Package 'GenomicRanges'

February 20, 2026

Title Representation and manipulation of genomic intervals

Description The ability to efficiently represent and manipulate genomic
annotations and alignments is playing a central role when it comes
to analyzing high-throughput sequencing data (a.k.a. NGS data).
The GenomicRanges package defines general purpose containers for
storing and manipulating genomic intervals and variables defined along
a genome. More specialized containers for representing and manipulating
short alignments against a reference genome, or a matrix-like
summarization of an experiment, are defined in the GenomicAlignments
and SummarizedExperiment packages, respectively. Both packages build
on top of the GenomicRanges infrastructure.

biocViews Genetics, Infrastructure, DataRepresentation, Sequencing,
Annotation, GenomeAnnotation, Coverage

URL https://bioconductor.org/packages/GenomicRanges

BugReports https://github.com/Bioconductor/GenomicRanges/issues

Version 1.62.1

License Artistic-2.0

Encoding UTF-8

Depends R (>= 4.0.0), methods, stats4, BiocGenerics (>= 0.53.2),
S4Vectors (>= 0.45.2), IRanges (>= 2.43.6), Seqinfo (>= 0.99.3)

Imports utils, stats

LinkingTo S4Vectors, IRanges

Suggests GenomeInfoDb, Biobase, AnnotationDbi, annotate, Biostrings
(>= 2.77.2), SummarizedExperiment (>= 1.39.1), Rsamtools,
GenomicAlignments, BSgenome, GenomicFeatures, UCSC.utils,
txdbmaker, Gviz, VariantAnnotation, AnnotationHub, DESeq2,
DEXSeq, edgeR, KEGGgraph, RNAseqData.HNRNPC.bam.chr14,
pasillaBamSubset, KEGGREST, hgu95av2.db, hgu95av2probe,
BSgenome.Scerevisiae.UCSC.sacCer2, BSgenome.Hsapiens.UCSC.hg38,
BSgenome.Mmusculus.UCSC.mm10,
TxDb.Athaliana.BioMart.plantsmart22,
TxDb.Dmelanogaster.UCSC.dm3.ensGene,
TxDb.Hsapiens.UCSC.hg38.knownGene,
TxDb.Mmusculus.UCSC.mm10.knownGene, RUnit, digest, knitr,
rmarkdown, BiocStyle

VignetteBuilder knitr

Collate normarg-utils.R utils.R phicoef.R transcript-utils.R
   constraint.R strand-utils.R genomic-range-squeezers.R
   GenomicRanges-class.R GenomicRanges-comparison.R
   GRanges-class.R GPos-class.R GRangesFactor-class.R
   DelegatingGenomicRanges-class.R GNCList-class.R
   GenomicRangesList-class.R GRangesList-class.R
   makeGRangesFromDataFrame.R makeGRangesListFromDataFrame.R
   RangedData-methods.R findOverlaps-methods.R
   intra-range-methods.R inter-range-methods.R coverage-methods.R
   setops-methods.R subtract-methods.R nearest-methods.R
   absoluteRanges.R tileGenome.R tile-methods.R genomicvars.R
   zzz.R

git_url https://git.bioconductor.org/packages/GenomicRanges

git_branch RELEASE_3_22

git_last_commit ce11a45

git_last_commit_date 2025-12-08

Repository Bioconductor 3.22

Date/Publication 2026-02-19

Author Patrick Aboyoun [aut],
   Hervé Pagès [aut, cre],
   Michael Lawrence [aut],
   Sonali Arora [ctb],
   Martin Morgan [ctb],
   Kayla Morrell [ctb],
   Valerie Obenchain [ctb],
   Marcel Ramos [ctb],
   Lori Shepherd [ctb],
   Dan Tenenbaum [ctb],
   Daniel van Twisk [ctb]

Maintainer Hervé Pagès <hpages.on.github@gmail.com>

Contents

---

absoluteRanges   *Transform genomic ranges into "absolute" ranges*

Description

absoluteRanges transforms the genomic ranges in x into *absolute* ranges i.e. into ranges counted
from the beginning of the virtual sequence obtained by concatenating all the sequences in the un-
derlying genome (in the order reported by seqlevels(x)).

relativeRanges performs the reverse transformation.

NOTE: These functions only work on *small* genomes. See Details section below.

Usage

```
absoluteRanges(x)
relativeRanges(x, seqlengths)

## Related utility:
isSmallGenome(seqlengths)
```

Arguments

x   For absoluteRanges: a [GenomicRanges](#) object with ranges defined on a *small*
                 genome (see Details section below).
                 For relativeRanges: an [IntegerRanges](#) object.

seqlengths   An object holding sequence lengths. This can be a named integer (or numeric)
                 vector with no duplicated names as returned by [seqlengths](#)(), or any object
                 from which sequence lengths can be extracted with [seqlengths](#)().
                 For relativeRanges, seqlengths must describe a *small* genome (see Details
                 section below).

Details

Because absoluteRanges returns the *absolute* ranges in an [IRanges](#) object, and because an [IRanges](#)
object cannot hold ranges with an end > .Machine$integer.max (i.e. >= 2^31 on most plat-
forms), absoluteRanges cannot be used if the size of the underlying genome (i.e. the total length
of the sequences in it) is > .Machine$integer.max. Utility function isSmallGenome is pro-
vided as a mean for the user to check upfront whether the genome is *small* (i.e. its size is <=
.Machine$integer.max) or not, and thus compatible with absoluteRanges or not.

relativeRanges applies the same restriction by looking at the seqlengths argument.

Value

An [IRanges](#) object for `absoluteRanges`.

A [GRanges](#) object for `relativeRanges`.

`absoluteRanges` and `relativeRanges` both return an object that is *parallel* to the input object (i.e. same length and names).

`isSmallGenome` returns TRUE if the total length of the underlying sequences is <= `.Machine$integer.max` (e.g. Fly genome), FALSE if not (e.g. Human genome), or NA if it cannot be computed (because some sequence lengths are NA).

Author(s)

H. Pagès

See Also

- [GRanges](#) objects.
- [IntegerRanges](#) objects in the **IRanges** package.
- [Seqinfo](#) objects and the [`seqlengths`](#) getter in the **Seqinfo** package.
- [genomicvars](#) for manipulating genomic variables.
- The [`tileGenome`](#) function for putting tiles on a genome.

Examples

```
## ---------------------------------------------------------------------
## TOY EXAMPLE
## ---------------------------------------------------------------------

gr <- GRanges(Rle(c("chr2", "chr1", "chr3", "chr1"), 4:1),
              IRanges(1:10, width=5),
              seqinfo=Seqinfo(c("chr1", "chr2", "chr3"), c(100, 50, 20)))

ar <- absoluteRanges(gr)
ar

gr2 <- relativeRanges(ar, seqlengths(gr))
gr2

## Sanity check:
stopifnot(all(gr == gr2))

## ---------------------------------------------------------------------
## ON REAL DATA
## ---------------------------------------------------------------------

## With a "small" genome

library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
ex <- exons(txdb)
ex

isSmallGenome(ex)
```

```
## Note that because isSmallGenome() can return NA (see Value section
## above), its result should always be wrapped inside isTRUE() when
## used in an if statement:
if (isTRUE(isSmallGenome(ex))) {
    ar <- absoluteRanges(ex)
    ar

    ex2 <- relativeRanges(ar, seqlengths(ex))
    ex2  # original strand is not restored

    ## Sanity check:
    strand(ex2) <- strand(ex)  # restore the strand
    stopifnot(all(ex == ex2))
}

## With a "big" genome (but we can reduce it)

library(TxDb.Hsapiens.UCSC.hg38.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
ex <- exons(txdb)
isSmallGenome(ex)
## Not run:
    absoluteRanges(ex)  # error!

## End(Not run)

## However, if we are only interested in some chromosomes, we might
## still be able to use absoluteRanges():
seqlevels(ex, pruning.mode="coarse") <- paste0("chr", 1:10)
isSmallGenome(ex)  # TRUE!
ar <- absoluteRanges(ex)
ex2 <- relativeRanges(ar, seqlengths(ex))

## Sanity check:
strand(ex2) <- strand(ex)
stopifnot(all(ex == ex2))
```

Constraints   *Enforcing constraints thru Constraint objects*

Description

Attaching a Constraint object to an object of class A (the "constrained" object) is meant to be a convenient/reusable/extensible way to enforce a particular set of constraints on particular instances of A.

THIS IS AN EXPERIMENTAL FEATURE AND STILL VERY MUCH A WORK-IN-PROGRESS!

Details

For the developer, using constraints is an alternative to the more traditional approach that consists in creating subclasses of A and implementing specific validity methods for each of them. However, using constraints offers the following advantages over the traditional approach:

- The traditional approach often tends to lead to a proliferation of subclasses of A.

- Constraints can easily be re-used across different classes without the need to create any new class.

- Constraints can easily be combined.

All constraints are implemented as concrete subclasses of the Constraint class, which is a virtual class with no slots. Like the Constraint virtual class itself, concrete Constraint subclasses cannot have slots.

Here are the 7 steps typically involved in the process of putting constraints on objects of class A:

1. Add a slot named `constraint` to the definition of class A. The type of this slot must be Constraint_OR_NULL. Note that any subclass of A will inherit this slot.

2. Implements the `constraint()` accessors (getter and setter) for objects of class A. This is done by implementing the `"constraint"` method (getter) and replacement method (setter) for objects of class A (see the examples below). As a convenience to the user, the setter should also accept the name of a constraint (i.e. the name of its class) in addition to an instance of that class. Note that those accessors will work on instances of any subclass of A.

3. Modify the validity method for class A so it also returns the result of checkConstraint(x, constraint(x)) (append this result to the result returned by the validity method).

4. Testing: Create x, an instance of class A (or subclass of A). By default there is no constraint on it (`constraint(x)` is NULL). `validObject(x)` should return TRUE.

5. Create a new constraint (MyConstraint) by extending the Constraint class, typically with `setClass("MyConstraint", contains="Constraint")`. This constraint is not enforcing anything yet so you could put it on x (with `constraint(x) <- "MyConstraint"`), but not much would happen. In order to actually enforce something, a `"checkConstraint"` method for signature `c(x="A", constraint="MyConstraint")` needs to be implemented.

6. Implement a `"checkConstraint"` method for signature `c(x="A", constraint="MyConstraint")`. Like validity methods, `"checkConstraint"` methods must return NULL or a character vector describing the problems found. Like validity methods, they should never fail (i.e. they should never raise an error). Note that, alternatively, an existing constraint (e.g. SomeConstraint) can be adapted to work on objects of class A by just defining a new `"checkConstraint"` method for signature `c(x="A", constraint="SomeConstraint")`. Also, stricter constraints can be built on top of existing constraints by extending one or more existing constraints (see the examples below).

7. Testing: Try `constraint(x) <- "MyConstraint"`. It will or will not work depending on whether x satisfies the constraint or not. In the former case, trying to modify x in a way that breaks the constraint on it will also raise an error.

Note

WARNING: This note is not true anymore as the `constraint` slot has been temporarily removed from [GenomicRanges](#) objects (starting with package GenomicRanges >= 1.7.9).

Currently, only [GenomicRanges](#) objects can be constrained, that is:

- they have a `constraint` slot;

- they have `constraint()` accessors (getter and setter) for this slot;

- their validity method has been modified so it also returns the result of checkConstraint(x, constraint(x)).

More classes in the GenomicRanges and IRanges packages will support constraints in the near future.

Author(s)

H. Pagès

See Also

[setClass](), [is](), [setMethod](), [showMethods](), [validObject](), [GenomicRanges-class]()

Examples

```
## The examples below show how to define and set constraints on
## GenomicRanges objects. Note that this is how the constraint()
## setter is defined for GenomicRanges objects:
#setReplaceMethod("constraint", "GenomicRanges",
#    function(x, value)
#    {
#        if (isSingleString(value))
#            value <- new(value)
#        if (!is(value, "Constraint_OR_NULL"))
#            stop("the supplied 'constraint' must be a ",
#                "Constraint object, a single string, or NULL")
#        x@constraint <- value
#        validObject(x)
#        x
#    }
#)

#selectMethod("constraint", "GenomicRanges")  # the getter
#selectMethod("constraint<-", "GenomicRanges")  # the setter

## We'll use the GRanges instance 'gr' created in the GRanges examples
## to test our constraints:
example(GRanges, echo=FALSE)
gr
#constraint(gr)

## ----------------------------------------------------------------------
## EXAMPLE 1: The HasRangeTypeCol constraint.
## ----------------------------------------------------------------------
## The HasRangeTypeCol constraint checks that the constrained object
## has a unique "rangeType" metadata column and that this column
## is a 'factor' Rle with no NAs and with the following levels
## (in this order): gene, transcript, exon, cds, 5utr, 3utr.

setClass("HasRangeTypeCol", contains="Constraint")

## Like validity methods, "checkConstraint" methods must return NULL or
## a character vector describing the problems found. They should never
## fail i.e. they should never raise an error.
setMethod("checkConstraint", c("GenomicRanges", "HasRangeTypeCol"),
    function(x, constraint, verbose=FALSE)
    {
        x_mcols <- mcols(x)
        idx <- match("rangeType", colnames(x_mcols))
        if (length(idx) != 1L || is.na(idx)) {
            msg <- c("'mcols(x)' must have exactly 1 column ",
                    "named \"rangeType\"")
```

```
            return(paste(msg, collapse=""))
        }
        rangeType <- x_mcols[[idx]]
        .LEVELS <- c("gene", "transcript", "exon", "cds", "5utr", "3utr")
        if (!is(rangeType, "Rle") ||
            anyNA(runValue(rangeType)) ||
            !identical(levels(rangeType), .LEVELS))
        {
            msg <- c("'mcols(x)$rangeType' must be a ",
                     "'factor' Rle with no NAs and with levels: ",
                     paste(.LEVELS, collapse=", "))
            return(paste(msg, collapse=""))
        }
        NULL
    }
)

#\dontrun{
#constraint(gr) <- "HasRangeTypeCol"  # will fail
#}
checkConstraint(gr, new("HasRangeTypeCol"))  # with GenomicRanges >= 1.7.9

levels <- c("gene", "transcript", "exon", "cds", "5utr", "3utr")
rangeType <- Rle(factor(c("cds", "gene"), levels=levels), c(8, 2))
mcols(gr)$rangeType <- rangeType
#constraint(gr) <- "HasRangeTypeCol"  # OK
checkConstraint(gr, new("HasRangeTypeCol"))  # with GenomicRanges >= 1.7.9

## Use is() to check whether the object has a given constraint or not:
#is(constraint(gr), "HasRangeTypeCol")  # TRUE
#\dontrun{
#mcols(gr)$rangeType[3] <- NA  # will fail
#}
mcols(gr)$rangeType[3] <- NA
checkConstraint(gr, new("HasRangeTypeCol"))  # with GenomicRanges >= 1.7.9

## ----------------------------------------------------------------------
## EXAMPLE 2: The GeneRanges constraint.
## ----------------------------------------------------------------------
## The GeneRanges constraint is defined on top of the HasRangeTypeCol
## constraint. It checks that all the ranges in the object are of type
## "gene".

setClass("GeneRanges", contains="HasRangeTypeCol")

## The checkConstraint() generic will check the HasRangeTypeCol constraint
## first, and, only if it's statisfied, it will then check the GeneRanges
## constraint.
setMethod("checkConstraint", c("GenomicRanges", "GeneRanges"),
    function(x, constraint, verbose=FALSE)
    {
        rangeType <- mcols(x)$rangeType
        if (!all(rangeType == "gene")) {
            msg <- c("all elements in 'mcols(x)$rangeType' ",
                     "must be equal to \"gene\"")
            return(paste(msg, collapse=""))
        }
```

```
        NULL
    }
)

#\dontrun{
#constraint(gr) <- "GeneRanges"  # will fail
#}
checkConstraint(gr, new("GeneRanges"))  # with GenomicRanges >= 1.7.9

mcols(gr)$rangeType[] <- "gene"
## This replace the previous constraint (HasRangeTypeCol):
#constraint(gr) <- "GeneRanges"  # OK
checkConstraint(gr, new("GeneRanges"))  # with GenomicRanges >= 1.7.9

#is(constraint(gr), "GeneRanges")  # TRUE
## However, 'gr' still indirectly has the HasRangeTypeCol constraint
## (because the GeneRanges constraint extends the HasRangeTypeCol
## constraint):
#is(constraint(gr), "HasRangeTypeCol")  # TRUE
#\dontrun{
#mcols(gr)$rangeType[] <- "exon"  # will fail
#}
mcols(gr)$rangeType[] <- "exon"
checkConstraint(gr, new("GeneRanges"))  # with GenomicRanges >= 1.7.9

## ----------------------------------------------------------------------
## EXAMPLE 3: The HasGCCol constraint.
## ----------------------------------------------------------------------
## The HasGCCol constraint checks that the constrained object has a
## unique "GC" metadata column, that this column is of type numeric,
## with no NAs, and that all the values in that column are >= 0 and <= 1.

setClass("HasGCCol", contains="Constraint")

setMethod("checkConstraint", c("GenomicRanges", "HasGCCol"),
    function(x, constraint, verbose=FALSE)
    {
        x_mcols <- mcols(x)
        idx <- match("GC", colnames(x_mcols))
        if (length(idx) != 1L || is.na(idx)) {
            msg <- c("'mcols(x)' must have exactly ",
                     "one column named \"GC\"")
            return(paste(msg, collapse=""))
        }
        GC <- x_mcols[[idx]]
        if (!is.numeric(GC) || anyNA(GC) || any(GC < 0) || any(GC > 1)) {
            msg <- c("'mcols(x)$GC' must be a numeric vector ",
                     "with no NAs and with values between 0 and 1")
            return(paste(msg, collapse=""))
        }
        NULL
    }
)

## This replace the previous constraint (GeneRanges):
#constraint(gr) <- "HasGCCol"  # OK
checkConstraint(gr, new("HasGCCol"))  # with GenomicRanges >= 1.7.9
```

```
#is(constraint(gr), "HasGCCol")  # TRUE
#is(constraint(gr), "GeneRanges")  # FALSE
#is(constraint(gr), "HasRangeTypeCol")  # FALSE

## ----------------------------------------------------------------------
## EXAMPLE 4: The HighGCRanges constraint.
## ----------------------------------------------------------------------
## The HighGCRanges constraint is defined on top of the HasGCCol
## constraint. It checks that all the ranges in the object have a GC
## content >= 0.5.

setClass("HighGCRanges", contains="HasGCCol")

## The checkConstraint() generic will check the HasGCCol constraint
## first, and, if it's statisfied, it will then check the HighGCRanges
## constraint.
setMethod("checkConstraint", c("GenomicRanges", "HighGCRanges"),
    function(x, constraint, verbose=FALSE)
    {
        GC <- mcols(x)$GC
        if (!all(GC >= 0.5)) {
            msg <- c("all elements in 'mcols(x)$GC' ",
                     "must be >= 0.5")
            return(paste(msg, collapse=""))
        }
        NULL
    }
)

#\dontrun{
#constraint(gr) <- "HighGCRanges"  # will fail
#}
checkConstraint(gr, new("HighGCRanges"))  # with GenomicRanges >= 1.7.9
mcols(gr)$GC[6:10] <- 0.5
#constraint(gr) <- "HighGCRanges"  # OK
checkConstraint(gr, new("HighGCRanges"))  # with GenomicRanges >= 1.7.9

#is(constraint(gr), "HighGCRanges")  # TRUE
#is(constraint(gr), "HasGCCol")  # TRUE

## ----------------------------------------------------------------------
## EXAMPLE 5: The HighGCGeneRanges constraint.
## ----------------------------------------------------------------------
## The HighGCGeneRanges constraint is the combination (AND) of the
## GeneRanges and HighGCRanges constraints.

setClass("HighGCGeneRanges", contains=c("GeneRanges", "HighGCRanges"))

## No need to define a method for this constraint: the checkConstraint()
## generic will automatically check the GeneRanges and HighGCRanges
## constraints.

#constraint(gr) <- "HighGCGeneRanges"  # OK
checkConstraint(gr, new("HighGCGeneRanges"))  # with GenomicRanges >= 1.7.9

#is(constraint(gr), "HighGCGeneRanges")  # TRUE
```

```
#is(constraint(gr), "HighGCRanges")  # TRUE
#is(constraint(gr), "HasGCCol")  # TRUE
#is(constraint(gr), "GeneRanges")  # TRUE
#is(constraint(gr), "HasRangeTypeCol")  # TRUE

## See how all the individual constraints are checked (from less
## specific to more specific constraints):
#checkConstraint(gr, constraint(gr), verbose=TRUE)
checkConstraint(gr, new("HighGCGeneRanges"), verbose=TRUE)  # with
                                                        # GenomicRanges
                                                        # >= 1.7.9

## See all the "checkConstraint" methods:
showMethods("checkConstraint")
```

---

coverage-methods   *Coverage of a GRanges or GRangesList object*

Description

[coverage](#) methods for [GRanges](#) and [GRangesList](#) objects.

NOTE: The [coverage](#) generic function and methods for [IntegerRanges](#) and [IntegerRangesList](#) objects are defined and documented in the **IRanges** package. Methods for [GAlignments](#) and [GAlignmentPairs](#) objects are defined and documented in the **GenomicAlignments** package.

Usage

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

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

Arguments

x
: A [GenomicRanges](#) or [GRangesList](#) object.

shift, weight
: A numeric vector or a list-like object. If numeric, it must be parallel to x (recycled if necessary). If a list-like object, it must have 1 list element per seqlevel in x, and its names must be exactly seqlevels(x).

  Alternatively, each of these arguments can also be specified as a single string naming a metadata column in x (i.e. a column in mcols(x)) to be used as the shift (or weight) vector.

  See ?[coverage](#) in the **IRanges** package for more information about these arguments.

  Note that when x is a [StitchedGPos](#) object, each of these arguments can only be a single number or a named list-like object.

width   Either NULL (the default), or an integer vector. If NULL, it is replaced with
                   seqlengths(x). Otherwise, the vector must have the length and names of
                   seqlengths(x) and contain NAs or non-negative integers.

                   See ?coverage in the **IRanges** package for more information about this argu-
                   ment.

method   See ?coverage in the **IRanges** package for a description of this argument.

Details

When x is a GRangesList object, coverage(x, ...) is equivalent to coverage(unlist(x), ...).

Value

A named RleList object with one coverage vector per seqlevel in x.

Author(s)

H. Pagès and P. Aboyoun

See Also

   - coverage in the **IRanges** package.
   - coverage-methods in the **GenomicAlignments** package.
   - RleList objects in the **IRanges** package.
   - GRanges, GPos, and GRangesList objects.

Examples

```
## Coverage of a GRanges object:
gr <- GRanges(
        seqnames=Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
        ranges=IRanges(1:10, end=10),
        strand=Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2)),
        seqlengths=c(chr1=11, chr2=12, chr3=13))
cvg <- coverage(gr)
pcvg <- coverage(gr[strand(gr) == "+"])
mcvg <- coverage(gr[strand(gr) == "-"])
scvg <- coverage(gr[strand(gr) == "*"])
stopifnot(identical(pcvg + mcvg + scvg, cvg))

## Coverage of a GPos object:
pos_runs <- GRanges(c("chr1", "chr1", "chr2"),
                    IRanges(c(1, 5, 9), c(10, 8, 15)))
gpos <- GPos(pos_runs)
coverage(gpos)

## Coverage of a GRangesList object:
gr1 <- GRanges(seqnames="chr2",
               ranges=IRanges(3, 6),
               strand = "+")
gr2 <- GRanges(seqnames=c("chr1", "chr1"),
               ranges=IRanges(c(7,13), width=3),
               strand=c("+", "-"))
gr3 <- GRanges(seqnames=c("chr1", "chr2"),
```

```
                ranges=IRanges(c(1, 4), c(3, 9)),
                strand=c("-", "-"))
grl <- GRangesList(gr1=gr1, gr2=gr2, gr3=gr3)
stopifnot(identical(coverage(grl), coverage(unlist(grl))))
```

DelegatingGenomicRanges-class

DelegatingGenomicRanges objects

Description

The DelegatingGenomicRanges class implements the virtual GenomicRanges class using a delegate GenomicRanges. This enables developers to create GenomicRanges subclasses that add specialized columns or other structure, while remaining agnostic to how the data are actually stored. See the Extending GenomicRanges vignette.

Author(s)

M. Lawrence

findOverlaps-methods   *Finding overlapping genomic ranges*

Description

Various methods for finding/counting overlaps between objects containing genomic ranges. This man page describes the methods that operate on [GenomicRanges](#) and [GRangesList](#) objects.

NOTE: The [findOverlaps](#) generic function and methods for [IntegerRanges](#) and [IntegerRanges-List](#) objects are defined and documented in the **IRanges** package. The methods for [GAlignments](#), [GAlignmentPairs](#), and [GAlignmentsList](#) objects are defined and documented in the **GenomicAlignments** package.

[GenomicRanges](#) and [GRangesList](#) objects also support countOverlaps, overlapsAny, and subsetByOverlaps thanks to the default methods defined in the **IRanges** package and to the findOverlaps and countOverlaps methods defined in this package and documented below.

Usage

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

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

```
        ignore.strand=FALSE)

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

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

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

Arguments

query, subject   A [GRanges](#) or [GRangesList](#) object.

maxgap, minoverlap, type

> See ?[findOverlaps](#) in the **IRanges** package for a description of these arguments.
>
> IMPORTANT NOTE about how minoverlap is interpreted when query or subject is a [GRangesList](#) object: In this case, *the total number of overlapping positions* between a given element in query and a given element in subject is taken into account. For example, if query is a [GRanges](#) object, and subject a [GRanges-List](#) object, then findOverlaps() will report an overlap between query[i] (a single range) and subject[[j]] (multiple ranges) only if the total number of positions in subject[[j]] that overlap with query[i] is equal to minoverlap or greater. In other words, the full overlap across all the ranges in subject[[j]] is looked at. See the Examples section below for an example illustrating this.

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

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

Details

When the query and the subject are [GRanges](#) or [GRangesList](#) objects, findOverlaps uses the triplet (sequence name, range, strand) to determine which features (see paragraph below for the definition of feature) from the query overlap which features in the subject, where a strand value of "*" is treated as occurring on both the "+" and "-" strand. An overlap is recorded when a feature in the query and a feature in the subject have the same sequence name, have a compatible pairing of strands (e.g. "+"/"+", "-"/"-", "*"/"+", "*"/"-", etc.), and satisfy the interval overlap requirements.

In the context of findOverlaps, a feature is a collection of ranges that are treated as a single entity. For GRanges objects, a feature is a single range; while for GRangesList objects, a feature is a list element containing a set of ranges. In the results, the features are referred to by number, which run from 1 to length(query)/length(subject).

For type="equal" with GRangesList objects, query[[i]] matches subject[[j]] iff for each range in query[[i]] there is an identical range in subject[[j]], and vice versa.

Value

For findOverlaps: either a Hits object when select="all" or an integer vector otherwise.

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

Author(s)

P. Aboyoun, S. Falcon, M. Lawrence, and H. Pagès

See Also

- The Hits class in the **S4Vectors** package for representing a set of hits between 2 vector-like objects.
- The findOverlaps generic function defined in the **IRanges** package.
- The GNCList constructor and class for preprocessing and representing a GenomicRanges or object as a data structure based on Nested Containment Lists.
- The GRanges and GRangesList classes.

Examples

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

## GRanges object:
gr <- GRanges(
        seqnames=Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
        ranges=IRanges(1:10, width=10:1, names=head(letters,10)),
        strand=Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2)),
        score=1:10,
        GC=seq(1, 0, length=10)
      )
gr

## GRangesList object:
gr1 <- GRanges(seqnames="chr2", ranges=IRanges(4:3, 6),
               strand="+", score=5:4, GC=0.45)
gr2 <- GRanges(seqnames=c("chr1", "chr1"),
               ranges=IRanges(c(7,13), width=3),
               strand=c("+", "-"), score=3:4, GC=c(0.3, 0.5))
gr3 <- GRanges(seqnames=c("chr1", "chr2"),
               ranges=IRanges(c(1, 4), c(3, 9)),
               strand=c("-", "-"), score=c(6L, 2L), GC=c(0.4, 0.1))
grl <- GRangesList("gr1"=gr1, "gr2"=gr2, "gr3"=gr3)

## Overlapping two GRanges objects:
table(!is.na(findOverlaps(gr, gr1, select="arbitrary")))
```

```
countOverlaps(gr, gr1)
findOverlaps(gr, gr1)
subsetByOverlaps(gr, gr1)

countOverlaps(gr, gr1, type="start")
findOverlaps(gr, gr1, type="start")
subsetByOverlaps(gr, gr1, type="start")

findOverlaps(gr, gr1, select="first")
findOverlaps(gr, gr1, select="last")

findOverlaps(gr1, gr)
findOverlaps(gr1, gr, type="start")
findOverlaps(gr1, gr, type="within")
findOverlaps(gr1, gr, type="equal")

## ---------------------------------------------------------------------
## MORE EXAMPLES
## ---------------------------------------------------------------------

table(!is.na(findOverlaps(gr, gr1, select="arbitrary")))
countOverlaps(gr, gr1)
findOverlaps(gr, gr1)
subsetByOverlaps(gr, gr1)

## Overlaps between a GRanges and a GRangesList object:

table(!is.na(findOverlaps(grl, gr, select="first")))
countOverlaps(grl, gr)
findOverlaps(grl, gr)
subsetByOverlaps(grl, gr)
countOverlaps(grl, gr, type="start")
findOverlaps(grl, gr, type="start")
subsetByOverlaps(grl, gr, type="start")
findOverlaps(grl, gr, select="first")

table(!is.na(findOverlaps(grl, gr1, select="first")))
countOverlaps(grl, gr1)
findOverlaps(grl, gr1)
subsetByOverlaps(grl, gr1)
countOverlaps(grl, gr1, type="start")
findOverlaps(grl, gr1, type="start")
subsetByOverlaps(grl, gr1, type="start")
findOverlaps(grl, gr1, select="first")

## Overlaps between two GRangesList objects:
countOverlaps(grl, rev(grl))
findOverlaps(grl, rev(grl))
subsetByOverlaps(grl, rev(grl))

## ---------------------------------------------------------------------
## INTERPRETATION OF 'minoverlap' WHEN 'query' OR 'subject' IS A
## GRangesList OBJECT
## ---------------------------------------------------------------------
gr1 <- GRanges("chr5:1-26")
gr2 <- GRanges("chr5:31-40")
gr3 <- c(GRanges("chr5:11-20"), gr2)
```

```
grl123 <- GRangesList(gr1, gr2, gr3)
grl123

query <- GRanges("chr5:17-35")

findOverlaps(query, grl123[[1]], minoverlap=8)  # 1 hit
findOverlaps(query, grl123[[2]], minoverlap=8)  # no hit
findOverlaps(query, grl123[[3]], minoverlap=8)  # no hit

## Using GRangesList object 'grl123' as the subject:
findOverlaps(query, grl123, minoverlap=8)

## As we can see, a hit is reported with the 3rd element in the subject.
## That's because the total number of positions in this overlap is 9:
## - positions 17 to 20 in the first range of grl123[[3]], so 4 positions
## - positions 31 to 35 in its second range, so 5 positions

## Sanity checks:
hits <- findOverlaps(query, grl123[[1]], minoverlap=8)
stopifnot(length(hits) == 1)
hits <- findOverlaps(query, grl123[[2]], minoverlap=8)
stopifnot(length(hits) == 0)
hits <- findOverlaps(query, grl123[[3]], minoverlap=8)
stopifnot(length(hits) == 0)
hits <- findOverlaps(query, grl123, minoverlap=8)
stopifnot(identical(subjectHits(hits), c(1L, 3L)))
hits <- findOverlaps(query, grl123, minoverlap=9)
stopifnot(identical(subjectHits(hits), c(1L, 3L)))
hits <- findOverlaps(query, grl123, minoverlap=10)
stopifnot(identical(subjectHits(hits), 1L))
hits <- findOverlaps(query, grl123, minoverlap=11)
stopifnot(length(hits) == 0)
```

---

genomic-range-squeezers

Squeeze the genomic ranges out of a range-based object

Description

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

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

Usage

```
granges(x, use.names=TRUE, use.mcols=FALSE, ...)
grglist(x, use.names=TRUE, use.mcols=FALSE, ...)
```

Arguments

x   An object containing genomic ranges e.g. a [GenomicRanges](#), [RangedSummarizedExperiment](#), [GAlignments](#), [GAlignmentPairs](#), or [GAlignmentsList](#) object, or a [Pairs](#) object containing genomic ranges.

```
use.names, use.mcols, ...
```
                    See ranges in the **IRanges** package for a description of these arguments.

Details

See ranges in the **IRanges** package for some details.

For some objects (e.g. GAlignments and GAlignmentPairs objects defined in the **GenomicAlign-ments** package), as(x, "GRanges") and as(x, "GRangesList"), are equivalent to granges(x, use.names=TRUE, use.mcols=TRUE) and grglist(x, use.names=TRUE, use.mcols=TRUE), re-spectively.

Value

A GRanges object for granges.

A GRangesList object for grglist.

If x is a vector-like object (e.g. GAlignments), the returned object is expected to be *parallel* to x, that is, the i-th element in the output corresponds to the i-th element in the input.

If use.names is TRUE, then the names on x (if any) are propagated to the returned object. If use.mcols is TRUE, then the metadata columns on x (if any) are propagated to the returned object.

Author(s)

H. Pagès

See Also

- GRanges and GRangesList objects.
- RangedSummarizedExperiment objects in the **SummarizedExperiment** packages.
- GAlignments, GAlignmentPairs, and GAlignmentsList objects in the **GenomicAlignments** package.

Examples

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

GenomicRanges-comparison
                    Comparing and ordering genomic ranges

Description

Methods for comparing and/or ordering GenomicRanges objects.

Usage

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

## S4 method for signature 'GenomicRanges'
duplicated(x, incomparables=FALSE, fromLast=FALSE,
           nmax=NA, method=c("auto", "quick", "hash"))

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

## S4 method for signature 'GenomicRanges,GenomicRanges'
match(x, table, nomatch=NA_integer_, incomparables=NULL,
      method=c("auto", "quick", "hash"), ignore.strand=FALSE)

## S4 method for signature 'GenomicRanges'
selfmatch(x, method=c("auto", "quick", "hash"), ignore.strand=FALSE)

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

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

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

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

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

## Generalized parallel comparison of 2 GenomicRanges objects
## ----------------------------------------------------------

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

Arguments

x, table, y   [GenomicRanges](#) objects.

incomparables   Not supported.

fromLast, method, nomatch, nmax, na.rm, strictly, na.last, decreasing
                  See ?`IPosRanges-comparison` in the **IRanges** package for a description of
                  these arguments.

ignore.strand   Whether or not the strand should be ignored when comparing 2 genomic ranges.

...	One or more GenomicRanges objects. The GenomicRanges objects after the first one are used to break ties.
ties.method	A character string specifying how ties are treated. Only `"first"` is supported for now.
by	An optional formula that is resolved against `as.env(x)`; the resulting variables are passed to `order` to generate the ordering permutation.

Details

Two elements of a GenomicRanges derivative (i.e. two genomic ranges) are considered equal iff they are on the same underlying sequence and strand, and share the same start and width. `duplicated()` and `unique()` on a GenomicRanges derivative are conforming to this.

The "natural order" for the elements of a GenomicRanges derivative is to order them (a) first by sequence level, (b) then by strand, (c) then by start, (d) and finally by width. This way, the space of genomic ranges is totally ordered. Note that, because we already do (c) and (d) for regular ranges (see ?`IPosRanges-comparison`), genomic ranges that belong to the same underlying sequence and strand are ordered like regular ranges.

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

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

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

Author(s)

H. Pagès, `is.unsorted` contributed by Pete Hickey

See Also

- The GenomicRanges class.
- IPosRanges-comparison in the **IRanges** package for comparing and ordering genomic ranges.
- findOverlaps-methods for finding overlapping genomic ranges.
- intra-range-methods and inter-range-methods for intra range and inter range transformations of a GRanges object.
- setops-methods for set operations on GenomicRanges objects.

Examples

```
gr0 <- GRanges(
    Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
    IRanges(c(1:9,7L), end=10),
    strand=Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2)),
    seqlengths=c(chr1=11, chr2=12, chr3=13)
)
gr <- c(gr0, gr0[7:3])
names(gr) <- LETTERS[seq_along(gr)]

## ---------------------------------------------------------------------
## A. ELEMENT-WISE (AKA "PARALLEL") COMPARISON OF 2 GenomicRanges OBJECTS
## ---------------------------------------------------------------------
```

```
gr[2] == gr[2]  # TRUE
gr[2] == gr[5]  # FALSE
gr == gr[4]
gr >= gr[3]

## ---------------------------------------------------------------------
## B. match(), selfmatch(), %in%, duplicated(), unique()
## ---------------------------------------------------------------------
table <- gr[1:7]
match(gr, table)
match(gr, table, ignore.strand=TRUE)

gr %in% table

duplicated(gr)
unique(gr)

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

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

gr_levels <- unique(gr)
countMatches(gr_levels, gr)

## ---------------------------------------------------------------------
## D. order() AND RELATED METHODS
## ---------------------------------------------------------------------
is.unsorted(gr)
order(gr)
sort(gr)
is.unsorted(sort(gr))

is.unsorted(gr, ignore.strand=TRUE)
gr2 <- sort(gr, ignore.strand=TRUE)
is.unsorted(gr2)  # TRUE
is.unsorted(gr2, ignore.strand=TRUE)  # FALSE

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

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

## TODO: Broken. Please fix!
#sort(gr, by = ~ score)

rank(gr, ties.method="first")
rank(gr, ties.method="first", ignore.strand=TRUE)

## ---------------------------------------------------------------------
## E. GENERALIZED ELEMENT-WISE COMPARISON OF 2 GenomicRanges OBJECTS
## ---------------------------------------------------------------------
gr3 <- GRanges(c(rep("chr1", 12), "chr2"), IRanges(c(1:11, 6:7), width=3))
```

```
strand(gr3)[12] <- "+"
gr4 <- GRanges("chr1", IRanges(5, 9))

pcompare(gr3, gr4)
rangeComparisonCodeToLetter(pcompare(gr3, gr4))
```

GenomicRangesList-class
                            GenomicRangesList objects

Description

The GenomicRangesList *virtual* class is a general container for storing a list of GenomicRanges objects.

Most users are probably more interested in the GRangesList container, a GenomicRangesList derivative for storing a list of GRanges objects.

Details

The place of GenomicRangesList in the *Vector class hierarchy*:

```
                                Vector
                                  ^
                                  |
                                 List
                                  ^
                                  |
                              RangesList
                             ^         ^
                            /           \
                           /             \
                          /               \
                         /                 \
                        /                   \
                       /                     \
            IntegerRangesList          GenomicRangesList
                   ^                           ^
                   |                           |
              IRangesList                  GRangesList
              ^       ^                    ^       ^
             /         \                  /         \
            /           \                /           \
           /             \              /             \
    SimpleIRangesList     \     SimpleGRangesList      \
             CompressedIRangesList        CompressedGRangesList
```
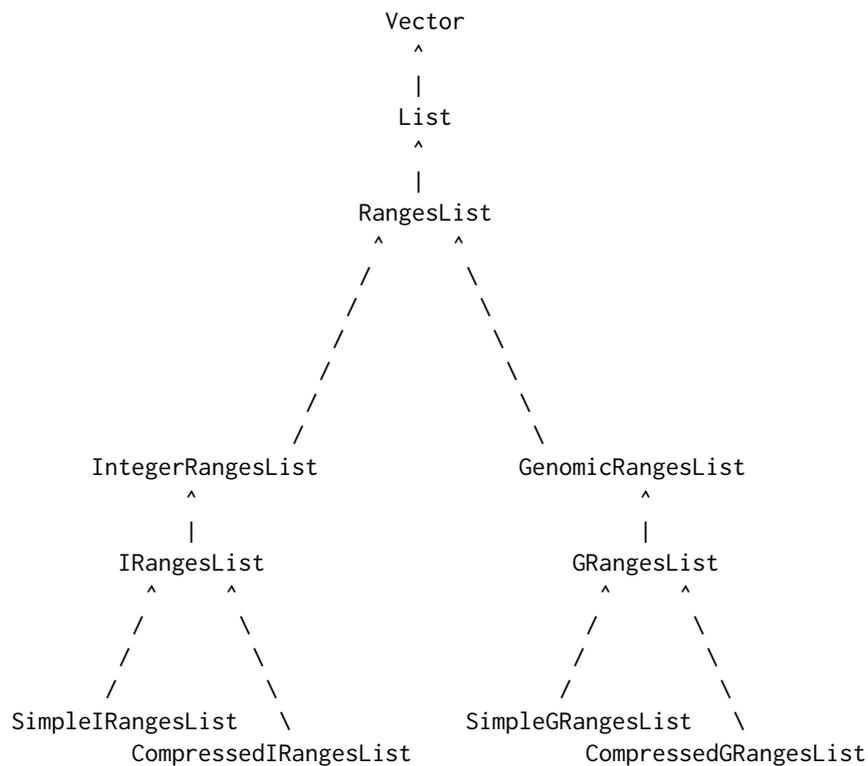
Note that the *Vector class hierarchy* has many more classes. In particular Vector, List, IRangesList, and IntegerRangesList have other subclasses not shown here.

Author(s)

H. Pagès and M. Lawrence

See Also

- GRangesList objects.

- GenomicRanges and GRanges objects.

---

genomicvars   *Manipulating genomic variables*

Description

A *genomic variable* is a variable defined along a genome. Here are 2 ways a genomic variable is generally represented in Bioconductor:

1. as a named RleList object with one list element per chromosome;

2. as a metadata column on a *disjoint* GRanges object.

This man page documents tools for switching from one form to the other.

Usage

```
bindAsGRanges(...)
mcolAsRleList(x, varname)
binnedAverage(bins, numvar, varname, na.rm=FALSE)
```

Arguments

`...`	One or more genomic variables in the form of named RleList objects.
`x`	A *disjoint* GRanges object with metadata columns on it. A GRanges object is said to be *disjoint* if it contains ranges that do not overlap with each other. This can be tested with isDisjoint. See ?`isDisjoint,GenomicRanges-method` for more information about the isDisjoint method for GRanges objects.
`varname`	The name of the genomic variable.
	For mcolAsRleList this must be the name of the metadata column on x to be turned into an RleList object.
	For binnedAverage this will be the name of the metadata column that contains the binned average in the returned object.
`bins`	A GRanges object representing the genomic bins. Typically obtained by calling tileGenome with cut.last.tile.in.chrom=TRUE.
`numvar`	A named RleList object representing a numerical variable defined along the genome covered by bins (which is the genome described by seqinfo(bins)).
`na.rm`	A logical value indicating whether NA values should be stripped before the average is computed.

Details

bindAsGRanges allows to switch the representation of one or more genomic variables from the *named RleList* form to the *metadata column on a disjoint GRanges object* form by binding the supplied named RleList objects together and putting them on the same GRanges object. This transformation is lossless.

mcolAsRleList performs the opposite transformation and is also lossless (however the circularity flags and genome information in seqinfo(x) won't propagate). It works for any metadata column on x that can be put in Rle form i.e. that is an atomic vector or a factor.

binnedAverage computes the binned average of a numerical variable defined along a genome.

Value

For bindAsGRanges: a GRanges object with 1 metadata column per supplied genomic variable.

For mcolAsRleList: a named RleList object with 1 list element per seqlevel in x.

For binnedAverage: input GRanges object bins with an additional metadata column named varname containing the binned average.

Author(s)

H. Pagès

See Also

- RleList objects in the **IRanges** package.
- coverage,GenomicRanges-method for computing the coverage of a GRanges object.
- The tileGenome function for putting tiles on a genome.
- GRanges objects and isDisjoint,GenomicRanges-method for the isDisjoint method for GenomicRanges objects.

Examples

```
## -----------------------------------------------------------------------
## A. TWO WAYS TO REPRESENT A GENOMIC VARIABLE
## -----------------------------------------------------------------

## 1) As a named RleList object
## ---------------------------
## Let's create a genomic variable in the "named RleList" form:
library(BSgenome.Scerevisiae.UCSC.sacCer2)
set.seed(55)
my_var <- RleList(
    lapply(seqlengths(Scerevisiae),
        function(seqlen) {
            tmp <- sample(50L, seqlen, replace=TRUE)
            Rle(cumsum(tmp - rev(tmp)))
        }
    ),
    compress=FALSE)
my_var

## 2) As a metadata column on a disjoint GRanges object
## ----------------------------------------------------
```

```
gr1 <- bindAsGRanges(my_var=my_var)
gr1

gr2 <- GRanges(c("chrI:1-150",
                 "chrI:211-285",
                 "chrI:291-377",
                 "chrV:51-60"),
               score=c(0.4, 8, -10, 2.2),
               id=letters[1:4],
               seqinfo=seqinfo(Scerevisiae))
gr2

## Going back to the "named RleList" form:
mcolAsRleList(gr1, "my_var")
score <- mcolAsRleList(gr2, "score")
score
id <- mcolAsRleList(gr2, "id")
id
bindAsGRanges(score=score, id=id)

## Bind 'my_var', 'score', and 'id' together:
gr3 <- bindAsGRanges(my_var=my_var, score=score, id=id)

## Sanity checks:
stopifnot(identical(my_var, mcolAsRleList(gr3, "my_var")))
stopifnot(identical(score, mcolAsRleList(gr3, "score")))
stopifnot(identical(id, mcolAsRleList(gr3, "id")))
gr2b <- bindAsGRanges(score=score, id=id)
seqinfo(gr2b) <- seqinfo(gr2)
stopifnot(identical(gr2, gr2b))

## ----------------------------------------------------------------------
## B. BIND TOGETHER THE COVERAGES OF SEVERAL BAM FILES
## ----------------------------------------------------------------------

library(pasillaBamSubset)
library(GenomicAlignments)
untreated1_cvg <- coverage(BamFile(untreated1_chr4()))
untreated3_cvg <- coverage(BamFile(untreated3_chr4()))
all_cvg <- bindAsGRanges(untreated1=untreated1_cvg,
                         untreated3=untreated3_cvg)

## Keep regions with coverage:
all_cvg[with(mcols(all_cvg), untreated1 + untreated3 >= 1)]

## Plot the coverage profiles with the Gviz package:
library(Gviz)
plotNumvars <- function(numvars, region, name="numvars", ...)
{
    stopifnot(is(numvars, "GRanges"))
    stopifnot(is(region, "GRanges"), length(region) == 1L)
    gtrack <- GenomeAxisTrack()
    dtrack <- DataTrack(numvars,
                        chromosome=as.character(seqnames(region)),
                        name=name,
                        groups=colnames(mcols(numvars)), type="l", ...)
    plotTracks(list(gtrack, dtrack), from=start(region), to=end(region))
```

```
}
plotNumvars(all_cvg, GRanges("chr4:1-25000"),
            "coverage", col=c("red", "blue"))
plotNumvars(all_cvg, GRanges("chr4:1.03e6-1.08e6"),
            "coverage", col=c("red", "blue"))

## Sanity checks:
stopifnot(identical(untreated1_cvg, mcolAsRleList(all_cvg, "untreated1")))
stopifnot(identical(untreated3_cvg, mcolAsRleList(all_cvg, "untreated3")))

## ---------------------------------------------------------------------
## C. COMPUTE THE BINNED AVERAGE OF A NUMERICAL VARIABLE DEFINED ALONG A
##    GENOME
## ---------------------------------------------------------------------

## In some applications (e.g. visualization), there is the need to compute
## the average of a genomic variable for a set of predefined fixed-width
## regions (sometimes called "bins").
## Let's use tileGenome() to create such a set of bins:
bins1 <- tileGenome(seqinfo(Scerevisiae), tilewidth=100,
                    cut.last.tile.in.chrom=TRUE)

## Compute the binned average for 'my_var' and 'score':
bins1 <- binnedAverage(bins1, my_var, "binned_var")
bins1
bins1 <- binnedAverage(bins1, score, "binned_score")
bins1

## Binned average in "named RleList" form:
binned_var1 <- mcolAsRleList(bins1, "binned_var")
binned_var1
stopifnot(all.equal(mean(my_var), mean(binned_var1)))  # sanity check

mcolAsRleList(bins1, "binned_score")

## With bigger bins:
bins2 <- tileGenome(seqinfo(Scerevisiae), tilewidth=50000,
                    cut.last.tile.in.chrom=TRUE)
bins2 <- binnedAverage(bins2, my_var, "binned_var")
bins2 <- binnedAverage(bins2, score, "binned_score")
bins2

binned_var2 <- mcolAsRleList(bins2, "binned_var")
binned_var2
stopifnot(all.equal(mean(my_var), mean(binned_var2)))  # sanity check

mcolAsRleList(bins2, "binned_score")

## Not surprisingly, the "binned" variables are much more compact in
## memory than the original variables (they contain much less runs):
object.size(my_var)
object.size(binned_var1)
object.size(binned_var2)

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

```
bins3 <- tileGenome(c(chr1=10, chr2=8), tilewidth=5,
                    cut.last.tile.in.chrom=TRUE)
my_var3 <- RleList(chr1=Rle(c(1:3, NA, 5:7)), chr2=Rle(c(-3, NA, -3, NaN)))
bins3 <- binnedAverage(bins3, my_var3, "binned_var3", na.rm=TRUE)
binned_var3 <- mcols(bins3)$binned_var3
stopifnot(
  identical(mean(my_var3$chr1[1:5], na.rm=TRUE),
            binned_var3[1]),
  identical(mean(c(my_var3$chr1, 0, 0, 0)[6:10], na.rm=TRUE),
            binned_var3[2]),
  #identical(mean(c(my_var3$chr2, 0), na.rm=TRUE),
  #          binned_var3[3]),
  identical(0, binned_var3[4])
)
```

GNCList-class   *GNCList objects*

Description

The GNCList class is a container for storing the Nested Containment List representation of a vector of genomic ranges (typically represented as a GRanges object). To preprocess a GRanges object, simply call the GNCList constructor function on it. The resulting GNCList object can then be used for efficient overlap-based operations on the genomic ranges.

Usage

```
GNCList(x)
```

Arguments

x   The GRanges (or more generally GenomicRanges) object to preprocess.

Details

The **IRanges** package also defines the NCList and NCLists constructors and classes for preprocessing and representing a IntegerRanges or IntegerRangesList object as a data structure based on Nested Containment Lists.

Note that GNCList objects (introduced in BioC 3.1) are replacements for GIntervalTree objects (BioC < 3.1).

See ?NCList in the **IRanges** package for some important differences between the new algorithm based on Nested Containment Lists and the old algorithm based on interval trees. In particular, the new algorithm supports preprocessing of a GenomicRanges object with ranges defined on circular sequences (e.g. on the mitochnodrial chromosome). See below for some examples.

Value

A GNCList object.

Author(s)

H. Pagès

References

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

See Also

- The NCList and NCLists constructors and classs defined in the **IRanges** package.
- findOverlaps for finding/counting interval overlaps between two *range-based* objects.
- GRanges objects.

Examples

```
## The examples below are for illustration purpose only and do 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).

## ---------------------------------------------------------------------
## PREPROCESS QUERY OR SUBJECT
## ---------------------------------------------------------------------

query <- GRanges(Rle(c("chrM", "chr1", "chrM", "chr1"), 4:1),
                 IRanges(1:10, width=5), strand=rep(c("+", "-"), 5))
subject <- GRanges(Rle(c("chr1", "chr2", "chrM"), 3:1),
                   IRanges(6:1, width=5), strand="+")

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

ppsubject <- GNCList(subject)
hits1a <- findOverlaps(query, ppsubject)
hits1a
hits1b <- findOverlaps(query, ppsubject, ignore.strand=TRUE)
hits1b

ppquery <- GNCList(query)
hits2a <- findOverlaps(ppquery, subject)
hits2a
hits2b <- findOverlaps(ppquery, subject, ignore.strand=TRUE)
hits2b

## Note that 'hits1a' and 'hits2a' contain the same hits but not
## necessarily in the same order.
stopifnot(identical(sort(hits1a), sort(hits2a)))
## Same for 'hits1b' and 'hits2b'.
stopifnot(identical(sort(hits1b), sort(hits2b)))

## ---------------------------------------------------------------------
## WITH CIRCULAR SEQUENCES
## ---------------------------------------------------------------------

seqinfo <- Seqinfo(c("chr1", "chr2", "chrM"),
                   seqlengths=c(100, 50, 10),
```

```
                          isCircular=c(FALSE, FALSE, TRUE))
seqinfo(query) <- seqinfo[seqlevels(query)]
seqinfo(subject) <- seqinfo[seqlevels(subject)]

ppsubject <- GNCList(subject)
hits3 <- findOverlaps(query, ppsubject)
hits3

## Circularity introduces more hits:

stopifnot(all(hits1a %in% hits3))
new_hits <- setdiff(hits3, hits1a)
new_hits  # 1 new hit
query[queryHits(new_hits)]
subject[subjectHits(new_hits)]  # positions 11:13 on chrM are the same
                                # as positions 1:3

## Sanity checks:
stopifnot(identical(new_hits, Hits(9, 6, 10, 6, sort.by.query=TRUE)))
ppquery <- GNCList(query)
hits4 <- findOverlaps(ppquery, subject)
stopifnot(identical(sort(hits3), sort(hits4)))
```

GPos-class   *Memory-efficient representation of genomic positions*

Description

The GPos class is a container for storing a set of *genomic positions* (a.k.a. *genomic loci*). It exists in 2 flavors: UnstitchedGPos and StitchedGPos. Each flavor uses a particular internal representation:

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

Because genomic positions can be seen as genomic ranges of width 1, the GPos class extends the GenomicRanges virtual class (via the GRanges class).

Usage

```
## Constructor function
GPos(seqnames=NULL, pos=NULL, strand=NULL,
     ..., seqinfo=NULL, seqlengths=NULL, stitch=NA)
```

Arguments

seqnames, strand, ..., seqinfo, seqlengths
               See documentation of the GRanges() constructor function for a description of these arguments.

pos   NULL, or an integer or numeric vector, or an [IRanges] or [IPos] object (or other
                       [IntegerRanges] derivative). If not NULL, GPos() will try to turn it into an [IPos]
                       derivative with IPos(pos, stitch=stitch).

                       When pos is an [IRanges] object (or other [IntegerRanges] derivative), each range
                       in it is interpreted as a run of consecutive positions.

stitch   TRUE, FALSE, or NA (the default).

                       Controls which internal representation should be used: StitchedGPos (when
                       stitch is TRUE) or UnstitchedGPos (when stitch is FALSE).

                       When stitch is NA (the default), which internal representation will be used de-
                       pends on the flavour of the [IPos] derivative returned by IPos(pos): UnstitchedG-
                       Pos if IPos(pos) returns an [UnstitchedIPos] instance, and StitchedGPos if it
                       returns a [StitchedIPos] instance.

Details

Even though a [GRanges] object can be used for storing genomic positions, using a GPos object is
more efficient. In particular the memory footprint of an UnstitchedGPos object is typically about
half that of a [GRanges] object.

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

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

Value

An UnstitchedGPos or StitchedGPos object.

Accessors

Getters: GPos objects support the same set of getters as other [GenomicRanges] derivatives
(i.e. seqnames(), ranges(), start(), end(), strand(), mcols(), seqinfo(), etc...), plus the
pos() getter which is equivalent to start() or end(). See ?[GenomicRanges] for the list of getters
supported by [GenomicRanges] derivatives.

Note that ranges() returns an [IPos] derivative instead of the [IRanges] object that one gets with
other [GenomicRanges] derivatives. To get an [IRanges] object, you need to call ranges() again on
this [IPos] derivative i.e. do ranges(ranges(x)) on GPos object x.

Setters: Like [GRanges] objects, GPos derivatives support the following setters:

- The seqnames() and strand() setters.
- The names(), mcols() and metadata() setters.
- The family of setters that operate on the seqinfo component of an object: [seqlevels](),
  [seqlevelsStyle](), [seqlengths](), [isCircular](), [genome](), and [seqinfo](). These set-
  ters are defined and documented in the **Seqinfo** and **GenomeInfoDb** packages.

However, there is no pos() setter for GPos derivatives at the moment (although one might be
added in the future).

Coercion

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

From GenomicRanges to UnstitchedGPos, StitchedGPos, or GPos: A GenomicRanges derivative x in which all the ranges have a width of 1 can be coerced to an UnstitchedGPos or StitchedGPos object with as(x, ″UnstitchedGPos″) or as(x, ″StitchedGPos″), respectively. For convenience as(x, ″GPos″) is supported and is equivalent to as(x, ″UnstitchedGPos″).

From GPos to GRanges: A GPos derivative x can be coerced to a GRanges object with as(x, ″GRanges″). However be aware that the resulting object can use thousands times (or more) memory than x! See "MEMORY USAGE" in the Examples section below.

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

Subsetting

A GPos derivative can be subsetted exactly like a GRanges object.

Concatenation

GPos derivatives can be concatenated with c() or append(). See ?c in the **S4Vectors** package for more information about concatenating Vector derivatives.

Splitting and Relisting

Like with any other GRanges object, split() and relist() work on a GPos derivative.

Note

Internal representation of GPos objects has changed in **GenomicRanges** 1.29.10 (Bioc 3.6). Update any old object x with: x <- updateObject(x, verbose=TRUE).

Author(s)

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

See Also

- The IPos class in the **IRanges** package for storing a set of *integer positions* (i.e. integer ranges of width 1).
- The GRanges class for storing a set of *genomic ranges* of arbitrary width.
- Seqinfo objects and the seqinfo accessor and family in the **Seqinfo** package for accessing/modifying information about the underlying sequences of a GenomicRanges derivative.
- GenomicRanges-comparison for comparing and ordering genomic ranges and/or positions.
- findOverlaps-methods for finding overlapping genomic ranges and/or positions.

- intra-range-methods and inter-range-methods for *intra range* and *inter range* transformations of GenomicRanges derivatives.

- coverage-methods for computing the coverage of a set of genomic ranges and/or positions.

- nearest-methods for finding the nearest genomic range/position neighbor.

- The snpsBySeqname, snpsByOverlaps, and snpsById methods for SNPlocs objects defined in the **BSgenome** package for extractors that return a GPos derivative.

- SummarizedExperiment objects and derivatives in the **SummarizedExperiment** package.

Examples

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

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

## Example 1:
gpos1a <- GPos(seqnames=Rle(c("chr1", "chr2", "chr1"), c(10, 6, 4)),
               pos=c(44:53, 5:10, 2:5))
gpos1a  # unstitched

length(gpos1a)
seqnames(gpos1a)
pos(gpos1a)  # same as 'start(gpos1a)' and 'end(gpos1a)'
strand(gpos1a)
as.character(gpos1a)
as.data.frame(gpos1a)
as(gpos1a, "GRanges")
as.data.frame(as(gpos1a, "GRanges"))
gpos1a[9:17]

gpos1b <- GPos(seqnames=Rle(c("chr1", "chr2", "chr1"), c(10, 6, 4)),
               pos=c(44:53, 5:10, 2:5), stitch=TRUE)
gpos1b  # stitched

## 'gpos1a' and 'gpos1b' are semantically equivalent, only their
## internal representations differ:
all(gpos1a == gpos1b)

gpos1c <- GPos(c("chr1:44-53", "chr2:5-10", "chr1:2-5"))
gpos1c  # stitched

identical(gpos1b, gpos1c)

## Example 2:
pos_runs <- GRanges("chrI", IRanges(c(1, 6, 12, 17), c(5, 10, 16, 20)),
                    strand=c("*", "-", "-", "+"))
gpos2 <- GPos(pos_runs)
gpos2  # stitched
strand(gpos2)

## Example 3:
gpos3A <- gpos3B <- GPos(c("chrI:1-1000", "chrI:1005-2000"))
npos <- length(gpos3A)
```

```
mcols(gpos3A)$sample <- Rle("sA")
sA_counts <- sample(10, npos, replace=TRUE)
mcols(gpos3A)$counts <- sA_counts

mcols(gpos3B)$sample <- Rle("sB")
sB_counts <- sample(10, npos, replace=TRUE)
mcols(gpos3B)$counts <- sB_counts

gpos3 <- c(gpos3A, gpos3B)
gpos3

## Example 4:
library(BSgenome.Scerevisiae.UCSC.sacCer2)
genome <- BSgenome.Scerevisiae.UCSC.sacCer2
gpos4 <- GPos(seqinfo(genome))
gpos4  # all the positions along the genome are represented
mcols(gpos4)$dna <- do.call("c", unname(as.list(genome)))
gpos4

## Note however that, like for any Vector derivative, the length of a
## GPos derivative cannot exceed '.Machine$integer.max' (i.e. 2^31 on
## most platforms) so the above only works with a "small" genome.
## For example it doesn't work with the Human genome:
library(TxDb.Hsapiens.UCSC.hg38.knownGene)
## Not run:
  GPos(seqinfo(TxDb.Hsapiens.UCSC.hg38.knownGene))  # error!

## End(Not run)

## You can use isSmallGenome() to check upfront whether the genome is
## "small" or not.
isSmallGenome(genome)  # TRUE
isSmallGenome(TxDb.Hsapiens.UCSC.hg38.knownGene)  # FALSE

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

## Coercion to GRanges works...
gr4 <- as(gpos4, "GRanges")
gr4
## ... but is generally not a good idea:
object.size(gpos4)
object.size(gr4)     # 8 times bigger than the StitchedGPos object!

## Shuffling the order of the positions impacts memory usage:
gpos4r <- rev(gpos4)
object.size(gpos4r)  # significantly
gpos4s <- sample(gpos4)
object.size(gpos4s)  # even worse!

## If one anticipates a lot of shuffling of the genomic positions,
## then an UnstitchedGPos object should be used instead:
gpos4b <- as(gpos4, "UnstitchedGPos")
object.size(gpos4b)  # initial size is bigger than stitched version
object.size(rev(gpos4b))  # size didn't change
object.size(sample(gpos4b))  # size increased, but is still < stitched
```

```
                                   # version

## AN IMPORTANT NOTE: In the worst situations, GPos still performs as
## good as a GRanges object.
object.size(as(gpos4r, "GRanges"))  # same size as 'gpos4r'
object.size(as(gpos4s, "GRanges"))  # same size as 'gpos4s'

## Best case scenario is when the object is strictly sorted (i.e.
## positions are in strict ascending order).
## This can be checked with:
is.unsorted(gpos4, strict=TRUE)  # 'gpos4' is strictly sorted

## ---------------------------------------------------------------------
## USING MEMORY-EFFICIENT METADATA COLUMNS
## ---------------------------------------------------------------------
## In order to keep memory usage as low as possible, it is recommended
## to use a memory-efficient representation of the metadata columns that
## we want to set on the object. Rle's are particularly well suited for
## this, especially if the metadata columns contain long runs of
## identical values. This is the case for example if we want to use a
## GPos object to represent the coverage of sequencing reads along a
## genome.

## Example 5:
library(pasillaBamSubset)
library(Rsamtools)  # for the BamFile() constructor function
bamfile1 <- BamFile(untreated1_chr4())
bamfile2 <- BamFile(untreated3_chr4())
gpos5 <- GPos(seqinfo(bamfile1))
library(GenomicAlignments)  # for "coverage" method for BamFile objects
cvg1 <- unlist(coverage(bamfile1), use.names=FALSE)
cvg2 <- unlist(coverage(bamfile2), use.names=FALSE)
mcols(gpos5) <- DataFrame(cvg1, cvg2)
gpos5

object.size(gpos5)  # lightweight

## Keep only the positions where coverage is at least 10 in one of the
## 2 samples:
gpos5[mcols(gpos5)$cvg1 >= 10 | mcols(gpos5)$cvg2 >= 10]

## ---------------------------------------------------------------------
## USING A GPos OBJECT IN A RangedSummarizedExperiment OBJECT
## ---------------------------------------------------------------------
## Because the GPos class extends the GenomicRanges virtual class, a
## GPos derivative can be used as the rowRanges component of a
## RangedSummarizedExperiment object.

## As a 1st example, we show how the counts for samples sA and sB in
## 'gpos3' can be stored in a SummarizedExperiment object where the rows
## correspond to unique genomic positions and the columns to samples:
library(SummarizedExperiment)
counts <- cbind(sA=sA_counts, sB=sB_counts)
mcols(gpos3A) <- NULL
rse3 <- SummarizedExperiment(list(counts=counts), rowRanges=gpos3A)
rse3
rowRanges(rse3)
```

```
head(assay(rse3))

## Finally we show how the coverage data from Example 5 can be easily
## stored in a lightweight SummarizedExperiment derivative:
cvg <- mcols(gpos5)
mcols(gpos5) <- NULL
rse5 <- SummarizedExperiment(list(cvg=cvg), rowRanges=gpos5)
rse5
rowRanges(rse5)
assay(rse5)

## Keep only the positions where coverage is at least 10 in one of the
## 2 samples:
rse5[assay(rse5)$cvg1 >= 10 | assay(rse5)$cvg2 >= 10]
```

GRanges-class   *GRanges objects*

Description

The GRanges class is a container for the genomic locations and their associated annotations.

Details

GRanges is a vector of genomic locations and associated annotations. Each element in the vector is comprised of a sequence name, an interval, a [strand], and optional metadata columns (e.g. score, GC content, etc.). This information is stored in four components:

seqnames a 'factor' [Rle] object containing the sequence names.

ranges an [IRanges] object containing the ranges.

strand a 'factor' [Rle] object containing the [strand] information.

mcols a [DataFrame] object containing the metadata columns. Columns cannot be named ″seqnames″, ″ranges″, ″strand″, ″seqlevels″, ″seqlengths″, ″isCircular″, ″start″, ″end″, ″width″, or ″element″.

seqinfo a [Seqinfo] object containing information about the set of genomic sequences present in the GRanges object.

Constructor

GRanges(seqnames=NULL, ranges=NULL, strand=NULL, ..., seqinfo=NULL, seqlengths=NULL): Creates a GRanges object.

seqnames NULL, or an [Rle] object, character vector, or factor containing the sequence names.

ranges NULL, or an [IRanges] object containing the ranges.

strand NULL, or an [Rle] object, character vector, or factor containing the strand information.

... Metadata columns to set on the GRanges object. All the metadata columns must be vector-like objects of the same length as the object to construct. They cannot be named ″start″, ″end″, ″width″, or ″element″.

seqinfo Either NULL, or a [Seqinfo] object, or a character vector of unique sequence names (a.k.a. *seqlevels*), or a named numeric vector of sequence lengths. When not NULL, seqinfo must be compatible with the sequence names in seqnames, that is, it must have one entry for each unique sequence name in seqnames. Note that it can have additional entries i.e. entries for seqlevels not present in seqnames.

seqlengths NULL, or an integer vector named with `levels(seqnames)` and containing the
lengths (or NA) for each level in `levels(seqnames)`.

If `ranges` is not supplied and/or NULL then the constructor proceeds in 2 steps:

1. An initial GRanges object is created with `as(seqnames, "GRanges")`.
2. Then this GRanges object is updated according to whatever non-NULL remaining arguments were passed to the call to `GRanges()`.

As a consequence of this behavior, `GRanges(x)` is equivalent to `as(x, "GRanges")`.

Accessors

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

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

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

`ranges(x)`, `ranges(x) <- value`: Get or set the ranges. `value` can be an [IntegerRanges](#) object.

`start(x)`, `start(x) <- value`: Get or set `start(ranges(x))`.

`end(x)`, `end(x) <- value`: Get or set `end(ranges(x))`.

`width(x)`, `width(x) <- value`: Get or set `width(ranges(x))`.

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

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

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

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

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

`seqlevels(x)`, `seqlevels(x, pruning.mode=c("error", "coarse", "fine", "tidy")) <- value`: Get or set the sequence levels. `seqlevels(x)` is equivalent to `seqlevels(seqinfo(x))` or to `levels(seqnames(x))`, those 2 expressions being guaranteed to return identical character vectors on a GRanges object. `value` must be a character vector with no NAs. See `?`[seqlevels](#) for more information.

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

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

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

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

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

granges(x, use.names=FALSE, use.mcols=FALSE): Squeeze the genomic ranges out of Genom-
icRanges object x and return them in a GRanges object *parallel* to x (i.e. same length as x).
If use.mcols is TRUE, the metadata columns are propagated. If x is a GenomicRanges deriva-
tive with *extra column slots*, these will be propagated as metadata columns on the returned
GRanges object.

Coercion

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

as(from, "GRanges"): Creates a GRanges object from a character vector, a factor, or IntegerRanges-
List object.

   When from is a character vector (or a factor), each element in it must represent a genomic
   range in format chr1:2501-2800 (unstranded range) or chr1:2501-2800:+ (stranded range).
   .. is also supported as a separator between the start and end positions. Strand can be +,
   -, *, or missing. The names on from are propagated to the returned GRanges object. See
   as.character() and as.factor() below for the reverse transformations.

   Coercing a data.frame or DataFrame into a GRanges object is also supported. See makeGRangesFromDataFrame
   for the details.

as(from, "IntegerRangesList"): Creates a IntegerRangesList object from a GRanges object.
   The strand and metadata columns become *inner* metadata columns (i.e. metadata columns
   on the ranges). The seqlengths(from), isCircular(from), and genome(from) vectors
   become the metadata columns.

as.character(x, ignore.strand=FALSE): Turn GRanges object x into a character vector where
   each range in x is represented by a string in format chr1:2501-2800:+. If ignore.strand is
   TRUE or if *all* the ranges in x are unstranded (i.e. their strand is set to *), then all the strings
   in the output are in format chr1:2501-2800.

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

   See as(from, "GRanges") above for the reverse transformation.

as.factor(x): Equivalent to

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

   See as(from, "GRanges") above for the reverse transformation.

   Note that table(x) is supported on a GRanges object. It is equivalent to, but much faster
   than, table(as.factor(x)).

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

as(from, "Grouping"): Creates a ManyToOneGrouping object that groups from by seqname, strand,
   start and end (same as the default sort order). This makes it convenient, for example, to ag-
   gregate a GenomicRanges object by range.

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

as(x, "GRanges"), as(x, "GenomicRanges"), as(x, "IntegerRangesList"): Turns Seqinfo ob-
   ject x (with no NA lengths) into a GRanges or IntegerRangesList.

Subsetting

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

x[i]: Return a new GRanges object made of the elements selected by i.

x[i, j]: Like the above, but allow the user to conveniently subset the metadata columns thru j.

x[i] <- value: Replacement version of x[i].

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

See ?`[` in the **S4Vectors** package for more information about subsetting Vector derivatives and
for an important note about the x[i, j] form.

Note that a GRanges object can be used as a subscript to subset a list-like object that has names
on it. In that case, the names on the list-like object are interpreted as sequence names. In the code
snippets below, x is a list or List object with names on it, and the subscript gr is a GRanges object
with all its seqnames being valid x names.

x[gr]: Return an object of the same class as x and *parallel* to gr. More precisely, it's conceptually
    doing:

        lapply(gr, function(gr1) x[[seqnames(gr1)]][ranges(gr1)])

Concatenation

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

Splitting

split(x, f, drop=FALSE): Splits GRanges object x according to f to create a GRangesList ob-
    ject. 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.

Displaying

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

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

Author(s)

P. Aboyoun and H. Pagès

See Also

- The IRanges class in the **IRanges** package for storing a set of *integer ranges*.
- The GPos class for representing a set of *genomic positions* (i.e. *genomic ranges* of width 1, a.k.a. *genomic loci*).
- makeGRangesFromDataFrame for making a GRanges object from a data.frame or DataFrame object.
- Seqinfo objects and the seqinfo accessor and family in the **Seqinfo** package for accessing/modifying information about the underlying sequences of a GenomicRanges derivative.
- GenomicRanges-comparison for comparing and ordering genomic ranges and/or positions.
- findOverlaps-methods for finding overlapping genomic ranges and/or positions.
- intra-range-methods and inter-range-methods for *intra range* and *inter range* transformations of GenomicRanges derivatives.
- coverage-methods for computing the coverage of a set of genomic ranges and/or positions.
- setops-methods for set operations on GRanges objects.
- subtract for subtracting a set of genomic ranges from a GRanges object (similar to bedtools subtract).
- nearest-methods for finding the nearest genomic range/position neighbor.
- absoluteRanges for transforming genomic ranges into *absolute* ranges (i.e. into ranges on the sequence obtained by virtually concatenating all the sequences in a genome).
- tileGenome for putting tiles on a genome.
- genomicvars for manipulating genomic variables.
- GRangesList objects.
- Vector, Rle, and DataFrame objects in the **S4Vectors** package.

Examples

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

## ---------------------------------------------------------------------
## CONSTRUCTION
## ---------------------------------------------------------------------
## Specifying the bare minimum i.e. seqnames and ranges only. The
## GRanges object will have no names, no strand information, and no
## metadata columns:
gr0 <- GRanges(Rle(c("chr2", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
               IRanges(1:10, width=10:1))
gr0

## Specifying names, strand, metadata columns. They can be set on an
## existing object:
names(gr0) <- head(letters, 10)
strand(gr0) <- Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2))
mcols(gr0)$score <- 1:10
mcols(gr0)$GC <- seq(1, 0, length=10)
gr0
```

```
## ... or specified at construction time:
gr <- GRanges(Rle(c("chr2", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
              IRanges(1:10, width=10:1, names=head(letters, 10)),
              Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2)),
              score=1:10, GC=seq(1, 0, length=10))
stopifnot(identical(gr0, gr))

## Specifying the seqinfo. It can be set on an existing object:
seqinfo <- Seqinfo(paste0("chr", 1:3), c(1000, 2000, 1500), NA, "mock1")
seqinfo(gr0) <- merge(seqinfo(gr0), seqinfo)
seqlevels(gr0) <- seqlevels(seqinfo)

## ... or specified at construction time:
gr <- GRanges(Rle(c("chr2", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
              IRanges(1:10, width=10:1, names=head(letters, 10)),
              Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2)),
              score=1:10, GC=seq(1, 0, length=10),
              seqinfo=seqinfo)
stopifnot(identical(gr0, gr))

## ---------------------------------------------------------------------
## COERCION
## ---------------------------------------------------------------------
## From GRanges:
as.character(gr)
as.factor(gr)
as.data.frame(gr)

## From character to GRanges:
x1 <- "chr2:56-125"
as(x1, "GRanges")
as(rep(x1, 4), "GRanges")
x2 <- c(A=x1, B="chr1:25-30:-")
as(x2, "GRanges")

## From data.frame to GRanges:
df <- data.frame(chrom="chr2", start=11:15, end=20:24)
gr3 <- as(df, "GRanges")

## Alternatively, coercion to GRanges can be done by just calling the
## GRanges() constructor on the object to coerce:
gr1 <- GRanges(x1)  # same as as(x1, "GRanges")
gr2 <- GRanges(x2)  # same as as(x2, "GRanges")
gr3 <- GRanges(df)  # same as as(df, "GRanges")

## Sanity checks:
stopifnot(identical(as(x1, "GRanges"), gr1))
stopifnot(identical(as(x2, "GRanges"), gr2))
stopifnot(identical(as(df, "GRanges"), gr3))

## ---------------------------------------------------------------------
## SUMMARIZING ELEMENTS
## ---------------------------------------------------------------------
table(seqnames(gr))
table(strand(gr))
sum(width(gr))
```

```
table(gr)
summary(mcols(gr)[,"score"])

## The number of lines displayed in the 'show' method are controlled
## with two global options:
longGR  <- sample(gr, 25, replace=TRUE)
longGR
options(showHeadLines=7)
options(showTailLines=2)
longGR

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


## ---------------------------------------------------------------------
## INVERTING THE STRAND
## ---------------------------------------------------------------------
invertStrand(gr)

## ---------------------------------------------------------------------
## RENAMING THE UNDERLYING SEQUENCES
## ---------------------------------------------------------------------
seqlevels(gr)
seqlevels(gr) <- sub("chr", "Chrom", seqlevels(gr))
gr
seqlevels(gr) <- sub("Chrom", "chr", seqlevels(gr)) # revert

## ---------------------------------------------------------------------
## COMBINING OBJECTS
## ---------------------------------------------------------------------
gr2 <- GRanges(seqnames=Rle(c('chr1', 'chr2', 'chr3'), c(3, 3, 4)),
               IRanges(1:10, width=5),
               strand='-',
               score=101:110, GC=runif(10),
               seqinfo=seqinfo)
gr3 <- GRanges(seqnames=Rle(c('chr1', 'chr2', 'chr3'), c(3, 4, 3)),
               IRanges(101:110, width=10),
               strand='-',
               score=21:30,
               seqinfo=seqinfo)
some.gr <- c(gr, gr2)

c(gr, gr2, gr3)
c(gr, gr2, gr3, ignore.mcols=TRUE)

## ---------------------------------------------------------------------
## USING A GRANGES OBJECT AS A SUBSCRIPT TO SUBSET ANOTHER OBJECT
## ---------------------------------------------------------------------
## Subsetting *by* a GRanges subscript is supported only if the object
## to subset is a named list-like object:
x <- RleList(chr1=101:120, chr2=2:-8, chr3=31:40)
x[gr]
```

GRangesFactor-class   *GRangesFactor objects*

Description

A GRangesFactor object is a [Factor](#) derivative where the levels are a [GRanges](#) object.

See ?`Factor` and in the **S4Vectors** package for general information about [Factor](#) objects.

Usage

```
GRangesFactor(x, levels, index=NULL, ...)  # constructor function
```

Arguments

x, levels   Like with the [`Factor`](#)() constructor function, at least one of x and `levels` must
                be specified. If `index` is NULL, both can be specified.

                When x and/or `levels` are specified, they must be [GRanges](#) objects or deriva-
                tives. In addition, `levels` cannot contain duplicate ranges (i.e. anyDuplicated(levels)
                must return 0).

                When x and `levels` are both specified, they should both be [GRanges](#) objects
                or [GRanges](#) derivatives of the same class, and all the elements in x must be
                represented in `levels` (i.e. the integer vector returned by match(x, levels)
                should contain no NAs).

index   NULL or an integer (or numeric) vector of valid positive indices (no NAs) into
                `levels`.

...   Optional metadata columns.

Details

Like with the [`Factor`](#)() constructor function, there are 4 different ways to use the GRangesFactor()
constructor function. See Details section in the man page for [Factor](#) objects for more information.

Value

A GRangesFactor object.

Accessors

GRangesFactor objects support the accessors documented in the man page for [Factor](#) objects.

In addition, the following getters are supported for convenience: seqnames(), start(), end(),
width(), strand(), seqinfo(), granges(), and ranges(). When called on GRangesFactor ob-
ject x, they all behave as if they were called on unfactor(x).

Decoding a Factor

Because a GRangesFactor object x is a [Factor](#) derivative, unfactor(x) can be used to *decode* it.
unfactor(x) returns an object of the same class as levels(x) (i.e. a [GRanges](#) object or derivative)
and same length as x.

See ?`unfactor` for more information.

Coercion

GRangesFactor objects support the coercions documented in the man page for [Factor](#) objects.

In addition, coercion back and forth between [GRanges](#) and GRangesFactor is supported via as(x,
"GRanges") and as(x, "GRangesFactor").

Subsetting

A GRangesFactor object can be subsetted with [, like a Factor object.

Concatenation

2 or more GRangesFactor objects can be concatenated with c(). The result of this concatenation is another GRangesFactor object.

See Concatenation section in ?`Factor`.

Comparing & ordering

See Comparing & Ordering section in ?`Factor`.

Author(s)

Hervé Pagès

See Also

- GRanges objects.
- Factor objects in the **S4Vectors** package for the parent class of GRangesFactor.
- anyDuplicated in the **BiocGenerics** package.

Examples

```
showClass("GRangesFactor")  # GRangesFactor extends Factor

## ---------------------------------------------------------------------
## CONSTRUCTOR & ACCESSORS
## ---------------------------------------------------------------------
set.seed(123)
ir0 <- IRanges(sample(5, 8, replace=TRUE), width=10, names=letters[1:8])
gr0 <- GRanges("chrA", ir0, ID=paste0("ID", 1:8))

## Use explicit levels:
gr1 <- GRanges("chrA", IRanges(1:6, width=10))
grf1 <- GRangesFactor(gr0, levels=gr1)
grf1
length(grf1)
names(grf1)
levels(grf1)  # gr1
nlevels(grf1)
as.integer(grf1)  # encoding

## If we don't specify the levels, they'll be set to unique(gr0):
grf2 <- GRangesFactor(gr0)
grf2
length(grf2)
names(grf2)
levels(grf2)  # unique(gr0)
nlevels(grf2)
as.integer(grf2)

## ---------------------------------------------------------------------
## DECODING
```

```
## ---------------------------------------------------------------------
unfactor(grf1)

stopifnot(identical(gr0, unfactor(grf1)))
stopifnot(identical(gr0, unfactor(grf2)))

unfactor(grf1, use.names=FALSE)
unfactor(grf1, ignore.mcols=TRUE)

## ---------------------------------------------------------------------
## COERCION
## ---------------------------------------------------------------------
grf2b <- as(gr0, "GRangesFactor")  # same as GRangesFactor(gr0)
stopifnot(identical(grf2, grf2b))

as.factor(grf2)
as.factor(grf1)

as.character(grf1)  # same as unfactor(as.factor(grf1)),
                    # and also same as as.character(unfactor(grf1))

## ---------------------------------------------------------------------
## CONCATENATION
## ---------------------------------------------------------------------
gr3 <- GRanges("chrA", IRanges(c(5, 2, 8:6), width=10))
grf3 <- GRangesFactor(levels=gr3, index=2:4)
grf13 <- c(grf1, grf3)
grf13
levels(grf13)

stopifnot(identical(c(unfactor(grf1), unfactor(grf3)), unfactor(grf13)))

## ---------------------------------------------------------------------
## COMPARING & ORDERING
## ---------------------------------------------------------------------
grf1 == grf2  # same as unfactor(grf1) == unfactor(grf2)

order(grf1)   # same as order(unfactor(grf1))
order(grf2)   # same as order(unfactor(grf2))

## The levels of the GRangesFactor influence the order of the table:
table(grf1)
table(grf2)
```

GRangesList-class   *GRangesList objects*

Description

The GRangesList class is a container for storing a collection of [GRanges](#) objects. It is a subclass of [GenomicRangesList](#). It exists in 2 flavors: SimpleGRangesList and CompressedGRangesList. Each flavor uses a particular internal representation. The CompressedGRangesList flavor is the default. It is particularly efficient for storing a large number of list elements and operating on them.

Constructors

GRangesList(..., compress=TRUE)**:** Creates a GRangesList object using the GRanges objects
supplied in ..., either consecutively or in a list. By default a CompressedGRangesList *in-stance* is returned, that is, a GRangesList object of the CompressedGRangesList flavor. Use
compress=FALSE to get a SimpleGRangesList *instance* instead.

makeGRangesListFromFeatureFragments(seqnames=Rle(factor()), fragmentStarts=list(), fragmentEnds=l
Constructs a GRangesList object from a list of fragmented features. See the Examples section
below.

Accessors

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

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

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

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

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

start(x)**,** start(x) <- value**:** Get or set start(ranges(x)).

end(x)**,** end(x) <- value**:** Get or set end(ranges(x)).

width(x)**,** width(x) <- value**:** Get or set width(ranges(x)).

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

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

elementNROWS(x)**:** Get a vector of the length of each of the list element.

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

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

seqlevels(x)**,** seqlevels(x, pruning.mode=c("error", "coarse", "fine", "tidy")) <- value**:**
Get or set the sequence levels. seqlevels(x) is equivalent to seqlevels(seqinfo(x)) or
to levels(seqnames(x)), those 2 expressions being guaranteed to return identical charac-
ter vectors on a GRangesList object. value must be a character vector with no NAs. See
?seqlevels for more information.

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

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

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

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

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

Coercion

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

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

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

as(x, "IRangesList"): Turns x into an IRangesList object.

When x is a list of GRanges, it can be coerced to a GRangesList.

as(x, "GRangesList"): Turns x into a GRangesList.

Subsetting

In the following code snippets, x is a GRangesList object.

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

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

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

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

rep(x, times, length.out, each): Repeats the values in x through one of the following conven-
tions:

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

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

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

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

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

Combining

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

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

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

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

Looping

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

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

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

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

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

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

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

> f A binary argument function.
>
> init An R object of the same kind as the elements of x.
>
> right A logical indicating whether to proceed from left to right (default) or from right to left.
>
> nomatch The value to be returned in the case when "no match" (no element satisfying the predicate) is found.

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

Author(s)

P. Aboyoun & H. Pagès

See Also

- [GRanges](#) objects.
- [seqinfo](#) in the **Seqinfo** package.
- [IntegerRangesList](#) objects in the **IRanges** package.
- [RleList](#) objects in the **IRanges** package.
- [DataFrameList](#) objects in the **IRanges** package.
- [intra-range-methods](#), [inter-range-methods](#), [coverage-methods](#), [setops-methods](#), and [findOverlaps-methods](#).
- [GenomicRangesList](#) objects.

Examples

```
## Construction with GRangesList():
gr1 <- GRanges("chr2", IRanges(3, 6),
               strand="+", score=5L, GC=0.45)
gr2 <- GRanges(c("chr1", "chr1"), IRanges(c(7,13), width=3),
               strand=c("+", "-"), score=3:4, GC=c(0.3, 0.5))
gr3 <- GRanges(c("chr1", "chr2"), IRanges(c(1, 4), c(3, 9)),
               strand=c("-", "-"), score=c(6L, 2L), GC=c(0.4, 0.1))
```

```
grl <- GRangesList(gr1=gr1, gr2=gr2, gr3=gr3)
grl

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

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

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

## Coerce to IRangesList (seqnames and strand information is lost):
as(grl, "IRangesList")

## isDisjoint():
isDisjoint(grl)

## disjoin():
disjoin(grl)  # metadata columns and order NOT preserved

## Construction with makeGRangesListFromFeatureFragments():
filepath <- system.file("extdata", "feature_frags.txt",
                        package="GenomicRanges")
featfrags <- read.table(filepath, header=TRUE, stringsAsFactors=FALSE)
grl2 <- with(featfrags,
             makeGRangesListFromFeatureFragments(seqnames=targetName,
                                                 fragmentStarts=targetStart,
                                                 fragmentWidths=blockSizes,
                                                 strand=strand))
names(grl2) <- featfrags$RefSeqID
grl2
```

---

inter-range-methods   *Inter range transformations of a GRanges or GRangesList object*

Description

This man page documents *inter range transformations* of a GenomicRanges object (i.e. of an object that belongs to the GenomicRanges class or one of its subclasses, this includes for example GRanges objects), or a GRangesList object.

See ?`intra-range-methods` and ?`inter-range-methods` in the **IRanges** package for a quick introduction to *intra range* and *inter range transformations*.

See ?`intra-range-methods` for *intra range transformations* of a GenomicRanges object or GRangesList object.

Usage

```
## S4 method for signature 'GenomicRanges'
```

```
range(x, ..., with.revmap=FALSE, ignore.strand=FALSE, na.rm=FALSE)
## S4 method for signature 'GRangesList'
range(x, ..., with.revmap=FALSE, ignore.strand=FALSE, na.rm=FALSE)

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

## S4 method for signature 'GenomicRanges'
gaps(x, start=1L, end=seqlengths(x), ignore.strand=FALSE)

## S4 method for signature 'GenomicRanges'
disjoin(x, with.revmap=FALSE, ignore.strand=FALSE)
## S4 method for signature 'GRangesList'
disjoin(x, with.revmap=FALSE, ignore.strand=FALSE)

## S4 method for signature 'GenomicRanges'
isDisjoint(x, ignore.strand=FALSE)
## S4 method for signature 'GRangesList'
isDisjoint(x, ignore.strand=FALSE)

## S4 method for signature 'GenomicRanges'
disjointBins(x, ignore.strand=FALSE)
```

Arguments

x   A GenomicRanges or GenomicRangesList object.

drop.empty.ranges, min.gapwidth, with.revmap, with.inframe.attrib,
start, end

                    See ?`inter-range-methods` in the **IRanges** package.

ignore.strand   TRUE or FALSE. Whether the strand of the input ranges should be ignored or not.
                    See details below.

...   For range, additional GenomicRanges objects to consider. Ignored otherwise.

na.rm   Ignored.

Details

On a GRanges object: range returns an object of the same type as x containing range bounds
for each distinct (seqname, strand) pairing. The names (names(x)) and the metadata columns in
x are dropped.

reduce returns an object of the same type as x containing reduced ranges for each distinct (seq-
name, strand) pairing. The names (names(x)) and the metadata columns in x are dropped. See
?reduce for more information about range reduction and for a description of the optional argu-
ments.

gaps returns an object of the same type as x containing complemented ranges for each distinct
(seqname, strand) pairing. The names (names(x)) and the metadata columns in x are dropped.
For the start and end arguments of this gaps method, it is expected that the user will supply a
named integer vector (where the names correspond to the appropriate seqlevels). See ?gaps for
more information about range complements and for a description of the optional arguments.

disjoin returns an object of the same type as x containing disjoint ranges for each distinct (se-qname, strand) pairing. The names (names(x)) and the metadata columns in x are dropped. If with.revmap=TRUE, a metadata column that maps the ouput ranges to the input ranges is added to the returned object. See ?disjoin for more information.

isDisjoint returns a logical value indicating whether the ranges in x are disjoint (i.e. non-overlapping).

disjointBins returns bin indexes for the ranges in x, such that ranges in the same bin do not overlap. If ignore.strand=FALSE, the two features cannot overlap if they are on different strands.

On a GRangesList/GenomicRangesList object: When they are supported on GRangesList object x, the above inter range transformations will apply the transformation to each of the list elements in x and return a list-like object *parallel* to x (i.e. with 1 list element per list element in x). If x has names on it, they're propagated to the returned object.

Author(s)

H. Pagès and P. Aboyoun

See Also

- The [GenomicRanges](#) and [GRanges](#) classes.
- The [IntegerRanges](#) class in the **IRanges** package.
- The [inter-range-methods](#) man page in the **IRanges** package.
- [GenomicRanges-comparison](#) for comparing and ordering genomic ranges.
- [endoapply](#) in the **S4Vectors** package.

Examples

```
gr <- GRanges(
        seqnames=Rle(paste("chr", c(1, 2, 1, 3), sep=""), c(1, 3, 2, 4)),
        ranges=IRanges(1:10, width=10:1, names=letters[1:10]),
        strand=Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2)),
        score=1:10,
        GC=seq(1, 0, length=10)
      )
gr

gr1 <- GRanges(seqnames="chr2", ranges=IRanges(3, 6),
               strand="+", score=5L, GC=0.45)
gr2 <- GRanges(seqnames="chr1",
               ranges=IRanges(c(10, 7, 19), width=5),
               strand=c("+", "-", "+"), score=3:5, GC=c(0.3, 0.5, 0.66))
gr3 <- GRanges(seqnames=c("chr1", "chr2"),
               ranges=IRanges(c(1, 4), c(3, 9)),
               strand=c("-", "-"), score=c(6L, 2L), GC=c(0.4, 0.1))
grl <- GRangesList(gr1=gr1, gr2=gr2, gr3=gr3)
grl

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

## On a GRanges object:
range(gr)
```

```
range(gr, with.revmap=TRUE)

## On a GRangesList object:
range(grl)
range(grl, ignore.strand=TRUE)
range(grl, with.revmap=TRUE, ignore.strand=TRUE)


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

gr2 <- reduce(gr, with.revmap=TRUE)
revmap <- mcols(gr2)$revmap  # an IntegerList

## Use the mapping from reduced to original ranges to group the original
## ranges by reduced range:
relist(gr[unlist(revmap)], revmap)

## Or use it to split the DataFrame of original metadata columns by
## reduced range:
relist(mcols(gr)[unlist(revmap), ], revmap)  # a SplitDataFrameList

## [For advanced users] Use this reverse mapping to compare the reduced
## ranges with the ranges they originate from:
expanded_gr2 <- rep(gr2, elementNROWS(revmap))
reordered_gr <- gr[unlist(revmap)]
codes <- pcompare(expanded_gr2, reordered_gr)
## All the codes should translate to "d", "e", "g", or "h" (the 4 letters
## indicating that the range on the left contains the range on the right):
alphacodes <-
    rangeComparisonCodeToLetter(pcompare(expanded_gr2, reordered_gr))
stopifnot(all(alphacodes %in% c("d", "e", "g", "h")))

## On a big GRanges object with a lot of seqlevels:
mcols(gr) <- NULL
biggr <- c(gr, GRanges("chr1", IRanges(c(4, 1), c(5, 2)), strand="+"))
seqlevels(biggr) <- paste0("chr", 1:2000)
biggr <- rep(biggr, 25000)
set.seed(33)
seqnames(biggr) <-
    sample(factor(seqlevels(biggr), levels=seqlevels(biggr)),
           length(biggr), replace=TRUE)

biggr2 <- reduce(biggr, with.revmap=TRUE)
revmap <- mcols(biggr2)$revmap
expanded_biggr2 <- rep(biggr2, elementNROWS(revmap))
reordered_biggr <- biggr[unlist(revmap)]
codes <- pcompare(expanded_biggr2, reordered_biggr)
alphacodes <-
    rangeComparisonCodeToLetter(pcompare(expanded_biggr2, reordered_biggr))
stopifnot(all(alphacodes %in% c("d", "e", "g", "h")))
table(alphacodes)

## On a GRangesList object:
reduce(grl)  # Doesn't really reduce anything but note the reordering
             # of the inner elements in the 2nd and 3rd list elements:
```

```
              # the ranges are reordered by sequence name first (which
              # should appear in the same order as in 'seqlevels(grl)'),
              # and then by strand.
reduce(grl, ignore.strand=TRUE)  # 2nd list element got reduced

## ---------------------------------------------------------------------
## gaps()
## ---------------------------------------------------------------------
gaps(gr, start=3, end=12)
gaps(gr, start=3, end=12, ignore.strand=TRUE)

## Note that if the lengths of the underlying sequences are known, then
## by default 'gaps(gr)' returns the regions of the sequences that are
## not covered by 'gr':
seqlengths(gr)  # lengths of underlying sequences are not known
seqlengths(gr) <- c(chr1=50, chr2=30, chr3=18)

gaps(gr)

gaps(gr, ignore.strand=TRUE)

## ---------------------------------------------------------------------
## disjoin(), isDisjoint(), disjointBins()
## ---------------------------------------------------------------------
disjoin(gr)
disjoin(gr, with.revmap=TRUE)
disjoin(gr, with.revmap=TRUE, ignore.strand=TRUE)
isDisjoint(gr)
stopifnot(isDisjoint(disjoin(gr)))
disjointBins(gr)
stopifnot(all(sapply(split(gr, disjointBins(gr)), isDisjoint)))

## On a GRangesList object:
disjoin(grl)  # doesn't really disjoin anything but note the reordering
disjoin(grl, with.revmap=TRUE)
```

---

intra-range-methods   *Intra range transformations of a GRanges or GRangesList object*

Description

This man page documents *intra range transformations* of a GenomicRanges object (i.e. of an object that belongs to the GenomicRanges class or one of its subclasses, this includes for example GRanges objects), or a GRangesList object.

See ?`intra-range-methods` and ?`inter-range-methods` in the **IRanges** package for a quick introduction to *intra range* and *inter range transformations*.

Intra range methods for GAlignments and GAlignmentsList objects are defined and documented in the **GenomicAlignments** package.

See ?`inter-range-methods` for *inter range transformations* of a GenomicRanges or GRanges-List object.

Usage

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

## S4 method for signature 'GenomicRanges'
narrow(x, start=NA, end=NA, width=NA, use.names=TRUE)

## S4 method for signature 'GenomicRanges'
resize(x, width, fix="start", use.names=TRUE, ignore.strand=FALSE)

## S4 method for signature 'GenomicRanges'
flank(x, width, start=TRUE, both=FALSE, use.names=TRUE,
      ignore.strand=FALSE)

## S4 method for signature 'GenomicRanges'
promoters(x, upstream=2000, downstream=200, use.names=TRUE)
## S4 method for signature 'GenomicRanges'
terminators(x, upstream=2000, downstream=200, use.names=TRUE)

## S4 method for signature 'GenomicRanges'
restrict(x, start=NA, end=NA, keep.all.ranges=FALSE, use.names=TRUE)

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

Arguments

x   A GenomicRanges object.

`shift, use.names, start, end, width, both, fix, keep.all.ranges, upstream, downstream`

See ?`intra-range-methods`.

`ignore.strand`   TRUE or FALSE. Whether the strand of the input ranges should be ignored or not. See details below.

Details

`shift`: behaves like the `shift` method for IntegerRanges objects. See ?`intra-range-methods` for the details.

`narrow`: on a GenomicRanges object behaves like on an IntegerRanges object. See ?`intra-range-methods` for the details.

A major difference though is that it returns a GenomicRanges object instead of an IntegerRanges object. The returned object is *parallel* (i.e. same length and names) to the original object x.

`resize`: returns an object of the same type and length as x containing intervals that have been resized to width `width` based on the `strand(x)` values. Elements where `strand(x) == "+"` or `strand(x) == "*"` are anchored at `start(x)` and elements where `strand(x) == "-"` are anchored at the `end(x)`. The `use.names` argument determines whether or not to keep the names on the ranges.

`flank`: returns an object of the same type and length as x containing intervals of width `width` that flank the intervals in x. The `start` argument takes a logical indicating whether x should be flanked at the "start" (TRUE) or the "end" (FALSE), which for `strand(x) != "-"` is `start(x)`

and end(x) respectively and for strand(x) == "-" is end(x) and start(x) respectively. The both argument takes a single logical value indicating whether the flanking region width positions extends *into* the range. If both=TRUE, the resulting range thus straddles the end point, with width positions on either side.

promoters: assumes that the ranges in x represent transcript regions and returns the ranges of the corresponding promoter regions. The result is another [GenomicRanges](#) derivative *parallel* to the input, that is, of the same length as x and with the i-th element in the output corresponding to the i-th element in the input.

The promoter regions extend around the transcription start sites (TSS) which are located at start(x) for ranges on the + or * strand, and at end(x) for ranges on the - strand. The upstream and downstream arguments define the number of nucleotides in the 5' and 3' direction, respectively. More precisely, the output range is defined as

(start(x) - upstream) to (start(x) + downstream - 1)

for ranges on the + or * strand, and as

(end(x) - downstream + 1) to (end(x) + upstream)

for ranges on the - strand.

Be aware that the returned object might contain *out-of-bound* ranges i.e. ranges that start before the first nucleotide position and/or end after the last nucleotide position of the underlying sequence.

The returned object will always have the same class as x, except when x is a [GPos](#) object in which case a [GRanges](#) instance is returned.

terminators: like promoters but returns the ranges of the terminator regions. These regions extend around the transcription end sites (TES) which are located at end(x) for ranges on the + or * strand, and at start(x) for ranges on the - strand.

restrict: returns an object of the same type and length as x containing restricted ranges for distinct seqnames. The start and end arguments can be a named numeric vector of seqnames for the ranges to be resticted or a numeric vector or length 1 if the restriction operation is to be applied to all the sequences in x. See ?`[intra-range-methods](#)` for more information about range restriction and for a description of the optional arguments.

trim: trims out-of-bound ranges located on non-circular sequences whose length is not NA.

Author(s)

P. Aboyoun, V. Obenchain, and H. Pagès

See Also

- [GenomicRanges](#), [GRanges](#), and [GRangesList](#) objects.
- The [intra-range-methods](#) man page in the **IRanges** package.
- The [IntegerRanges](#) class in the **IRanges** package.

Examples

```
## -------------------------------------------------------------------
## A. ON A GRanges OBJECT
## -------------------------------------------------------------------
gr <- GRanges(
```

```
            seqnames=Rle(paste("chr", c(1, 2, 1, 3), sep=""), c(1, 3, 2, 4)),
            ranges=IRanges(1:10, width=10:1, names=letters[1:10]),
            strand=Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2)),
            score=1:10,
            GC=seq(1, 0, length=10)
        )
gr

shift(gr, 1)
narrow(gr[-10], start=2, end=-2)
resize(gr, width=10)
flank(gr, width=10)
restrict(gr, start=3, end=7)

gr <- GRanges("chr1", IRanges(rep(10, 3), width=8), c("+", "-", "*"))
promoters(gr, 2, 5)
promoters(gr, upstream=0, downstream=1)  # TSS
terminators(gr, 2, 5)
terminators(gr, upstream=0, downstream=1)  # TES

## ---------------------------------------------------------------------
## B. ON A GRangesList OBJECT
## ---------------------------------------------------------------------
gr1 <- GRanges("chr2", IRanges(3, 6))
gr2 <- GRanges(c("chr1", "chr1"), IRanges(c(7,13), width=3),
               strand=c("+", "-"))
gr3 <- GRanges(c("chr1", "chr2"), IRanges(c(1, 4), c(3, 9)),
               strand="-")
grl <- GRangesList(gr1= gr1, gr2=gr2, gr3=gr3)
grl

resize(grl, width=20)
flank(grl, width=20)
restrict(grl, start=3)
```

---

makeGRangesFromDataFrame

Make a GRanges object from a data.frame or DataFrame

Description

makeGRangesFromDataFrame and makeGPosFromDataFrame both take a data-frame-like object as input and try to automatically find the columns that describe genomic ranges (for makeGRangesFromDataFrame) or genomic positions (for makeGPosFromDataFrame). If successful, they return them in a GRanges or GPos object.

The two functions are also the workhorses behind the coercion methods from data.frame (or DataFrame) to GRanges or GPos.

Usage

```
makeGRangesFromDataFrame(df, keep.extra.columns=FALSE,
        ignore.strand=FALSE, seqinfo=NULL,
        seqnames.field=c("seqnames", "seqname",
```

```
                          "chromosome", "chrom", "chr", "chromosome_name",
                          "seqid"),
        start.field="start",
        end.field=c("end", "stop"),
        strand.field="strand",
        starts.in.df.are.0based=FALSE,
        na.rm=FALSE)

makeGPosFromDataFrame(df, keep.extra.columns=FALSE,
        ignore.strand=FALSE, seqinfo=NULL,
        seqnames.field=c("seqnames", "seqname",
                          "chromosome", "chrom", "chr", "chromosome_name",
                          "seqid"),
        pos.field=c("pos", "position", "positions"),
        strand.field="strand",
        na.rm=FALSE)
```

Arguments

df   A data.frame or [DataFrame] object. If not, then the function first tries to turn df
                   into a data frame with as.data.frame(df).

keep.extra.columns

                   TRUE or FALSE (the default). If TRUE, then the columns in df that are not used
                   to form the genomic ranges or genomic positions of the returned [GRanges] or
                   [GPos] object are returned as metadata columns on the object. Otherwise, they
                   are ignored.

                   Note that if df has a width column, then makeGRangesFromDataFrame will
                   always ignore it.

ignore.strand   TRUE or FALSE (the default). If TRUE, then the strand of the returned [GRanges] or
                   [GPos] object is set to "*".

seqinfo   Either NULL, or a [Seqinfo] object, or a character vector of unique sequence names
                   (a.k.a. *seqlevels*), or a named numeric vector of sequence lengths. When not
                   NULL, seqinfo must be compatible with the genomic ranges in df, that is, it
                   must have one entry for each unique sequence name represented in df. Note
                   that it can have additional entries i.e. entries for seqlevels not represented in df.

seqnames.field   A character vector of recognized names for the column in df that contains the
                   chromosome name (a.k.a. sequence name) associated with each genomic range.
                   Only the first name in seqnames.field that is found in colnames(df) is used.
                   If no one is found, then an error is raised.

start.field   A character vector of recognized names for the column in df that contains the
                   start positions of the genomic ranges. Only the first name in start.field that
                   is found in colnames(df) is used. If no one is found, then an error is raised.

end.field   A character vector of recognized names for the column in df that contains the
                   end positions of the genomic ranges. Only the first name in start.field that
                   is found in colnames(df) is used. If no one is found, then an error is raised.

pos.field   A character vector of recognized names for the column in df that contains the
                   genomic positions to use to make the [GPos] object. Only the first name in
                   pos.field that is found in colnames(df) is used. If no one is found, then
                   an error is raised.

strand.field   A character vector of recognized names for the column in df that contains the
                   strand associated with each genomic range. Only the first name in strand.field
```

that is found in `colnames(df)` is used. If no one is found or if `ignore.strand` is TRUE, then the strand of the returned [GRanges](#) object is set to `"*"`.

starts.in.df.are.0based

TRUE or FALSE (the default). If TRUE, then the start positions of the genomic ranges in `df` are considered to be *0-based* and are converted to *1-based* in the returned [GRanges](#) object. This feature is intended to make it more convenient to handle input that contains data obtained from resources using the "0-based start" convention. A notorious example of such resource is the UCSC Table Browser (<http://genome.ucsc.edu/cgi-bin/hgTables>).

na.rm               TRUE or FALSE (the default).

If TRUE, then rows in the `df` with missing start, end, or position values (i.e. the value is NA) are ignored. Otherwise, they trigger an error.

## Value

A [GRanges](#) or [GPos](#) object.

If `na.rm` is set to FALSE (the default), then the returned object is guaranteed to have one element per row in the input. However, if `na.rm` is set to TRUE, then the length of the returned object can be less than `nrow(df)`.

If the `seqinfo` argument was supplied, the returned object will have exactly the seqlevels specified in `seqinfo` and in the same order. Otherwise, the seqlevels are ordered according to the output of the [rankSeqlevels](#) function (except if `df` contains the seqnames in the form of a factor or factor-Rle, in which case the `levels()` of the seqnames become the seqlevels of the returned object as-is, that is, without any re-ordering).

If `df` has non-automatic row names (i.e. `rownames(df)` is not NULL and is not `seq_len(nrow(df))`), then they will be used to set names on the returned [GRanges](#) or [GPos](#) object.

## Note

Coercing a data.frame or [DataFrame](#) `df` to [GRanges](#) (with `as(df, "GRanges")`), or calling `GRanges(df)`, are both equivalent to calling `makeGRangesFromDataFrame(df, keep.extra.columns=TRUE)`.

Coercing a data.frame or [DataFrame](#) `df` to [GPos](#) (with `as(df, "GPos")`) is equivalent to calling `makeGPosFromDataFrame(df, keep.extra.columns=TRUE)`.

## Author(s)

H. Pagès, based on a proposal by Kasper Daniel Hansen

## See Also

- [GRanges](#) and [GPos](#) objects.
- [Seqinfo](#) objects and the [rankSeqlevels](#) function in the **Seqinfo** package.
- The [makeGRangesListFromFeatureFragments](#) function for making a [GRangesList](#) object from a list of fragmented features.
- [makeIRangesFromDataFrame](#) in the **IRanges** package to make an [IRanges](#) object from a data.frame or [DataFrame](#).
- [DataFrame](#) objects in the **S4Vectors** package.

## Examples

```
## ---------------------------------------------------------------------
## BASIC makeGRangesFromDataFrame() EXAMPLES
## ---------------------------------------------------------------------

df <- data.frame(chr="chr1", start=11:15, end=12:16,
                 strand=c("+","-","+","*","."), score=1:5)
df
makeGRangesFromDataFrame(df)  # strand value "." is replaced with "*"

## With NAs in range-defining columns:
df$start[5] <- df$end[2] <- NA
df
#makeGRangesFromDataFrame(df)  # error!
makeGRangesFromDataFrame(df, na.rm=TRUE)  # rows with NAs got dropped

## The strand column is optional:
df <- data.frame(chr="chr1", start=11:15, end=12:16, score=1:5)
makeGRangesFromDataFrame(df)

gr <- makeGRangesFromDataFrame(df, keep.extra.columns=TRUE)
gr2 <- as(df, "GRanges")  # equivalent to the above
stopifnot(identical(gr, gr2))
gr2 <- GRanges(df)        # equivalent to the above
stopifnot(identical(gr, gr2))

makeGRangesFromDataFrame(df, ignore.strand=TRUE)
makeGRangesFromDataFrame(df, keep.extra.columns=TRUE,
                             ignore.strand=TRUE)

makeGRangesFromDataFrame(df, seqinfo=paste0("chr", 4:1))
makeGRangesFromDataFrame(df, seqinfo=c(chrM=NA, chr1=500, chrX=100))
makeGRangesFromDataFrame(df, seqinfo=Seqinfo(paste0("chr", 4:1)))

## ---------------------------------------------------------------------
## BASIC makeGPosFromDataFrame() EXAMPLES
## ---------------------------------------------------------------------

df <- data.frame(
    rsids=    c("rs7927381", "rs79273813", "rs79273815",
                "rs79273819", "rs79273817", "rs79273811", "rs79273814"),
    seqnames= c("11", "1", "11", "1", "5", "8", "8"),
    positions=c("67579271", "179599437", "70746832",
                "5066529", "107006951", "95077418", "43582071"),
    alleles=  c("T/C", "A/G", "C/G, C/T", "G/A, G/C", "T/C, T/G",
                "G/A, G/T", "G/A, G/T"),
    genes=    c(NA, "TDRD5", "SHANK2", NA, "LOC102467213", "NDUFAF6", NA),
    row.names=letters[1:7]
)

makeGPosFromDataFrame(df)
makeGPosFromDataFrame(df, keep.extra.columns=TRUE)
as(df, "GPos")  # same as above

## With missing positions:
df$positions[2L] <- NA
```

```
df
#makeGPosFromDataFrame(df)  # error!
makeGPosFromDataFrame(df, na.rm=TRUE)  # rows with NAs got dropped

## ---------------------------------------------------------------------
## ABOUT AUTOMATIC DETECTION OF THE seqnames/start/end/strand COLUMNS
## ---------------------------------------------------------------------

## Automatic detection of the seqnames/start/end/strand columns is
## case insensitive:
df <- data.frame(ChRoM="chr1", StarT=11:15, stoP=12:16,
                 STRAND=c("+","-","+","*","."), score=1:5)
makeGRangesFromDataFrame(df)

## It also ignores a common prefix between the start and end columns:
df <- data.frame(seqnames="chr1", tx_start=11:15, tx_end=12:16,
                 strand=c("+","-","+","*","."), score=1:5)
makeGRangesFromDataFrame(df)

## The common prefix between the start and end columns is used to
## disambiguate between more than one seqnames column:
df <- data.frame(chrom="chr1", tx_start=11:15, tx_end=12:16,
                 tx_chr="chr2", score=1:5)
makeGRangesFromDataFrame(df)

## ---------------------------------------------------------------------
## 0-BASED VS 1-BASED START POSITIONS
## ---------------------------------------------------------------------

if (require(UCSC.utils)) {
  ## Use list_UCSC_tracks() to lookup the primary table associated with
  ## a given track:
  subset(list_UCSC_tracks("sacCer2"), track == "Assembly")

  df <- fetch_UCSC_track_data("sacCer2", primary_table="gold")
  head(df)

  ## A common pitfall is to forget that UCSC uses the "0-based start"
  ## convention to store genomic ranges in their databases:
  gr0 <- makeGRangesFromDataFrame(df, keep.extra.columns=TRUE,
                                      start.field="chromStart",
                                      end.field="chromEnd")
  head(gr0)

  ## The start positions need to be converted into 1-based positions,
  ## to adhere to the convention used in Bioconductor:
  gr1 <- makeGRangesFromDataFrame(df, keep.extra.columns=TRUE,
                                      start.field="chromStart",
                                      end.field="chromEnd",
                                      starts.in.df.are.0based=TRUE)
  head(gr1)

  ## IMPORTANT NOTE: The start positions in the "fragStart" metadata
  ## column are still 0-based! That's because using
  ## 'keep.extra.columns=TRUE' only takes care of converting the
  ## start positions of the genomic ranges that define the GRanges
  ## object itself, but it doesn't meddle with its metadata columns.
```

```
}
```

---

makeGRangesListFromDataFrame

Make a GRangesList object from a data.frame or DataFrame

Description

makeGRangesListFromDataFrame extends the [makeGRangesFromDataFrame](#) functionality from GenomicRanges. It can take a data-frame-like object as input and tries to automatically find the columns that describe the genomic ranges. It returns a [GRangesList](#) object. This is different from the makeGRangesFromDataFrame function by requiring a split.field. The split.field acts like the "f" argument in the [split](#) function. This factor must be of the same length as the number of rows in the DataFrame argument. The split.field may also be a character vector.

Usage

```
makeGRangesListFromDataFrame(df,
                             split.field = NULL,
                             names.field = NULL,
                             ...)
```

Arguments

df	A DataFrame or data.frame class object
split.field	A character string of a recognized column name in df that contains the grouping. This column defines how the rows of df are split and is typically a factor or character vector. When split.field is not provided the df will be split by the number of rows.
names.field	An optional single character string indicating the name of the column in df that designates the names for the ranges in the elements of the [GRangesList](#).
...	Additional arguments passed on to [makeGRangesFromDataFrame](#)

Value

A [GRangesList](#) of the same length as the number of levels or unique character strings in the df column indicated by split.field. When split.field is not provided the df is split by row and the resulting [GRangesList](#) has the same length as nrow(df).

Names on the individual ranges are taken from the names.field argument. Names on the outer list elements of the [GRangesList](#) are propagated from split.field.

Author(s)

M. Ramos

See Also

- [makeGRangesFromDataFrame](#)

Examples

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

df <- data.frame(chr="chr1", start=11:15, end=12:16,
                 strand=c("+","-","+","*","."), score=1:5,
                 specimen = c("a", "a", "b", "b", "c"),
                 gene_symbols = paste0("GENE", letters[1:5]))
df

grl <- makeGRangesListFromDataFrame(df, split.field = "specimen",
                                    names.field = "gene_symbols")
grl
names(grl)

## Keep metadata columns
makeGRangesListFromDataFrame(df, split.field = "specimen",
                             keep.extra.columns = TRUE)
```

---

nearest-methods   *Finding the nearest genomic range/position neighbor*

Description

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

Usage

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

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

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

## S4 method for signature 'GenomicRanges,GenomicRanges'
```

```
nearestKNeighbors(x, subject, k=1L,
    select=c("arbitrary", "all"), ignore.strand=FALSE)
## S4 method for signature 'GenomicRanges,missing'
nearestKNeighbors(x, subject, k=1L,
    select=c("arbitrary", "all"), ignore.strand=FALSE)

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

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

Arguments

x	The query [GenomicRanges](#) instance.
subject	The subject [GenomicRanges](#) instance within which the nearest neighbors are found. Can be missing, in which case x is also the subject.
y	For the `distance` method, a GRanges 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.
k	For the `nearestKNeighbors` method, an integer declaring how many nearest neighbors to find.
select	Logic for handling ties. By default, all methods select a single interval (arbitrary for `nearest`, the first by order in `subject` for `precede`, and the last for `follow`). When select="all" a [Hits](#) object is returned with all matches for x.
ignore.strand	A `logical` indicating if the strand of the input ranges should be ignored. When TRUE, strand is set to '+'.
...	Additional arguments for methods.

Details

nearest: Performs conventional nearest neighbor finding. Returns an integer vector containing the index of the nearest neighbor range in `subject` for each range in `x`. If there is no nearest neighbor NA is returned. For details of the algorithm see the man page in the **IRanges** package (?nearest).

precede: For each range in `x`, precede returns the index of the range in `subject` that is directly preceded by the range in `x`. Overlapping ranges are excluded. NA is returned when there are no qualifying ranges in `subject`.

follow: The opposite of precede, follow returns the index of the range in `subject` that is directly followed by the range in `x`. Overlapping ranges are excluded. NA is returned when there are no qualifying ranges in `subject`.

nearestKNeighbors: Performs conventional k-nearest neighbor finding. Returns an [IntegerList](#) containing the index of the k-nearest neighbors in `subject` for each range in `x`. If there is no nearest neighbor NA is returned. If select="all" is specified, ties will be included in the resulting [IntegerList](#).

Orientation and strand for precede **and** follow**:** Orientation is 5' to 3', consistent with the direction of translation. Because positional numbering along a chromosome is from left to right and transcription takes place from 5' to 3', precede and follow can appear to have 'opposite' behavior on the + and − strand. Using positions 5 and 6 as an example, 5 precedes 6 on the + strand but follows 6 on the − strand.

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

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

distanceToNearest**:** Returns the distance for each range in x to its nearest neighbor in the subject.

distance**:** Returns the distance for each range in x to the range in y. The behavior of distance has changed in Bioconductor 2.12. See the man page ?distance in the **IRanges** package for details.

Value

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

For nearestKNeighbors, an IntegerList of vertices in subject.

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

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

Author(s)

P. Aboyoun and V. Obenchain

See Also

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

Examples

```
## ---------------------------------------------------------
## precede() and follow()
## ---------------------------------------------------------
query <- GRanges("A", IRanges(c(5, 20), width=1), strand="+")
subject <- GRanges("A", IRanges(rep(c(10, 15), 2), width=1),
                        strand=c("+", "+", "-", "-"))
precede(query, subject)
follow(query, subject)

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

## ties choose first in order
query <- GRanges("A", IRanges(10, width=1), c("+", "-", "*"))
subject <- GRanges("A", IRanges(c(5, 5, 5, 15, 15, 15), width=1),
                        rep(c("+", "-", "*"), 2))
precede(query, subject)
precede(query, rev(subject))

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

## ---------------------------------------------------------
## nearest()
## ---------------------------------------------------------
## When multiple ranges overlap an "arbitrary" range is chosen
query <- GRanges("A", IRanges(5, 15))
subject <- GRanges("A", IRanges(c(1, 15), c(5, 19)))
nearest(query, subject)

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

## Ranges in 'x' will self-select when 'subject' is present
query <- GRanges("A", IRanges(c(1, 10), width=5))
nearest(query, query)

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

## ---------------------------------------------------------
## nearestKNeighbors()
## ---------------------------------------------------------
## Without an argument, k defaults to 1
query <- GRanges("A", IRanges(c(2, 5), c(8, 15)))
subject <- GRanges("A", IRanges(c(1, 4, 10, 15), c(5, 7, 12, 19)))
nearestKNeighbors(query, subject)

## Return multiple neighbors with k > 1
nearestKNeighbors(query, subject, k=3)

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

```
## ----------------------------------------------------------
## distance(), distanceToNearest()
## ----------------------------------------------------------
## Adjacent, overlap, separated by 1
query <- GRanges("A", IRanges(c(1, 2, 10), c(5, 8, 11)))
subject <- GRanges("A", IRanges(c(6, 5, 13), c(10, 10, 15)))
distance(query, subject)

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

## zero-width ranges
zw <- GRanges("A", IRanges(4,3))
stopifnot(distance(zw, GRanges("A", IRanges(3,4))) == 0L)
sapply(-3:3, function(i)
    distance(shift(zw, i), GRanges("A", IRanges(4,3))))

query <- GRanges(c("A", "B"), IRanges(c(1, 5), width=1))
distanceToNearest(query, subject)

## distance() with GRanges and TxDb see the
## ?'distance,GenomicRanges,TxDb-method' man
## page in the GenomicFeatures package.
```

---

phicoef	*Calculate the "phi coefficient" between two binary variables*

Description

The `phicoef` function calculates the "phi coefficient" between two binary variables.

Usage

```
phicoef(x, y=NULL)
```

Arguments

x, y   Two logical vectors of the same length. If y is not supplied, x must be a 2x2 integer matrix (or an integer vector of length 4) representing the contingency table of two binary variables.

Value

The "phi coefficient" between the two binary variables. This is a single numeric value ranging from -1 to +1.

Author(s)

H. Pagès

References

http://en.wikipedia.org/wiki/Phi_coefficient

Examples

```
set.seed(33)
x <- sample(c(TRUE, FALSE), 100, replace=TRUE)
y <- sample(c(TRUE, FALSE), 100, replace=TRUE)
phicoef(x, y)
phicoef(rep(x, 10), c(rep(x, 9), y))

stopifnot(phicoef(table(x, y)) == phicoef(x, y))
stopifnot(phicoef(y, x) == phicoef(x, y))
stopifnot(phicoef(x, !y) == - phicoef(x, y))
stopifnot(phicoef(x, x) == 1)
```

---

setops-methods   *Set operations on genomic ranges*

Description

Performs set operations on GRanges and GRangesList objects.

NOTE: The `punion`, `pintersect`, `psetdiff`, and `pgap` generic functions and methods for IntegerRanges objects are defined and documented in the **IRanges** package.

Usage

```
## Vector-wise set operations
## ------------------------

## S4 method for signature 'GenomicRanges,GenomicRanges'
union(x, y, ignore.strand=FALSE)

## S4 method for signature 'GenomicRanges,GenomicRanges'
intersect(x, y, ignore.strand=FALSE)

## S4 method for signature 'GenomicRanges,GenomicRanges'
setdiff(x, y, ignore.strand=FALSE)

## Element-wise (aka "parallel") set operations
## -------------------------------------------

## S4 method for signature 'GRanges,GRanges'
punion(x, y, fill.gap=FALSE, ignore.strand=FALSE)

## S4 method for signature 'GRanges,GRanges'
pintersect(x, y, drop.nohit.ranges=FALSE,
           ignore.strand=FALSE, strict.strand=FALSE)

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

Arguments

x, y   For union, intersect, and setdiff: 2 GenomicRanges objects or 2 GRanges-List objects.

              For punion and pintersect: 2 GRanges objects, or 1 GRanges object and 1 GRangesList object.

              For psetdiff: x must be a GRanges object and y can be a GRanges or GRanges-List object.

              For pgap: 2 GRanges objects.

              In addition, for the *parallel* operations, x and y must be of equal length (i.e. length(x) == length(y)).

fill.gap   Logical indicating whether or not to force a union by using the rule start = min(start(x), start(y)), end = max(end(x), end(y)).

ignore.strand For set operations: If set to TRUE, then the strand of x and y is set to "*" prior to any computation.

              For parallel set operations: If set to TRUE, the strand information is ignored in the computation and the result has the strand information of x.

drop.nohit.ranges

              If TRUE then elements in x that don't intersect with their corresponding element in y are removed from the result (so the returned object is no more parallel to the input).

              If FALSE (the default) then nothing is removed and a hit metadata column is added to the returned object to indicate elements in x that intersect with the corresponding element in y. For those that don't, the reported intersection is a zero-width range that has the same start as x.

strict.strand If set to FALSE (the default), features on the "*" strand are treated as occurring on both the "+" and "-" strand. If set to TRUE, the strand of intersecting elements must be strictly the same.

Details

The pintersect methods involving GRanges and/or GRangesList objects use the triplet (sequence name, range, strand) to determine the element by element intersection of features, where a strand value of "*" is treated as occurring on both the "+" and "-" strand (unless strict.strand is set to TRUE, in which case the strand of intersecting elements must be strictly the same).

The psetdiff methods involving GRanges and/or GRangesList objects use the triplet (sequence name, range, strand) to determine the element by element set difference of features, where a strand value of "*" is treated as occurring on both the "+" and "-" strand.

Value

For union, intersect, and setdiff: a GRanges object if x and y are GenomicRanges objects, and a GRangesList object if they are GRangesList objects.

For punion and pintersect: when x or y is not a GRanges object, an object of the same class as this non-GRanges object. Otherwise, a GRanges object.

For psetdiff: either a GRanges object when both x and y are GRanges objects, or a GRangesList object when y is a GRangesList object.

For pgap: a GRanges object.

Author(s)

P. Aboyoun and H. Pagès

See Also

- subtract for subtracting a set of genomic ranges from a GRanges object (similar to bedtools subtract).

- setops-methods in the **IRanges** package for set operations on IntegerRanges and IntegerRanges-List objects.

- findOverlaps-methods for finding/counting overlapping genomic ranges.

- intra-range-methods and inter-range-methods for *intra range* and *inter range* transformations of a GRanges object.

- GRanges and GRangesList objects.

- mendoapply in the **S4Vectors** package.

Examples

```
## ---------------------------------------------------------------------
## A. SET OPERATIONS
## ---------------------------------------------------------------------

x <- GRanges("chr1", IRanges(c(2, 9) , c(7, 19)), strand=c("+", "-"))
y <- GRanges("chr1", IRanges(5, 10), strand="-")

union(x, y)
union(x, y, ignore.strand=TRUE)

intersect(x, y)
intersect(x, y, ignore.strand=TRUE)

setdiff(x, y)
setdiff(x, y, ignore.strand=TRUE)

## With 2 GRangesList objects:
gr1 <- GRanges(seqnames="chr2",
               ranges=IRanges(3, 6))
gr2 <- GRanges(seqnames=c("chr1", "chr1"),
               ranges=IRanges(c(7,13), width = 3),
               strand=c("+", "-"))
gr3 <- GRanges(seqnames=c("chr1", "chr2"),
               ranges=IRanges(c(1, 4), c(3, 9)),
               strand=c("-", "-"))
grlist <- GRangesList(gr1=gr1, gr2=gr2, gr3=gr3)

union(grlist, shift(grlist, 3))
intersect(grlist, shift(grlist, 3))
setdiff(grlist, shift(grlist, 3))

## Sanity checks:
grlist2 <- shift(grlist, 3)
stopifnot(identical(
    union(grlist, grlist2),
    mendoapply(union, grlist, grlist2)
))
```

```
stopifnot(identical(
    intersect(grlist, grlist2),
    mendoapply(intersect, grlist, grlist2)
))
stopifnot(identical(
    setdiff(grlist, grlist2),
    mendoapply(setdiff, grlist, grlist2)
))

## ---------------------------------------------------------------------
## B. PARALLEL SET OPERATIONS
## ---------------------------------------------------------------------

punion(x, shift(x, 6))
## Not run:
punion(x, shift(x, 7))  # will fail

## End(Not run)
punion(x, shift(x, 7), fill.gap=TRUE)

pintersect(x, shift(x, 6))
pintersect(x, shift(x, 7))

psetdiff(x, shift(x, 7))


## ---------------------------------------------------------------------
## C. MORE EXAMPLES
## ---------------------------------------------------------------------

## GRanges object:
gr <- GRanges(seqnames=c("chr2", "chr1", "chr1"),
              ranges=IRanges(1:3, width = 12),
              strand=Rle(strand(c("-", "*", "-"))))

## Parallel intersection of a GRanges and a GRangesList object
pintersect(gr, grlist)
pintersect(grlist, gr)

## For a fast 'mendoapply(intersect, grlist, as(gr, "GRangesList"))'
## call pintersect() with 'strict.strand=TRUE' and call reduce() on
## the result with 'drop.empty.ranges=TRUE':
reduce(pintersect(grlist, gr, strict.strand=TRUE),
       drop.empty.ranges=TRUE)

## Parallel set difference of a GRanges and a GRangesList object
psetdiff(gr, grlist)
```

---

strand-utils   *Strand utilities*

Description

A bunch of useful `strand` and `invertStrand` methods.

Usage

```
## S4 method for signature 'missing'
strand(x)
## S4 method for signature 'character'
strand(x)
## S4 method for signature 'factor'
strand(x)
## S4 method for signature 'integer'
strand(x)
## S4 method for signature 'logical'
strand(x)
## S4 method for signature 'Rle'
strand(x)
## S4 method for signature 'RleList'
strand(x)
## S4 method for signature 'DataFrame'
strand(x)
## S4 replacement method for signature 'DataFrame,ANY'
strand(x) <- value

## S4 method for signature 'character'
invertStrand(x)
## S4 method for signature 'factor'
invertStrand(x)
## S4 method for signature 'integer'
invertStrand(x)
## S4 method for signature 'logical'
invertStrand(x)
## S4 method for signature 'Rle'
invertStrand(x)
## S4 method for signature 'RleList'
invertStrand(x)
```

Arguments

x   The object from which to obtain a *strand factor*, *strand factor Rle*, or *strand factor RleList* object. Can be missing. See Details and Value sections below for more information.

value   Replacement value for the strand.

Details

All the `strand` and `invertStrand` methods documented here return either a *strand factor*, *strand factor Rle*, or *strand factor RleList* object. These are factor, factor-Rle, or factor-RleList objects containing the "standard strand levels" (i.e. +, -, and *) and no NAs.

Value

All the `strand` and `invertStrand` methods documented here return an object that is *parallel* to input object x when x is a character, factor, integer, logical, Rle, or RleList object.

For the `strand` methods:

- If x is missing, returns an empty factor with the "standard strand levels" i.e. +, -, and *.
- If x is a character vector or factor, it is coerced to a factor with the levels listed above. NA values in x are not accepted.
- If x is an integer vector, it is coerced to a factor with the levels listed above. 1, -1, and NA values in x are mapped to the +, -, and * levels respectively.
- If x is a logical vector, it is coerced to a factor with the levels listed above. FALSE, TRUE, and NA values in x are mapped to the +, -, and * levels respectively.
- If x is a character-, factor-, integer-, or logical-Rle, it is transformed with runValue(x) <- strand(runValue(x)) and returned.
- If x is an RleList object, each list element in x is transformed by calling strand() on it and the resulting RleList object is returned. More precisely the returned object is endoapply(x, strand). Note that in addition to being *parallel* to x, this object also has the same *shape* as x (i.e. its list elements have the same lengths as in x).
- If x is a DataFrame object, the "strand" column is passed thru strand() and returned. If x has no "strand" column, this return value is populated with *s.

Each invertStrand method returns the same object as its corresponding strand method but with "+" and "-" switched.

Author(s)

M. Lawrence and H. Pagès

See Also

strand

Examples

```
strand()

x1 <- c("-", "*", "*", "+", "-", "*")
x2 <- factor(c("-", "-", "+", "-"))
x3 <- c(-1L, NA, NA, 1L, -1L, NA)
x4 <- c(TRUE, NA, NA, FALSE, TRUE, NA)

strand(x1)
invertStrand(x1)
strand(x2)
invertStrand(x2)
strand(x3)
invertStrand(x3)
strand(x4)
invertStrand(x4)

strand(Rle(x1))
invertStrand(Rle(x1))
strand(Rle(x2))
invertStrand(Rle(x2))
strand(Rle(x3))
invertStrand(Rle(x3))
strand(Rle(x4))
invertStrand(Rle(x4))
```

```
x5 <- RleList(x1, character(0), as.character(x2))
strand(x5)
invertStrand(x5)

strand(DataFrame(score=2:-3))
strand(DataFrame(score=2:-3, strand=x3))
strand(DataFrame(score=2:-3, strand=Rle(x3)))

## Sanity checks:
target <- strand(x1)
stopifnot(identical(target, strand(x3)))
stopifnot(identical(target, strand(x4)))

stopifnot(identical(Rle(strand(x1)), strand(Rle(x1))))
stopifnot(identical(Rle(strand(x2)), strand(Rle(x2))))
stopifnot(identical(Rle(strand(x3)), strand(Rle(x3))))
stopifnot(identical(Rle(strand(x4)), strand(Rle(x4))))
```

---

subtract-methods   *Subtract a set of genomic ranges from a GRanges object*

Description

Similar to bedtools subtract.

Usage

```
subtract(x, y, minoverlap=1L, ...)

## S4 method for signature 'GenomicRanges,GenomicRanges'
subtract(x, y, minoverlap=1L, ignore.strand=FALSE)
```

Arguments

x, y   Two [GRanges](#) objects, typically, but any [GenomicRanges](#) derivative should be
                supported. Note that y gets immediately replaced with:

                    reduce(y, ignore.strand=ignore.strand)

                internally.

minoverlap   Minimum overlap (in number of genomic positions) between a range in x and
                a range in reduce(y, ignore.strand=ignore.strand) for the 2 ranges to be
                considered overlapping, and for their overlapping portion to be removed from
                the range in x.

ignore.strand   If set to TRUE, the strand information is ignored in the computation and the
                strand of x is propagated to the result.

...   Further arguments to be passed to specific methods.

Details

subtract() first replaces its second argument y with:

```
reduce(y, ignore.strand=ignore.strand)
```

Then it searches for genomic ranges in y that overlap genomic ranges in x by at least the number of base pairs specified via the minoverlap argument. If an overlapping range is found in y, the overlapping portion is removed from any range in x involved in the overlap.

Note that by default subtract(x, y) is equivalent to:

```
psetdiff(x, rep(GRangesList(y), length(x)))
```

but will typically be hundred times more efficient.

Value

A GRangesList object *parallel* to x, that is, with one list element per range in x. The names and metadata columns on x are propagated to the result.

Author(s)

H. Pagès

See Also

- bedtools subtract at https://bedtools.readthedocs.io/en/latest/content/tools/subtract.html

- setops-methods for set operations on GRanges objects.

- findOverlaps-methods for finding/counting overlapping genomic ranges.

- intra-range-methods and inter-range-methods for *intra range* and *inter range* transformations of a GRanges object.

- GRanges and GRangesList objects.

Examples

```
x <- GRanges(c(A="chr1:1-50", B="chr1:40-110", C="chrX:1-500"))
y <- GRanges(c("chr1:21-25", "chr1:38-150"))
z <- subtract(x, y)
z

unlist(z)
```

---

tile-methods   *Generate windows for a GenomicRanges*

Description

[tile](#) and [slidingWindows](#) methods for [GenomicRanges](#). tile partitions each range into a set
of tiles, which are defined in terms of their number or width. slidingWindows generates sliding
windows of a specified width and frequency.

Usage

```
## S4 method for signature 'GenomicRanges'
tile(x, n, width)
## S4 method for signature 'GenomicRanges'
slidingWindows(x, width, step=1L)
```

Arguments

x	A [GenomicRanges](#) object, like a GRanges.
n	The number of tiles to generate. See ?[tile](#) in the **IRanges** package for more information about this argument.
width	The (maximum) width of each tile. See ?[tile](#) in the **IRanges** package for more information about this argument.
step	The distance between the start positions of the sliding windows.

Details

The tile function splits x into a GRangesList, each element of which corresponds to a tile, or
partition, of x. Specify the tile geometry with either n or width (not both). Passing n creates n tiles
of approximately equal width, truncated by sequence end, while passing width tiles the region with
ranges of the given width, again truncated by sequence end.

The slidingWindows function generates sliding windows within each range of x, according to
width and step, returning a GRangesList. If the sliding windows do not exactly cover a range in
x, the last window is partial.

Value

A GRangesList object, each element of which corresponds to a window.

Author(s)

M. Lawrence

See Also

[tile](#) in the **IRanges** package.

Examples

```
gr <- GRanges(
        seqnames=Rle(c("chr1", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
        ranges=IRanges(1:10, end=11),
        strand=Rle(strand(c("-", "+", "*", "+", "-")), c(1, 2, 2, 3, 2)),
        seqlengths=c(chr1=11, chr2=12, chr3=13))

# split every range in half
tiles <- tile(gr, n = 2L)
stopifnot(all(elementNROWS(tiles) == 2L))

# split ranges into subranges of width 2
# odd width ranges must contain one subrange of width 1
tiles <- tile(gr, width = 2L)
stopifnot(all(all(width(tiles) %in% c(1L, 2L))))

windows <- slidingWindows(gr, width=3L, step=2L)
width(windows[[1L]]) # last range is truncated
```

---

tileGenome	*Put (virtual) tiles on a given genome*

Description

`tileGenome` returns a set of genomic regions that form a partitioning of the specified genome. Each region is called a "tile".

Usage

```
tileGenome(seqlengths, ntile, tilewidth, cut.last.tile.in.chrom=FALSE)
```

Arguments

seqlengths   Either a named numeric vector of chromosome lengths or a [Seqinfo](#) object. More precisely, if a named numeric vector, it must have a length >= 1, cannot contain NAs or negative values, and cannot have duplicated names. If a [Seqinfo](#) object, then it's first replaced with the vector of sequence lengths stored in the object (extracted from the object with the [seqlengths](#) getter), then the restrictions described previously apply to this vector.

ntile   The number of tiles to generate.

tilewidth   The desired tile width. The effective tile width might be slightly different but is guaranteed to never be more than the desired width.

cut.last.tile.in.chrom

               Whether or not to cut the last tile in each chromosome. This is set to `FALSE` by default. Can be set to `TRUE` only when `tilewidth` is specified. In that case, a tile will never overlap with more than 1 chromosome and a [GRanges](#) object is returned with one element (i.e. one genomic range) per tile.

Value

If cut.last.tile.in.chrom is FALSE (the default), a GRangesList object with one list element per tile, each of them containing a number of genomic ranges equal to the number of chromosomes it overlaps with. Note that when the tiles are small (i.e. much smaller than the chromosomes), most of them only overlap with a single chromosome.

If cut.last.tile.in.chrom is TRUE, a GRanges object with one element (i.e. one genomic range) per tile.

Author(s)

H. Pagès, based on a proposal by M. Morgan

See Also

- genomicvars for an example of how to compute the binned average of a numerical variable defined along a genome.
- GRangesList and GRanges objects.
- Seqinfo objects and the seqlengths getter.
- IntegerList objects.
- Views objects.

Examples

```
## ---------------------------------------------------------------------
## A. WITH A TOY GENOME
## ---------------------------------------------------------------------

seqlengths <- c(chr1=60, chr2=20, chr3=25)

## Create 5 tiles:
tiles <- tileGenome(seqlengths, ntile=5)
tiles
elementNROWS(tiles)  # tiles 3 and 4 contain 2 ranges

width(tiles)
## Use sum() on this IntegerList object to get the effective tile
## widths:
sum(width(tiles))  # each tile covers exactly 21 genomic positions

## Create 9 tiles:
tiles <- tileGenome(seqlengths, ntile=9)
elementNROWS(tiles)  # tiles 6 and 7 contain 2 ranges

table(sum(width(tiles)))  # some tiles cover 12 genomic positions,
                          # others 11

## Specify the tile width:
tiles <- tileGenome(seqlengths, tilewidth=20)
length(tiles)  # 6 tiles
table(sum(width(tiles)))  # effective tile width is <= specified

## Specify the tile width and cut the last tile in each chromosome:
tiles <- tileGenome(seqlengths, tilewidth=24,
                    cut.last.tile.in.chrom=TRUE)
```

```
tiles
width(tiles)  # each tile covers exactly 24 genomic positions, except
              # the last tile in each chromosome

## Partition a genome by chromosome ("natural partitioning"):
tiles <- tileGenome(seqlengths, tilewidth=max(seqlengths),
                    cut.last.tile.in.chrom=TRUE)
tiles  # one tile per chromosome

## sanity check
stopifnot(all.equal(setNames(end(tiles), seqnames(tiles)), seqlengths))

## ---------------------------------------------------------------------
## B. WITH A REAL GENOME
## ---------------------------------------------------------------------

library(BSgenome.Scerevisiae.UCSC.sacCer2)
tiles <- tileGenome(seqinfo(Scerevisiae), ntile=20)
tiles

tiles <- tileGenome(seqinfo(Scerevisiae), tilewidth=50000,
                    cut.last.tile.in.chrom=TRUE)
tiles

## ---------------------------------------------------------------------
## C. AN APPLICATION: COMPUTE THE BINNED AVERAGE OF A NUMERICAL VARIABLE
##    DEFINED ALONG A GENOME
## ---------------------------------------------------------------------

## See '?genomicvars' for an example of how to compute the binned
## average of a numerical variable defined along a genome.
```

Index