intervals is finding which intervals in one set overlap those in another. An efficient family of algorithms for answering such queries is known as the Interval Tree. The `IntervalForest` class stores a set of Interval Trees corresponding to intervals that are partitioned into disjoint sets. The most efficient way to construct `IntervalForest` objects is to call the constructor below on a [CompressedIRangesList](#) object. See the [IntervalTree](#) class for the underlying Interval Tree data structure.

A canonical example of a compressed ranges list are [GenomicRanges](#) objects, where intervals are partitioned by their seqnames. See the [GIntervalTree](#) class to see the use of `IntervalForest` objects in this case.

The simplest approach for finding overlaps is to call the [findOverlaps](#) function on a [RangesList](#) object. See the man page of [findOverlaps-methods](#) for how to use this and other related functions.

## Constructor

`IntervalForest(rangesList)`: Creates an `IntervalForest` from the ranges list in `rangesList`, an object coercible to `CompressedIRangesList`.

## Accessors

`length(x)`: Gets the number of ranges stored in the forest. This is a fast operation that does not bring the ranges into R.

`start(x)`: Get the starts of the ranges as a `CompressedIntegerList`.

`end(x)`: Get the ends of the ranges as `CompressedIntegerList`.

`x@partitioning`: The range partitioning of class `PartitioningByEnd`.

`names(x)`: Get the names of the range partitioning.

`elementLengths(x)`: The number of ranges in each partition.

## Author(s)

Hector Corrada Bravo, Michael Lawrence

## See Also

[findOverlaps-methods](#) for finding/counting interval overlaps between two compressed lists of "range-based" objects, [RangesList](#), the parent of this class, [CompressedHitsList](#), set of hits between 2 list-like objects, [GIntervalTree](#), which uses `IntervalForest` objects.

## Examples

```
## IntervalForest objects are defunct. Please use NCLists objects
## instead. See ?NCLists for more information.
```



## Description

Efficiently perform overlap queries with an interval tree.

WARNING: IntervalTree objects are defunct. Please use [NCList](#) objects instead. See [?NCList](#) for more information.

## Details

A common type of query that arises when working with intervals is finding which intervals in one set overlap those in another. An efficient family of algorithms for answering such queries is known as the Interval Tree. This implementation makes use of the augmented tree algorithm from the reference below, but heavily adapts it for the use case of large, sorted query sets.

The simplest approach for finding overlaps is to call the [findOverlaps](#) function on a [Ranges](#) or other object with range information. See the man page of [findOverlaps](#) for how to use this and other related functions.

An IntervalTree object is a derivative of [Ranges](#) and stores its ranges as a tree that is optimized for overlap queries. Thus, for repeated queries against the same subject, it is more efficient to create an IntervalTree once for the subject using the constructor described below and then perform the queries against the IntervalTree instance.

## Constructor

`IntervalTree(ranges)`: Creates an IntervalTree from the ranges in ranges, an object coercible to IntervalTree, such as an [IRanges](#) object.

## Coercion

`as(from, "IRanges")`: Imports the ranges in from, an IntervalTree, to an [IRanges](#).

`as(from, "IntervalTree")`: Constructs an IntervalTree representing from, a Ranges object that is coercible to IRanges.

## Accessors

`length(x)`: Gets the number of ranges stored in the tree. This is a fast operation that does not bring the ranges into R.

`start(x)`: Get the starts of the ranges.

`end(x)`: Get the ends of the ranges.

### Notes on Time Complexity

The cost of constructing an instance of the interval tree is a  $O(n \cdot \lg(n))$ , which makes it about as fast as other types of overlap query algorithms based on sorting. The good news is that the tree need only be built once per subject; this is useful in situations of frequent querying. Also, in this implementation the data is stored outside of `R`, avoiding needless copying. Of course, external storage is not always convenient, so it is possible to coerce the tree to an instance of `IRanges` (see the Coercion section).

For the query operation, the running time is based on the query size  $m$  and the average number of hits per query  $k$ . The output size is then  $\max(mk, m)$ , but we abbreviate this as  $mk$ . Note that when the `multiple` parameter is set to `FALSE`,  $k$  is fixed to 1 and drops out of this analysis. We also assume here that the query is sorted by start position (the `findOverlaps` function sorts the query if it is unsorted).

An upper bound for finding overlaps is  $O(\min(mk \cdot \lg(n), n + mk))$ . The fastest interval tree algorithm known is bounded by  $O(\min(m \cdot \lg(n), n) + mk)$  but is a lot more complicated and involves two auxiliary trees. The lower bound is  $\Omega(\lg(n) + mk)$ , which is almost the same as for returning the answer,  $\Omega(mk)$ . The average is of course somewhere in between.

This analysis informs the choice of which set of ranges to process into a tree, i.e. assigning one to be the subject and the other to be the query. Note that if  $m > n$ , then the running time is  $O(m)$ , and the total operation of complexity  $O(n \cdot \lg(n) + m)$  is better than if  $m$  and  $n$  were exchanged. Thus, for once-off operations, it is often most efficient to choose the smaller set to become the tree (but  $k$  also affects this). This is reinforced by the realization that if  $mk$  is about the same in either direction, the running time depends only on  $n$ , which should be minimized. Even in cases where a tree has already been constructed for one of the sets, it can be more efficient to build a new tree when the existing tree of size  $n$  is much larger than the query set of size  $m$ , roughly when  $n > m \cdot \lg(n)$ .

### Author(s)

Michael Lawrence

### References

Interval tree algorithm from: Cormen, Thomas H.; Leiserson, Charles E.; Rivest, Ronald L.; Stein, Clifford. Introduction to Algorithms, second edition, MIT Press and McGraw-Hill. ISBN 0-262-53196-8

### See Also

`findOverlaps` for finding/counting interval overlaps between two "range-based" objects, `Ranges`, the parent of this class, `Hits`, set of hits between 2 vector-like objects.

### Examples

```
## IntervalTree objects are defunct. Please use NList objects instead.
## See ?NList for more information.
```

---

intra-range-methods    *Intra range transformations of a Ranges, Views, RangesList, or MaskCollection object*

---

## Description

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.

Range-based endomorphisms are grouped in 2 categories:

1. Intra range transformations like `shift()` that transform each range individually (and independently of the other ranges) and return an object of the *same length* as the input object. Those transformations are described in this man page.
2. Inter range transformations like `reduce()` that transform all the ranges together as a set to produce a new set of ranges and return an object not necessarily of the same length as the input object. Those transformations are described in the [inter-range-methods](#) man page (see `?`inter-range-methods``).

## Usage

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

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

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

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

## promoters()
promoters(x, upstream=2000, downstream=200, ...)

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

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

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

**Arguments**

x	A <a href="#">Ranges</a> , <a href="#">Views</a> , <a href="#">RangesList</a> , or <a href="#">MaskCollection</a> object.
shift	An integer vector containing the shift information. Recycled as necessary so that each element corresponds to a range in x. It can also be an <a href="#">IntegerList</a> object if x is a <a href="#">RangesList</a> object.
use.names	TRUE or FALSE. Should names be preserved?
start, end	<ul style="list-style-type: none"> <li>• If x is a <a href="#">Ranges</a> or <a href="#">Views</a> object: A vector of integers for all functions except for flank. For restrict, the supplied start and end 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 x. Same thing for narrow and threebands, except that here start and end must contain coordinates relative to the ranges in x. See the Details section below. For flank, start is a logical indicating whether x should be flanked at the start (TRUE) or the end (FALSE). Recycled as necessary so that each element corresponds to a range in x.</li> <li>• If x is a <a href="#">RangesList</a> object: For flank, start must be either a logical vector or a <a href="#">LogicalList</a> object indicating whether x should be flanked at the start (TRUE) or the end (FALSE). Recycled as necessary so that each element corresponds to a range in x. For narrow, start and end must be either an integer vector or an <a href="#">IntegerList</a> object containing coordinates relative to the current ranges. For restrict, start and end must be either an integer vector or an <a href="#">IntegerList</a> object (possibly containing NA's).</li> </ul>
width	<ul style="list-style-type: none"> <li>• If x is a <a href="#">Ranges</a> or <a href="#">Views</a> object: For narrow and threebands, a vector of integers, eventually with NAs. See the SEW (Start/End/Width) interface for the details (?solveUserSEW). For resize and flank, the width of the resized or flanking regions. Note that if both is TRUE, this is effectively doubled. Recycled as necessary so that each element corresponds to a range in x.</li> <li>• If x is a <a href="#">RangesList</a> object: For resize and flank, either an integer vector or an <a href="#">IntegerList</a> object containing the width of the flanking or resized regions. Recycled as necessary so that each element corresponds to a range in x. (Note for flank: if both is TRUE, this is effectively doubled.) For narrow, either an integer vector or a <a href="#">IntegerList</a> object containing the widths to narrow to. See the SEW (Start/End/Width) interface for the details (?solveUserSEW).</li> </ul>
both	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.
bounds	An <a href="#">IRanges</a> object to serve as the reference bounds for the reflection, see below.
fix	<ul style="list-style-type: none"> <li>• If x is a <a href="#">Ranges</a> or <a href="#">Views</a> object: A character vector or character-Rle of length 1 or length(x) containing the values "start", "end", and "center" denoting what to use as an anchor for each element in x.</li> <li>• If x is a <a href="#">RangesList</a> object: A character vector of length 1, a <a href="#">CharacterList</a> object, or a character-RleList object containing the values "start", "end", and "center" denoting what to use as an anchor for each element in x.</li> </ul>

upstream, downstream

Single integer values  $\geq 0$ . upstream defines the number of nucleotides toward the 5' end and downstream 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 upstream and downstream 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.

keep.all.ranges

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  $start - 1$  or start strictly after  $end + 1$ . Ranges that end at  $start - 1$  or start at  $end + 1$  are always kept and their width is set to zero in the returned [IRanges](#) object.

...

Additional arguments for methods.

## Details

Here we start by describing how each transformation operates on a [Ranges](#) object  $x$ .

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

`narrow` narrows the ranges in  $x$  i.e. each range in the returned [Ranges](#) object is a subrange 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` resizes the ranges to the specified width where either the start, end, or center is used as an anchor.

`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)`:

```
---***XXXX
```

`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,  $(\text{start}(x) - \text{upstream})$  to  $(\text{start}(x) + \text{downstream} - 1)$ . For documentation for using `promoters` on `GenomicRanges` objects see `?promoters, GRanges-method`.

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

`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=`

When `x` in a `RangesList` object, doing any of the transformation above is equivalent to applying the transformation to each `RangesList` top-level element separately.

### Author(s)

H. Pages, M. Lawrence, P. Aboyoun

### See Also

- [inter-range-methods](#) for inter range transformations.
- The [Ranges](#), [Views](#), [RangesList](#), and [MaskCollection](#) classes.
- The [intra-range-methods](#) man page in the `XVector` package for methods that operate on `XVectorList` objects.
- The [intra-range-methods](#) man page in the `GenomicRanges` package for methods that operate on [GenomicRanges](#) and other objects.
- [setops-methods](#) for set operations on [IRanges](#) objects.
- [solveUserSEW](#) for the SEW (Start/End/Width) interface.

**Examples**

```

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

## On a Ranges object
ir1 <- successiveIRanges(c(19, 5, 0, 8, 5))
ir1
shift(ir1, shift=-3)

## On a RangesList 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)

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

## On a Ranges 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 a RangesList 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 a Ranges object
resize(ir2, 200)
resize(ir2, 2, fix="end")

## On a RangesList object
resize(collection, width=200)

## -----

```

```

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

## On a Ranges object
ir3 <- IRanges(c(2,5,1), 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 a RangesList object
flank(collection, width=10)

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

## On a Ranges object
ir4 <- IRanges(20:23, width=3)
promoters(ir4, upstream=0, downstream=0) ## no change
promoters(ir4, upstream=0, downstream=1) ## start value only
promoters(ir4, upstream=1, downstream=0) ## single upstream nucleotide

## On a RangesList object
promoters(collection, upstream=5, downstream=2)

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

## On a Ranges object
bounds <- IRanges(c(0, 5, 3), c(10, 6, 9))
reflect(ir3, bounds)

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

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

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

## On a RangesList object
restrict(collection, start=2, end=8)

## -----

```



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

## On a Ranges 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 RangesList objects.
```

---

IRanges-class

*IRanges and NormalIRanges objects*


---

### Description

The IRanges class is a simple implementation of the [Ranges](#) container where 2 integer vectors of the same length are used to store the start and width values. See the [Ranges](#) virtual class for a formal definition of [Ranges](#) 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 [Ranges](#) objects for the definition and properties of "normal" [Ranges](#) objects.

### Constructor

See `?`IRanges-constructor``.

### Coercion

`as(from, "IRanges")`: Creates an IRanges instance from a Ranges object, logical vector, 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.

### Combining

`c(x, ..., ignore.mcols=FALSE)` Combining IRanges objects is straightforward when they do not have any metadata columns. If only one of the IRanges object has metadata columns, then the corresponding metadata columns are attached to the other IRanges object and set to NA. When multiple IRanges object have their own metadata columns, the user must ensure that each such `linkS4class{DataFrame}` have identical layouts to each other (same columns defined), in order for the combination to be successful, otherwise an error will be thrown. The user can call `c(x, ..., ignore.mcols=TRUE)` in order to combine IRanges objects with differing sets of metadata columns, which will result in the combined object having NO metadata columns.

**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)**

H. Pages

**See Also**

[Ranges-class](#),  
[IRanges-constructor](#), [IRanges-utils](#),  
[intra-range-methods](#) for intra range transformations,  
[inter-range-methods](#) for inter range transformations,  
[setops-methods](#)

**Examples**

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

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

## Combining 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 <- 5000000L
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.

solveUserSEW0 and solveUserSEW are utility functions that solve a set of user-supplied start/end/width values.

## Usage

```

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

## Supporting functions (not for the end user):
solveUserSEW0(start=NULL, end=NULL, width=NULL)
solveUserSEW(refwidths, start=NA, end=NA, width=NA,
             rep.refwidths=FALSE,
             translate.negative.coord=TRUE,
             allow.nonnarrowing=FALSE)

```

## Arguments

start, end, width	For IRanges and solveUserSEW0: NULL, or vector of integers (eventually with NAs). For solveUserSEW: vector of integers (eventually with NAs).
names	A character vector or NULL.
refwidths	Vector of non-NA non-negative integers containing the reference widths.
rep.refwidths	TRUE or FALSE. Use of rep.refwidths=TRUE is supported only when refwidths is of length 1.
translate.negative.coord, allow.nonnarrowing	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

`solveUserSEW0(start=NULL, end=NULL, width=NULL):`

`solveUserSEW(refwidths, start=NA, end=NA, width=NA, rep.refwidths=FALSE,`

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)**

H. Pages

**See Also**[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 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)
```

**Description**

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

**Usage**

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

## 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.
chunksize	A single positive integer. The size of the chunks (last chunk might be smaller).
nchunk	A single positive integer. The number of chunks.
x	A logical vector for whichAsIRanges. 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.

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)**

H. Pages

**See Also**

[Ranges-class](#), [IRanges-class](#),  
[intra-range-methods](#) for intra range transformations,  
[inter-range-methods](#) for inter range transformations,  
[setops-methods](#), [solveUserSEW](#), [successiveViews](#)

**Examples**

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

successiveIRanges(vec)

breakInChunks(600999, 50000) # 13 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(..., universe = NULL, 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 compressed, the internal storage of the data is compressed.

### Coercion

`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

### See Also

[RangesList](#), the parent of this class, for more functionality.

[intra-range-methods](#) and [inter-range-methods](#) for intra and inter range transformations of `IRangesList` objects.

[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)
```

---

List-class-leftovers *List objects (old man page)*

---

### Description

IMPORTANT NOTE - 9/4/2014: This man page is being refactored. Most of the things that used to be documented here have been moved to the man page for [List](#) objects located in the **S4Vectors** package.



**Details**

The only thing left here is the documentation of the `stack` method for [List](#) objects. In the code snippets below, `x` is a `List` object.

```
stack(x, index.var = "name", value.var = "value"): As with stack on a list, constructs a DataFrame with two columns: one for the unlisted values, the other indicating the name of the element from which each value was obtained. index.var specifies the column name for the index (source name) column and value.var specifies the column name for the values.
```

**See Also**

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

**Examples**

```
starts <- IntegerList(c(1, 5), c(2, 8))
ends <- IntegerList(c(3, 8), c(5, 9))
rgl <- IRangesList(start=starts, end=ends)
rangeDataFrame <- stack(rgl, "space", "ranges")
```

---

mapCoords-methods

*Mapping of ranges to another sequence*


---

**Description**

DEFUNCT! Use [mapToTranscripts](#) from the **GenomicFeatures** package or [mapToAlignments](#) from the **GenomicAlignments** package instead.

The `mapCoords` generic converts a set of ranges to the equivalent ranges on another sequence through some sort of alignment between sequences. The output is an object of the same class as from and in general will contain the mapped ranges with the matching data as metadata. Matching data are the result of calling `findOverlaps` with `type = "within"`. This operation matches each input range to a destination sequence (useful when the alignment is one/many to many).

The `pmapCoords` function is simpler: it treats the two inputs as parallel vectors, maps each input range via the corresponding alignment, and returns the mapped ranges. There is one result per input element, instead of the many-to-many result from `mapCoords`.

**Usage**

```
mapCoords(from, to, ...)
pmapCoords(from, to, ...)
```

**Arguments**

<code>from</code>	Typically an object containing ranges to map.
<code>to</code>	Typically an object representing an alignment.
<code>...</code>	Arguments to pass to methods

**Value**

An object the same class as from.

In the case of `mapCoords`, the result of `findOverlaps` with type = "within" are included as metadata columns ('queryHits' and 'subjectHits').

**Author(s)**

Michael Lawrence

**See Also**

- See `?mapCoords-methods` in the **GenomicRanges** package for the `mapCoords` method on `GRanges` objects
- See `?mapCoords-methods` in the **GenomicAlignments** package for the `mapCoords` method on `GAlignments` objects

**Examples**

```
## DEFUNCT! See ?mapToTranscripts in the GenomicFeatures package and  
## ?mapToAlignments in the GenomicAlignments package.
```

---

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)**

H. Pages

**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	<i>Split elements belonging to multiple groups</i>
------------	--

---

**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**

x	The object to split, like a vector.
f	A list-like object of vectors, the same length as x, where each element indicates the groups to which each element of x 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]))
```

---

NCList-class	<i>Nested Containment List objects</i>
--------------	--

---

**Description**

The NCList class is a container for storing the Nested Containment List representation of a [Ranges](#) object. Preprocessing a [Ranges](#) object as a Nested Containment List allows efficient overlap-based operations like [findOverlaps](#).

The NCLists class is a container for storing a collection of NCList objects. An NCLists object is typically the result of preprocessing each list element of a [RangesList](#) object as a Nested Containment List. Like with NCList, the NCLists object can then be used for efficient overlap-based operations.

To preprocess a [Ranges](#) or [RangesList](#) object, simply call the NCList or NCLists constructor function on it.

## Usage

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

## Arguments

`x` The [Ranges](#) or [RangesList](#) object to preprocess.

`circle.length` Use only if the space (or spaces if `x` is a [RangesList](#) 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.

Note that `NCList`, `NCLists`, and [GNCList](#) objects, are replacements for [IntervalTree](#), [IntervalForest](#), and [GIntervalTree](#) objects, respectively. The latter are defunct starting with BioC 3.2.

Some important differences between the new `findOverlaps`/`countOverlaps` implementation based on Nested Containment Lists and the old implementation based on Interval Trees:

- 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 [Ranges](#) object (replacement for [IntervalTree](#)), `NCLists` for a [RangesList](#) 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 [Ranges](#) 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)

H. Pages

### 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.
- [Ranges](#) and [RangesList](#) 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 neighbor*

---

## Description

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

## Usage

```
## S4 method for signature 'Ranges,RangesORmissing'
nearest(x, subject, select = c("arbitrary", "all"),
        algorithm = c("nclist", "intervaltree"))

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

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

## S4 method for signature 'Ranges,RangesORmissing'
distanceToNearest(x, subject, select = c("arbitrary", "all"),
                  algorithm = c("nclist", "intervaltree"))

## S4 method for signature 'Ranges,Ranges'
distance(x, y)
```

## Arguments

x	The query <a href="#">Ranges</a> instance.
subject	The subject <a href="#">Ranges</a> instance, within which the nearest neighbors are found. Can be missing, in which case x is also the subject.
select	Logic for handling ties. By default, all the methods select a single interval (arbitrary for nearest, the first by order in subject for precede, and the last for follow). To get all matchings, as a <a href="#">Hits</a> object, use "all".
algorithm	This argument is passed to <a href="#">findOverlaps</a> , which nearest and distanceToNearest use internally. See <a href="#">?findOverlaps</a> for more information. Note that it will be removed in BioC 3.3 so please don't use it unless you have a good reason to do so (e.g. troubleshooting).
y	For the distance method, a <a href="#">Ranges</a> instance. Cannot be missing. If x and y are not the same length, the shortest will be recycled to match the length of the longest.
...	Additional arguments for methods



## Details

- `nearest`: The conventional nearest neighbor finder. Returns a 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`: 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`: 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`.
  - `distanceToNearest`: Returns the distance for each range in `x` to its nearest neighbor in `subject`.
  - `distance`: 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`

## Value

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

For `distanceToNearest`, a `Hits` object with an `elementMetadata` column of the distance between the pair. Access distance with `mcols` accessor.

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

**Author(s)**

M. Lawrence

**See Also**

- The [Ranges](#) and [Hits](#) classes.
- The [GenomicRanges](#) and [GRanges](#) classes in the GenomicRanges package.
- [findOverlaps](#) for finding just the overlapping ranges.
- GenomicRanges methods for
  - precede
  - follow
  - nearest
  - distance
  - distanceToNearest

are documented at [?nearest-methods](#) or [?precede,GenomicRanges,GenomicRanges-method](#)

**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)))
```

---

RangedData-class      *Data on ranges*

---

## Description

**IMPORTANT NOTE:** Starting with BioC 2.12, the use of RangedData and RangedDataList objects is discouraged in favor of GRanges and GRangesList objects (those classes are defined in the **GenomicRanges** package).

RangedData supports storing data, i.e. a set of variables, on a set of ranges spanning multiple spaces (e.g. chromosomes). Although the data is split across spaces, it can still be treated as one cohesive dataset when desired and extends `DataTable`. In order to handle large datasets, the data values are stored externally to avoid copying, and the `rdapply` function facilitates the processing of each space separately (divide and conquer).

## Details

A RangedData object consists of two primary components: a `RangesList` holding the ranges over multiple spaces and a parallel `SplitDataFrameList`, holding the split data. There is also an universe slot for denoting the source (e.g. the genome) of the ranges and/or data.

There are two different modes of interacting with a RangedData. The first mode treats the object as a contiguous "data frame" annotated with range information. The accessors `start`, `end`, and `width` get the corresponding fields in the ranges as atomic integer vectors, undoing the division over the spaces. The `[[` and matrix-style `[`, extraction and subsetting functions unroll the data in the same way. `[[<-` does the inverse. The number of rows is defined as the total number of ranges and the number of columns is the number of variables in the data. It is often convenient and natural to treat the data this way, at least when the data is small and there is no need to distinguish the ranges by their space.

The other mode is to treat the RangedData as a list, with an element (a virtual `Ranges/DataFrame` pair) for each space. The length of the object is defined as the number of spaces and the value returned by the `names` accessor gives the names of the spaces. The list-style `[` subset function behaves analogously. The `rdapply` function provides a convenient and formal means of applying an operation over the spaces separately. This mode is helpful when ranges from different spaces must be treated separately or when the data is too large to process over all spaces at once.

## Accessor methods

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

The following accessors treat the data as a contiguous dataset, ignoring the division into spaces:

Array accessors:

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

`ncol(x)`: The number of data variables in `x`.

`dim(x)`: An integer vector of length two, essentially `c(nrow(x), ncol(x))`.  
`rownames(x), rownames(x) <- value`: Gets or sets the names of the ranges in `x`.  
`colnames(x), colnames(x) <- value`: Gets the names of the variables in `x`.  
`dimnames(x)`: A list with two elements, essentially `list(rownames(x), colnames(x))`.  
`dimnames(x) <- value`: Sets the row and column names, where `value` is a list as described above.  
`columnMetadata(x)`: Get the `DataFrame` of metadata along the value columns, i.e., where each column in `x` is represented by a row in the metadata. Note that calling `mcols(x)` returns the metadata on each space in `x`.  
`columnMetadata(x) <- value`: Set the `DataFrame` of metadata for the columns.  
`within(data, expr, ...)`: Evaluates `expr` within `data`, a `RangedData`. Any values assigned in `expr` will be stored as value columns in `data`, unless they match one of the reserved names: `ranges`, `start`, `end`, `width` and `space`. Behavior is undefined if any of the range symbols are modified inconsistently. Modifications to `space` are ignored.

Range accessors. The type of the return value depends on the type of `Ranges`. For `IRanges`, an integer vector. Regardless, the number of elements is always equal to `nrow(x)`.

`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(elementLengths(ranges(x)))` or an `IntegerList` object of length `length(ranges(x))` and names `names(ranges(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(elementLengths(ranges(x)))` or an `IntegerList` object of length `length(ranges(x))` and names `names(ranges(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(elementLengths(ranges(x)))` or an `IntegerList` object of length `length(ranges(x))` and names `names(ranges(x))`.

These accessors make the object seem like a list along the spaces:

`length(x)`: The number of spaces (e.g. chromosomes) in `x`.  
`names(x), names(x) <- value`: Get or set the names of the spaces (e.g. "chr1"). `NULL` or a character vector of the same length as `x`.

Other accessors:

`universe(x), universe(x) <- value`: Get or set the scalar string identifying the scope of the data in some way (e.g. genome, experimental platform, etc). The universe may be `NULL`.  
`ranges(x), ranges(x) <- value`: Gets or sets the ranges in `x` as a `RangesList`.  
`space(x)`: Gets the spaces from `ranges(x)`.  
`values(x), values(x) <- value`: Gets or sets the data values in `x` as a `SplitDataFrameList`.  
`score(x), score(x) <- value`: Gets or sets the column representing a "score" in `x`, as a vector. This is the column named `score`, or, if this does not exist, the first column, if it is numeric. The get method return `NULL` if no suitable score column is found. The set method takes a numeric vector as its value.

**Constructor**

`RangedData(ranges = IRanges(), ..., space = NULL, universe = NULL)`:  
 Creates a `RangedData` with the ranges in `ranges` and variables given by the arguments in `...`.  
 See the constructor `DataFrame` for how the `...` arguments are interpreted.

If `ranges` is a `Ranges` object, the `space` argument is used to split of the data into spaces.  
 If `space` is `NULL`, all of the ranges and values are placed into the same space, resulting in a single-space (length one) `RangedData` object. Otherwise, the ranges and values are split into spaces according to `space`, which is treated as a factor, like the `f` argument in `split`.

If `ranges` is a `RangesList` object, then the supplied `space` argument is ignored and its value is derived from `ranges`.

If `ranges` is not a `Ranges` or `RangesList` object, this function calls `as(ranges, "RangedData")` and returns the result if successful.

The universe may be specified as a scalar string by the `universe` argument.

**Coercion**

`as.data.frame(x, row.names=NULL, optional=FALSE, ...)`: Copy the start, end, width of the ranges and all of the variables as columns in a `data.frame`. This is a bridge to existing functionality in R, but of course care must be taken if the data is large. Note that `optional` and `...` are ignored.

`as(from, "DataFrame")`: Like `as.data.frame` above, except the result is an `DataFrame` and it probably involves less copying, especially if there is only a single space.

`as(from, "RangedData")`: Coerce `from` to a `RangedData`, according to the type of `from`:

- `Rle, RleList` Converts each run to a range and stores the run values in a column named "score".
- `RleViewsList` Creates a `RangedData` using the ranges given by the runs of `subject(from)` in each of the windows, with a value column `score` taken as the corresponding subject values.
- `Ranges` Creates a `RangedData` with only the ranges in `from`; no data columns.
- `RangesList` Creates a `RangedData` with the ranges in `from`. Also propagates the *inner* metadata columns of the `RangesList` (accessed with `mcols(unlist(from))`) to the data columns (aka values) of the `RangedData`. This makes it a *lossless* coercion and the exact reverse of the coercion from `RangedData` to `RangesList`.
- `data.frame` or `DataTable` Constructs a `RangedData`, using the columns "start", "end", and, optionally, "space" columns in `from`. The other columns become data columns in the result. Any "width" column is ignored.

`as(from, "RangesList")`: Creates a `CompressedIRangesList` (a subclass of `RangesList`) made of the ranges in `from`. Also propagates the data columns (aka values) of the `RangedData` to the inner metadata columns of the `RangesList`. This makes it a *lossless* coercion and the exact reverse of the coercion from `RangesList` to `RangedData`.

`as.env(x, enclos = parent.frame())`: Creates an environment with a symbol for each variable in the frame, as well as a `ranges` symbol for the ranges. This is efficient, as no copying is performed.

## Subsetting and Replacement

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

`x[i]`: Subsets `x` by indexing into its spaces, so the result is of the same class, with a different set of spaces. `i` can be numerical, logical, `NULL` or missing.

`x[i, j]`: Subsets `x` by indexing into its rows and columns. The result is of the same class, with a different set of rows and columns. The row index `i` can either treat `x` as a flat table by being a character, integer, or logical vector or treat `x` as a partitioned table by being a [RangesList](#), [LogicalList](#), or [IntegerList](#) of the same length as `x`.

`x[[i]]`: Extracts a variable from `x`, where `i` can be a character, numeric, or logical scalar that indexes into the columns. The variable is unlisted over the spaces.

For convenience, values of `"space"` and `"ranges"` are equivalent to `space(x)` and `unlist(ranges(x))` respectively.

`x$name`: similar to above, where `name` is taken literally as a column name in the data.

`x[[i]] <- value`: Sets `value` as column `i` in `x`, where `i` can be a character, numeric, or logical scalar that indexes into the columns. The length of `value` should equal `nrow(x)`. `x[[i]]` should be identical to `value` after this operation.

For convenience, `i="ranges"` is equivalent to `ranges(x) <- value`.

`x$name <- value`: similar to above, where `name` is taken literally as a column name in the data.

## Splitting and Combining

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

`split(x, f, drop = FALSE)`: Split `x` according to `f`, which should be of length equal to `nrow(x)`. Note that `drop` is ignored here. The result is a [RangedDataList](#) where every element has the same length (number of spaces) but different sets of ranges within each space.

`rbind(...)`: Matches the spaces from the `RangedData` objects in `...` by name and combines them row-wise. In a way, this is the reverse of the `split` operation described above.

`c(x, ..., recursive = FALSE)`: Combines `x` with arguments specified in `...`, which must all be `RangedData` objects. This combination acts as if `x` is a list of spaces, meaning that the result will contain the spaces of the first concatenated with the spaces of the second, and so on. This function is useful when creating `RangedData` objects on a space-by-space basis and then needing to combine them.

## Applying

There are two ways explicitly supported ways to apply a function over the spaces of a `RangedData`. The richest interface is [rdapply](#), which is described in its own man page. The simpler interface is an `lapply` method:

`lapply(X, FUN, ...)`: Applies `FUN` to each space in `X` with extra parameters in `...`

## Author(s)

Michael Lawrence

**See Also**

[DataTable](#), the parent of this class, with more utilities. The `rdapply` function for applying a function to each space separately.

**Examples**

```

ranges <- IRanges(c(1,2,3),c(4,5,6))
filter <- c(1L, 0L, 1L)
score <- c(10L, 2L, NA)

## constructing RangedData instances

## no variables
rd <- RangedData()
rd <- RangedData(ranges)
ranges(rd)
## one variable
rd <- RangedData(ranges, score)
rd[["score"]]
## multiple variables
rd <- RangedData(ranges, filter, vals = score)
rd[["vals"]] # same as rd[["score"]] above
rd$vals
rd[["filter"]]
rd <- RangedData(ranges, score + score)
rd[["score...score"]] # names made valid
## use a universe
rd <- RangedData(ranges, universe = "hg18")
universe(rd)

## split some data over chromosomes

range2 <- IRanges(start=c(15,45,20,1), end=c(15,100,80,5))
both <- c(ranges, range2)
score <- c(score, c(0L, 3L, NA, 22L))
filter <- c(filter, c(0L, 1L, NA, 0L))
chrom <- paste("chr", rep(c(1,2), c(length(ranges), length(range2))), sep="")

rd <- RangedData(both, score, filter, space = chrom, universe = "hg18")
rd[["score"]] # identical to score
rd[1][["score"]] # identical to score[1:3]

## subsetting

## list style: [i]

rd[numeric()] # these three are all empty
rd[logical()]
rd[NULL]
rd[] # missing, full instance returned
rd[FALSE] # logical, supports recycling
rd[c(FALSE, FALSE)] # same as above

```

```

rd[TRUE] # like rd[]
rd[c(TRUE, FALSE)]
rd[1] # numeric index
rd[c(1,2)]
rd[-2]

## matrix style: [i,j]

rd[,NULL] # no columns
rd[NULL,] # no rows
rd[,1]
rd[,1:2]
rd[, "filter"]
rd[1,] # now by the rows
rd[c(1,3),]
rd[1:2, 1] # row and column
rd[c(1:2,1,3),1] ## repeating rows

## dimnames

colnames(rd)[2] <- "foo"
colnames(rd)
rownames(rd) <- head(letters, nrow(rd))
rownames(rd)

## space names

names(rd)
names(rd)[1] <- "chr1"

## variable replacement

count <- c(1L, 0L, 2L)
rd <- RangedData(ranges, count, space = c(1, 2, 1))
## adding a variable
score <- c(10L, 2L, NA)
rd[["score"]] <- score
rd[["score"]] # same as 'score'
## replacing a variable
count2 <- c(1L, 1L, 0L)
rd[["count"]] <- count2
## numeric index also supported
rd[[2]] <- score
rd[[2]] # gets 'score'
## removing a variable
rd[[2]] <- NULL
ncol(rd) # is only 1
rd$score2 <- score

## combining/splitting

rd <- RangedData(ranges, score, space = c(1, 2, 1))
c(rd[1], rd[2]) # equal to 'rd'

```



```
rd2 <- RangedData(ranges, score)
unlist(split(rd2, c(1, 2, 1))) # same as 'rd'

## applying

lapply(rd, `[`, 1) # get first column in each space
```

---

RangedDataList-class    *Lists of RangedData*

---

### Description

IMPORTANT NOTE: Starting with BioC 2.12, the use of `RangedData` and `RangedDataList` objects is discouraged in favor of `GRanges` and `GRangesList` objects (those classes are defined in the **GenomicRanges** package).

A formal list of `RangedData` objects. Extends and inherits all its methods from `List`. One use case is to group together all of the samples from an experiment generating data on ranges.

### Constructor

`RangedDataList(...)`: Concatenates the `RangedData` objects in ... into a new `RangedDataList`.

### Other methods

`stack(x, index.var = "name")`: Concatenates the elements of `x` into a `RangedData`, with a column named by `index.var` that groups the records by their original element in `x`.

### Author(s)

Michael Lawrence

### See Also

[RangedData](#), the element type of this `List`.

### Examples

```
ranges <- IRanges(c(1,2,3),c(4,5,6))
a <- RangedData(IRanges(c(1,2,3),c(4,5,6)), score = c(10L, 2L, NA))
b <- RangedData(IRanges(c(1,2,4),c(4,7,5)), score = c(3L, 5L, 7L))
RangedDataList(sample1 = a, sample2 = b)
```

---

**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 = RangesList(), 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 `RangesList`, 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 `RangesList`, 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 <- RangesList(chr1 = IRanges(c(1, 5), c(3, 6)))
```

```
RangedSelection(r1)
as(r1, "RangedSelection") # same as above
```

```
RangedSelection(r1, "score")
```

---

Ranges-class

*Ranges objects*

---

## Description

The Ranges virtual class is a general container for storing a set of integer ranges.

## Details

A Ranges object is a vector-like object where each element describes a "range of integer values".

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 a Ranges object is the number of ranges in it, not the number of integer values in its ranges.

A Ranges object is considered empty iff all its ranges are empty.

Ranges 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 Ranges class itself is a virtual class. The following classes derive directly from the Ranges class: [IRanges](#), [NCList](#), [PartitioningByEnd](#).

## Methods

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

Note that many more operations on Ranges 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 [RangesList](#) objects where the `split` method for Ranges objects 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)`: `start(x) + width(x) - 1L`
- `mid(x)`: returns the midpoint of the range, `start(x) + floor((width(x) - 1)/2)`.
- `names(x)`: NULL or a character vector of the same length as `x`.
- `update(object, ...)`: Convenience method for combining multiple modifications of `object` in one single call. For example `object <- update(object, start=start(object)-2L, is.equivalent.to=start(object) <- start(object)-2L; end(object) <- end(object)+2L`.
- `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`. Ranges with a width less than the `width` argument are returned unchanged.
- `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` and any additional argument (...) is ignored. See [?as.data.frame](#) for more information about these arguments.
- `as.integer(x)`: Convert `x` into an integer vector, by converting each range into the integer sequence formed by `from:to` and concatenating them together.
- `unlist(x, recursive = TRUE, use.names = TRUE)`: Similar to `as.integer(x)` except can add names to elements.
- `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 `Ranges` 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 `Ranges` 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, ...)`: Combine `x` and the `Ranges` objects in ... together. Any object in ... must belong to the same class as `x`, or to one of its subclasses, or must be NULL. The result is an object of the same class as `x`. NOTE: Only works for `IRanges` (and derived) objects for now.
- `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 `GRanges`, `GAlignments`, `Ranges` and `XString` objects.

## Normality

A `Ranges` 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 `Ranges` 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 a `Ranges` 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" `Ranges` 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" `Ranges`:

`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".

## Disjoint ranges

A `Ranges` object `x` is considered to be "disjoint" if its ranges are disjoint (i.e. non-overlapping).

The `isDisjoint` function is provided for testing whether a `Ranges` object is "disjoint" or not:

`isDisjoint(x)`: Return `TRUE` or `FALSE` indicating whether `x` is "disjoint" or not.

`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`). In other words, 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:

```
start(B) < start(A) <= end(B)
```

and also equivalent to:

```
start(B) <= end(A) < end(B)
```

Finally, it is also equivalent to:

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

See `?`Ranges-comparison`` for the meaning of the codes returned by the `compare` function.

Note that a "normal" Ranges object is always "disjoint" but the opposite is not true.

### Author(s)

H. Pages and M. Lawrence

### See Also

[IRanges-class](#), [Ranges-comparison](#), [intra-range-methods](#), [inter-range-methods](#), [IRanges-utils](#), [setops-methods](#), [RangedData-class](#), [NCList-class](#), [PartitioningByEnd-class](#), [update](#), [as.matrix](#), [as.data.frame](#), [rep](#)

### 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

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

## On a Ranges 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) compare(IRanges(i, width=0), IRanges(12, 15)))

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

```

---

Ranges-comparison      *Comparing and ordering ranges*

---

## Description

Methods for comparing and/or ordering [Ranges](#) objects.

## Usage

```

## Element-wise (aka "parallel") comparison of 2 Ranges objects
## -----

## S4 method for signature 'Ranges,Ranges'
compare(x, y)

rangeComparisonCodeToLetter(code)

```

```

## match()
## -----

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

## selfmatch()
## -----

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

## order()
## -----

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

```

### Arguments

<code>x, y, table</code>	<a href="#">Ranges</a> objects.
<code>code</code>	A vector of codes as returned by <code>compare</code> .
<code>nomatch</code>	The value to be returned in the case when no match is found. It is coerced to an integer.
<code>incomparables</code>	Not supported.
<code>method</code>	Use a Quicksort-based ( <code>method="quick"</code> ) or a hash-based ( <code>method="hash"</code> ) algorithm. The latter tends to give better performance, except maybe for some pathological input that we've not been able to determine so far. When <code>method="auto"</code> 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.
<code>...</code>	One or more <a href="#">Ranges</a> objects. The additional <a href="#">Ranges</a> objects are used to break ties.
<code>na.last</code>	Ignored.
<code>decreasing</code>	TRUE or FALSE.

### Details

Two ranges are considered equal iff they share the same start and width. 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.



Ranges are ordered by starting position first, and then by width. This way, the space of ranges is totally ordered. On a [Ranges](#) object, `order`, `sort`, and `rank` are consistent with this order.

`compare(x, y)`: Performs element-wise (aka "parallel") comparison of 2 [Ranges](#) 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> <code>y[i]: .....0000.</code>	6 m: <code>x[i]: .....0000.</code> <code>y[i]: .0000.....</code>
-5 b: <code>x[i]: ..0000.....</code> <code>y[i]: .....0000..</code>	5 l: <code>x[i]: .....0000..</code> <code>y[i]: ..0000.....</code>
-4 c: <code>x[i]: ...0000.....</code> <code>y[i]: .....0000...</code>	4 k: <code>x[i]: .....0000...</code> <code>y[i]: ...0000.....</code>
-3 d: <code>x[i]: ...000000...</code> <code>y[i]: .....0000...</code>	3 j: <code>x[i]: .....0000...</code> <code>y[i]: ...000000...</code>
-2 e: <code>x[i]: ..00000000..</code> <code>y[i]: ....0000....</code>	2 i: <code>x[i]: ....0000....</code> <code>y[i]: ..00000000..</code>
-1 f: <code>x[i]: ...0000.....</code> <code>y[i]: ...000000...</code>	1 h: <code>x[i]: ...000000...</code> <code>y[i]: ...0000.....</code>
0 g: <code>x[i]: ...000000...</code> <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 `compare` method for [Ranges](#) objects 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 `compare`. 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 a [Ranges](#) object. 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 a [Ranges](#) object. 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 (a [Ranges](#) object) into ascending order, breaking ties by further arguments (also [Ranges](#) objects).

`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)

H. Pages

### See Also

- The [Ranges](#) 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.
- [intra-range-methods](#) and [inter-range-methods](#) for intra and inter range transformations.
- [setops-methods](#) for set operations on [IRanges](#) objects.
- [findOverlaps](#) for finding overlapping ranges.

### Examples

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

```

compare(x0, y0) > 0 # equivalent to 'x0 > y0'

rangeComparisonCodeToLetter(-10:10)
rangeComparisonCodeToLetter(compare(x0, y0))

## Handling of zero-width ranges (a.k.a. empty ranges):
x1 <- IRanges(11:17, width=0)
x1
compare(x1, x1[4])
compare(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, compare()
## considers x1[2] and x1[6] to be *adjacent* to IRanges(12, 15), and
## thus returns codes -5 and 5:
compare(x1[2], IRanges(12, 15)) # -5
compare(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
## -----
order(x2)

```

```
sort(x2)
rank(x2, ties.method="first")
```

---

RangesList-class      *List of Ranges*

---

### Description

An extension of [List](#) that holds only [Ranges](#) objects. Useful for storing ranges over a set of spaces (e.g. chromosomes), each of which requires a separate Ranges object. As a Vector, RangesList may be annotated with its universe identifier (e.g. a genome) in which all of its spaces exist.

### Accessors

In the code snippets below, `x` is a RangesList 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(elementLengths(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 starts, `value` can be an integer vector of length(`sum(elementLengths(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 starts, `value` can be an integer vector of length(`sum(elementLengths(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.

These accessors are for the universe identifier:

`universe(x)`: gets the name of the universe as a single string, if one has been specified, NULL otherwise.

`universe(x) <- value`: sets the name of the universe to `value`, a single string or NULL.

### Constructor

`RangesList(..., universe = NULL)`: Each Ranges in `...` becomes an element in the new RangesList, in the same order. This is analogous to the [list](#) constructor, except every argument in `...` must be derived from Ranges. The universe is specified by the `universe` parameter, which should be a single string or NULL, to leave unspecified.

**Coercion**

In the code snippets below, `x` and `from` are a `RangesList` object.

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

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

```
as(from, "CompressedIRangesList"): Coerces from, to a CompressedIRangesList, requir-
  ing that all Ranges elements are coerced to internal IRanges elements. This is a convenient
  way to ensure that all Ranges have been imported into R (and that there is no unwanted over-
  head when accessing them).
```

```
as(from, "SimpleNormalIRangesList"): Coerces from, to a SimpleNormalIRangesList, re-
  quiring that all Ranges elements are coerced to internal NormalIRanges elements.
```

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

**Arithmetic Operations**

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

**Author(s)**

Michael Lawrence

**See Also**

[List](#), the parent of this class, for more functionality.

**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 <- RangesList(one = range1, two = range2)
length(named) # 2
start(named) # same as start(c(range1, range2))
names(named) # "one" and "two"
named[[1]] # range1
unnamed <- RangesList(range1, range2)
names(unnamed) # NULL

# edit the width of the ranges in the list
```

```

edited <- named
width(edited) <- rep(c(3,2), elementLengths(named))
edited

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

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

# set the universe
universe(named) <- "hg18"
universe(named)
RangesList(range1, range2, universe = "hg18")

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

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

range3 <- IRanges(start=c(-2, 6, 7), width=c(8, 0, 0)) # with empty ranges
collection <- IRangesList(one=range1, range2, range3)

isDisjoint(collection)

```

---

rdapply

*Applying over spaces*


---

### Description

The `rdapply` function applies a user function over the spaces of a [RangedData](#). The parameters to `rdapply` are collected into an instance of `RDApplyParams`, which is passed as the sole parameter to `rdapply`.

### Usage

```
rdapply(x, ...)
```

### Arguments

<code>x</code>	The <code>RDApplyParams</code> instance, see below for how to make one.
<code>...</code>	Additional arguments for methods

## Details

The `rdapply` function is an attempt to facilitate the common operation of performing the same operation over each space (e.g. chromosome) in a `RangedData`. To facilitate a wide array of such tasks, the function takes a large number of options. The `RDApplyParams` class is meant to help manage this complexity. In particular, it facilitates experimentation through its support for incremental changes to parameter settings.

There are two `RangedData` settings that are required: the user function object and the `RangedData` over which it is applied. The rest of the settings determine what is actually passed to the user function and how the return value is processed before relaying it to the user. The following is the description and rationale for each setting.

`rangedData` **REQUIRED.** The `RangedData` instance over which `applyFun` is applied.

`applyFun` **REQUIRED.** The user function to be applied to each space in the `RangedData`. The function must expect the `RangedData` as its first parameter and also accept the parameters specified in `applyParams`.

`applyParams` The list of additional parameters to pass to `applyFun`. Usually empty.

`filterRules` The instance of `FilterRules` that is used to filter each subset of the `RangedData` passed to the user function. This is an efficient and convenient means for performing the same operation over different subsets of the data on a space-by-space basis. In particular, this avoids the need to store subsets of the entire `RangedData`. A common workflow is to invoke `rdapply` with one set of active filters, enable different filters, reinvoke `rdapply`, and compare the results.

`simplify` A scalar logical (TRUE or FALSE) indicating whether the list to be returned from `rdapply` should be simplified as by `sapply`. Defaults to FALSE.

`reducerFun` The function that is used to convert the list that would otherwise be returned from `rdapply` to something more convenient. The function should take the list as its first parameter and also accept the parameters specified in `reducerParams`. This is an alternative to the primitive behavior of the `simplify` option (so `simplify` must be FALSE if this option is set). The aim is to orthogonalize the `applyFun` operation (i.e. the statistics) from the data structure of the result.

`reducerParams` A list of additional parameters to pass to `reducerFun`. Can only be set if `reducerFun` is set. Usually empty.

`iteratorFun` The function used for applying over the `RangedData`. By default, this is `lapply`, but it could also be a specialized function, like `mclapply`.

## Value

By default a list holding the result of each invocation of the user function, but see details.

## Constructing an `RDApplyParams` object

`RDApplyParams(rangedData, applyFun, applyParams, filterRules, simplify, reducerFun, reducerParams)`  
 Constructs a `RDApplyParams` object with each setting specified by the argument of the same name. See the Details section for more information.

## Accessors

In the following code snippets, `x` is an `RDApplyParams` object.

```
rangedData(x), rangedData(x) <- value: Get or set the RangedData instance over which
  applyFun is applied.
applyFun(x), applyFun(x) <- value: Get or set the user function to be applied to each space
  in the RangedData.
applyParams(x), applyParams(x) <- value: Get or set the list of additional parameters to
  pass to applyFun.
filterRules(x), filterRules(x) <- value: Get or set the instance of FilterRules that is
  used to filter each subset of the RangedData passed to the user function.
simplify(x), simplify(x) <- value: Get or set a scalar logical (TRUE or FALSE) indicating
  whether the list to be returned from rdapply should be simplified as by sapply.
reducerFun(x), reducerFun(x) <- value: Get or set the function that is used to convert the
  list that would otherwise be returned from rdapply to something more convenient.
reducerParams(x), reducerParams(x) <- value: Get or set a list of additional parameters
  to pass to reducerFun.
iteratorFun(x), iteratorFun(x) <- value: Get or set the function used for applying over the
  RangedData.
```

## Author(s)

Michael Lawrence

## See Also

[RangedData](#), [FilterRules](#)

## Examples

```
ranges <- IRanges(c(1,2,3),c(4,5,6))
score <- c(2L, 0L, 1L)
rd <- RangedData(ranges, score, space = c("chr1","chr2","chr1"))

## a single function
countrows <- function(rd) nrow(rd)
params <- RDApplyParams(rd, countrows)
rdapply(params) # list(chr1 = 2L, chr2 = 1L)

## with a parameter
params <- RDApplyParams(rd, function(rd, x) nrow(rd)*x, list(x = 2))
rdapply(params) # list(chr1 = 4L, chr2 = 2L)

## add a filter
cutoff <- 0
rules <- FilterRules(filter = score > cutoff)
params <- RDApplyParams(rd, countrows, filterRules = rules)
rdapply(params) # list(chr1 = 2L, chr2 = 0L)
```



```

rules <- FilterRules(list(fun = function(rd) rd[["score"]] < 2),
                     filter = score > cutoff)
params <- RDAApplyParams(rd, countrows, filterRules = rules)
rdapply(params) # list(chr1 = 1L, chr2 = 0L)
active(filterRules(params))["filter"] <- FALSE
rdapply(params) # list(chr1 = 1L, chr2 = 1L)

## simplify
params <- RDAApplyParams(rd, countrows, simplify = TRUE)
rdapply(params) # c(chr1 = 2L, chr2 = 1L)

## reducing
params <- RDAApplyParams(rd, countrows, reducerFun = unlist,
                         reducerParams = list(use.names = FALSE))
rdapply(params) ## c(2L, 1L)

```

---

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)

```

### Arguments

file	Either a character string naming a file or a connection open for reading.
seqname	The name of the sequence for which the mask must be extracted. If no sequence is specified (i.e. seqname="?") then an error is raised and the sequence names found in the file are displayed. If the file doesn't contain any information for the specified sequence, then a warning is issued and an empty mask of width mask.width is returned.
mask.width	The width of the mask to return i.e. the length of the sequence this mask will be put on. See ?`MaskCollection-class` for more information about the width of a <a href="#">MaskCollection</a> object.

gap.types	NULL or a character vector containing gap types. Use this argument to filter the assembly gaps that are to be extracted from the "agp" or "gap" file based on their type. Most common gap types are "contig", "clone", "centromere", "telomere", "heterochromatin", "short_arm" and "fragment". With gap.types=NULL, all the assembly gaps described in the file are extracted. With gap.types="?", an error is raised and the gap types found in the file for the specified sequence are displayed.
use.gap.types	Whether or not the gap types provided in the "agp" or "gap" file should be used to name the ranges constituting the returned mask. See <code>?IRanges-class</code> for more information about the names of an <code>IRanges</code> object.
use.IDs	Whether or not the repeat IDs provided in the RepeatMasker .out file should be used to name the ranges constituting the returned mask. See <code>?IRanges-class</code> for more information about the names of an <code>IRanges</code> object.

### See Also

[MaskCollection-class](#), [IRanges-class](#)

### Examples

```
## -----
## A. Extract a mask of assembly gaps ("AGAPS" mask) with read.agpMask()
## -----
## Note: The hs_b36v3_chrY.agp file was obtained by downloading,
## extracting and renaming the hs_ref_chrY.agp.gz file from
##
## ftp://ftp.ncbi.nih.gov/genomes/H_sapiens/Assembled_chromosomes/
##   hs_ref_chrY.agp.gz      5 KB  24/03/08  04:33:00 PM
##
## on May 9, 2008.

chrY_length <- 57772954
file1 <- system.file("extdata", "hs_b36v3_chrY.agp", package="IRanges")
mask1 <- read.agpMask(file1, seqname="chrY", mask.width=chrY_length,
                     use.gap.types=TRUE)

mask1
mask1[[1]]

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

`x` A vector-like or list-like object.  
`...` 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

[reverse-methods](#), [Views-class](#), [MaskCollection-class](#), [endoapply](#), [rev](#)

## 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, universe = NULL)`: 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 Ranges objects respectively that are meshed together for form the RleViewsList. The universe is specified by the `universe` parameter, which should be a single string or NULL, to leave unspecified.

`Views(subject, start=NULL, end=NULL, width=NULL, names=NULL)`: Same as `RleViewsList(rleList = subject,`

## Coercion

In the code snippets below, `from` is an RleViewsList object:

`as(from, "IRangesList")`: Creates a `CompressedIRangesList` object containing the view locations in `from`.

`as(from, "CompressedIRangesList")`: Creates a `CompressedIRangesList` object containing the view locations in `from`.

`as(from, "SimpleIRangesList")`: Creates a `SimpleIRangesList` 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 RangesList 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 IRanges and RangesList objects*

---

**Description**

Performs set operations on [IRanges](#) objects.

**Usage**

```
## Vector-wise operations:
## S4 method for signature 'Ranges,Ranges'
union(x, y,...)
## S4 method for signature 'Ranges,Ranges'
intersect(x, y,...)
## S4 method for signature 'Ranges,Ranges'
setdiff(x, y,...)

## Element-wise (aka "parallel") operations:
## S4 method for signature 'Ranges,Ranges'
punion(x, y, fill.gap=FALSE, ...)
## S4 method for signature 'Ranges,Ranges'
pintersect(x, y, resolve.empty=c("none", "max.start", "start.x"), ...)
## S4 method for signature 'Ranges,Ranges'
psetdiff(x, y, ...)
## S4 method for signature 'Ranges,Ranges'
pgap(x, y, ...)
```

**Arguments**

x, y	<a href="#">IRanges</a> objects.
fill.gap	Logical indicating whether or not to force a union by using the rule <code>start = min(start(x), start(y))</code> .
resolve.empty	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.)

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

## Details

The `union`, `intersect` and `setdiff` methods for [IRanges](#) objects return a "normal" [IRanges](#) object (of the same class as `x`) 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 [IRanges](#) objects are defined. For these methods, `x` and `y` must have the same length (i.e. same number of ranges) and they return an [IRanges](#) instance of the same length as `x` and `y` where each range represents the union/intersection/difference/gap of/between the corresponding ranges in `x` and `y`.

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 range 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.

## Author(s)

H. Pages 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.

[union](#),

[Ranges-class](#),

[intra-range-methods](#) for intra range transformations,

[inter-range-methods](#) for inter range transformations,

[IRanges-class](#), [IRanges-utils](#)

## 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 RangesList 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**

x	An <a href="#">Rle</a> or <a href="#">RleList</a> object, or any object coercible to an Rle object.
lower, upper	The lower and upper bounds for the slice.
includeLower, includeUpper	Logical indicating whether or not the specified boundary is open or closed.
rangesOnly	A logical indicating whether or not to drop the original data from the output.
...	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)
```

---

updateObject-methods    *Update an object of a class defined in the IRanges package to its current class definition*

---

## Description

The IRanges package provides an extensive collection of [updateObject](#) methods for updating almost any instance of a class defined in the package.

## Usage

```
## Showing usage of method defined for IntegerList objects only (usage
## is the same for all methods).
```

```
## S4 method for signature 'IntegerList'
updateObject(object, ..., verbose=FALSE)
```

## Arguments

object	Object to be updated. Many (but not all) IRanges classes are supported. If no specific method is available for the object, then the default method (defined in the BiocGenerics package) is used. See <a href="#">?updateObject</a> for a description of the default method.
..., verbose	See <a href="#">?updateObject</a> .

## Value

Returns a valid instance of object.

## Author(s)

The Bioconductor Dev Team

## See Also

[updateObject](#)

---

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)`: Extract the subsequence `window` from the Vector object using:

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

`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.

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

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

`rev(x)`: Return a new Vector object made of the original elements in the reverse order.

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

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

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

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

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

**Combining**

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

`mstack(..., .index.var = "name")`: A variant of `stack`, where the list is taken as the list of arguments in `...`, each of which should be a Vector or vector (mixing the two will not work).

**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.

`shiftApply(SHIFT, X, Y, FUN, ..., OFFSET = 0L, simplify = TRUE, verbose = FALSE)`: Let `i` be the indices in `SHIFT`, `X_i = window(X, 1 + OFFSET, length(X) - SHIFT[i])`, and `Y_i = window(Y, 1 + SHIFT[i], length(Y) - OFFSET)`. Calculates the set of `FUN(X_i, Y_i, ...)` values and return the results in a convenient form:

`SHIFT` A non-negative integer vector of shift values.

`X, Y` The Vector or R vector objects to shift.

`FUN` The function, found via `match.fun`, to be applied to each set of shifted vectors.

`...` Further arguments for `FUN`.

**OFFSET** A non-negative integer offset to maintain throughout the shift operations.

`simplify` A logical value specifying whether or not the result should be simplified to a vector or matrix if possible.

`verbose` A logical value specifying whether or not to print the `i` indices to track the iterations.

**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 a [Ranges](#) 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 [Ranges](#) 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))`).

**Combining**

`c(x, ..., ignore.mcols=FALSE)`: Combine 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)`.

`subviews(x, start=NA, end=NA, width=NA, use.names=TRUE)`: `start`, `end`, and `width` arguments must be vectors of integers, eventually with NAs, 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=width, gapwidth=gapwidth, from=from))`. See `?successiveIRanges` for a description of the `width`, `gapwidth` and `from` arguments.

**Author(s)**

H. Pages

**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	<i>List of Views</i>
-----------------	----------------------

---

**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 [Vector](#) subclass, ViewsList may be annotated with its universe identifier (e.g. a genome) in which all of its spaces exist.

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. Pages

**See Also**

[List-class](#), [RleViewsList-class](#),  
[findOverlaps](#).

**Examples**

```
showClass("ViewsList")
```

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