Package ‘GenomicAlignments’

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Title Representation and manipulation of short genomic alignments

Description Provides efficient containers for storing and manipulating short genomic alignments (typically obtained by aligning short reads to a reference genome). This includes read counting, computing the coverage, junction detection, and working with the nucleotide content of the alignments.

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Encoding UTF-8

Author Hervé Pagès, Valerie Obenchain, Martin Morgan

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

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Imports methods, utils, stats, BiocGenerics, S4Vectors, IRanges, GenomicRanges, Biostrings, Rsamtools, BiocParallel

LinkingTo S4Vectors, IRanges


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Video https://www.youtube.com/watch?v=2KqBShkfhRo, https://www.youtube.com/watch?v=3PK_jx44QTs
cigar-utils

Description
Utility functions for low-level CIGAR manipulation.

Usage
## -=-= Supported CIGAR operations -=-=
CIGAR_OPS

## -=-= Transform CIGARs into other useful representations -=-=
explodeCigarOps(cigar, ops=CIGAR_OPS)
explodeCigarOpLengths(cigar, ops=CIGAR_OPS)
cigarToRleList(cigar)

## -=-= Summarize CIGARs -=-=
cigarOpTable(cigar)

## -=-= From CIGARs to ranges -=-=
cigarRangesAlongReferenceSpace(cigar, flag=NULL,
   N.regions.removed=FALSE, pos=1L, f=NULL,
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ops=CIGAR_OPS, drop.empty.ranges=FALSE, reduce.ranges=FALSE, with.ops=FALSE)

cigarRangesAlongQuerySpace(cigar, flag=NULL,
before.hard.clipping=FALSE, after.soft.clipping=FALSE,
ops=CIGAR_OPS, drop.empty.ranges=FALSE, reduce.ranges=FALSE, with.ops=FALSE)

cigarRangesAlongPairwiseSpace(cigar, flag=NULL,
N.regions.removed=FALSE, dense=FALSE,
ops=CIGAR_OPS, drop.empty.ranges=FALSE, reduce.ranges=FALSE, with.ops=FALSE)

extractAlignmentRangesOnReference(cigar, pos=1L,
drop.D.ranges=FALSE, f=NULL)

## -=-= From CIGARs to sequence lengths =-=-
cigarWidthAlongReferenceSpace(cigar, flag=NULL,
N.regions.removed=FALSE)
cigarWidthAlongQuerySpace(cigar, flag=NULL,
before.hard.clipping=FALSE, after.soft.clipping=FALSE)
cigarWidthAlongPairwiseSpace(cigar, flag=NULL,
N.regions.removed=FALSE, dense=FALSE)

## -=-= Narrow CIGARs =-=-
cigarNarrow(cigar, start=NA, end=NA, width=NA)
cigarQNarrow(cigar, start=NA, end=NA, width=NA)

## -=-= Translate coordinates between query and reference spaces =-=-
queryLoc2refLoc(qloc, cigar, pos=1L)
queryLocs2refLocs(qlocs, cigar, pos=1L, flag=NULL)

Arguments

cigar A character vector or factor containing the extended CIGAR strings. It can be of arbitrary length except for queryLoc2refLoc which only accepts a single CIGAR (as a character vector or factor of length 1).

ops Character vector containing the extended CIGAR operations to actually consider. Zero-length operations or operations not listed ops are ignored.

flag NULL or an integer vector containing the SAM flag for each read. According to the SAM Spec v1.4, flag bit 0x4 is the only reliable place to tell whether a segment (or read) is mapped (bit is 0) or not (bit is 1). If flag is supplied, then cigarRangesAlongReferenceSpace, cigarRangesAlongQuerySpace, cigarRangesAlongPairwiseSpace, and extractAlignmentRangesOnReference don’t produce any range for unmapped reads i.e. they treat them as if their CIGAR was empty (independently of what their CIGAR is). If flag is supplied, then cigarWidthAlongReferenceSpace, cigarWidthAlongQuerySpace, and cigarWidthAlongPairwiseSpace return NA for unmapped reads.

N.regions.removed TRUE or FALSE. If TRUE, then cigarRangesAlongReferenceSpace and cigarWidthAlongReference
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Report ranges/widths with respect to the "reference" space from which the N regions have been removed, and `cigarRangesAlongPairwiseSpace` and `cigarWidthAlongPairwiseSpace` report them with respect to the "pairwise" space from which the N regions have been removed.

pos
An integer vector containing the 1-based leftmost position/coordinate for each (eventually clipped) read sequence. Must have length 1 (in which case it's recycled to the length of `cigar`), or the same length as `cigar`.

f
NULL or a factor of length `cigar`. If NULL, then the ranges are grouped by alignment i.e. the returned `IRangesList` object has 1 list element per element in `cigar`. Otherwise they are grouped by factor level i.e. the returned `IRangesList` object has 1 list element per level in `f` and is named with those levels.

For example, if `f` is a factor containing the chromosome for each read, then the returned `IRangesList` object will have 1 list element per chromosome and each list element will contain all the ranges on that chromosome.

drop.empty.ranges
Should empty ranges be dropped?

reduce.ranges
Should adjacent ranges coming from the same cigar be merged or not? Using TRUE can significantly reduce the size of the returned object.

with.ops
TRUE or FALSE indicating whether the returned ranges should be named with their corresponding CIGAR operation.

before.hard.clipping
TRUE or FALSE. If TRUE, then `cigarRangesAlongQuerySpace` and `cigarWidthAlongQuerySpace` report ranges/widths with respect to the "query" space to which the H regions have been added. `before.hard.clipping` and `after.soft.clipping` cannot both be TRUE.

after.soft.clipping
TRUE or FALSE. If TRUE, then `cigarRangesAlongQuerySpace` and `cigarWidthAlongQuerySpace` report ranges/widths with respect to the "query" space from which the S regions have been removed. `before.hard.clipping` and `after.soft.clipping` cannot both be TRUE.

dense
TRUE or FALSE. If TRUE, then `cigarRangesAlongPairwiseSpace` and `cigarWidthAlongPairwiseSpace` report ranges/widths with respect to the "pairwise" space from which the I, D, and N regions have been removed. `N.regions.removed` and `dense` cannot both be TRUE.

drop.D.ranges
Should the ranges corresponding to a deletion from the reference (encoded with a D in the CIGAR) be dropped? By default we keep them to be consistent with the pileup tool from SAMtools. Note that, when `drop.D.ranges` is TRUE, then Ds and Ns in the CIGAR are equivalent.

start,end,width
Vectors of integers. NAs and negative values are accepted and "solved" according to the rules of the SEW (Start/End/Width) interface (see `solveUserSEW` for the details).

qloc
An integer vector containing "query-based locations" i.e. 1-based locations relative to the query sequence stored in the SAM/BAM file.

qlocs
A list of the same length as `cigar` where each element is an integer vector containing "query-based locations" i.e. 1-based locations relative to the corresponding query sequence stored in the SAM/BAM file.
CIGAR_OPS is a predefined character vector containing the supported extended CIGAR operations: M, I, D, N, S, H, P, =, X. See p. 4 of the SAM Spec v1.4 at http://samtools.sourceforge.net/ for the list of extended CIGAR operations and their meanings.

For explodeCigarOps and explodeCigarOpLengths: Both functions return a list of the same length as cigar where each list element is a character vector (for explodeCigarOps) or an integer vector (for explodeCigarOpLengths). The 2 lists have the same shape, that is, same length() and same elementNROWS(). The i-th character vector in the list returned by explodeCigarOps contains one single-letter string per CIGAR operation in cigar[i]. The i-th integer vector in the list returned by explodeCigarOpLengths contains the corresponding CIGAR operation lengths. Zero-length operations or operations not listed in ops are ignored.

For cigarToRleList: A CompressedRleList object.

For cigarOpTable: An integer matrix with number of rows equal to the length of cigar and nine columns, one for each extended CIGAR operation.

For cigarRangesAlongReferenceSpace, cigarRangesAlongQuerySpace, cigarRangesAlongPairwiseSpace, and extractAlignmentRangesOnReference: An IRangesList object (more precisely a CompressedIRangesList object) with 1 list element per element in cigar. However, if f is a factor, then the returned IRangesList object can be a SimpleIRangesList object (instead of CompressedIRangesList), and in that case, has 1 list element per level in f and is named with those levels.

For cigarWidthAlongReferenceSpace and cigarWidthAlongPairwiseSpace: An integer vector of the same length as cigar where each element is the width of the alignment with respect to the "reference" and "pairwise" space, respectively. More precisely, for cigarWidthAlongReferenceSpace, the returned widths are the lengths of the alignments on the reference, N gaps included (except if N.regions.removed is TRUE). NAs or "*" in cigar will produce NAs in the returned vector.

For cigarWidthAlongQuerySpace: An integer vector of the same length as cigar where each element is the length of the corresponding query sequence as inferred from the CIGAR string. Note that, by default (i.e. if before.hard.clipping and after.soft.clipping are FALSE), this is the length of the query sequence stored in the SAM/BAM file. If before.hard.clipping or after.soft.clipping is TRUE, the returned widths are the lengths of the query sequences before hard clipping or after soft clipping. NAs or "*" in cigar will produce NAs in the returned vector.

For cigarNarrow and cigarQNarrow: A character vector of the same length as cigar containing the narrowed cigars. In addition the vector has an "rshift" attribute which is an integer vector of the same length as cigar. It contains the values that would need to be added to the POS field of a SAM/BAM file as a consequence of this cigar narrowing.

For queryLoc2refLoc: An integer vector of the same length as qloc containing the "reference-based locations" (i.e. the 1-based locations relative to the reference sequence) corresponding to the "query-based locations" passed in qloc.

For queryLocs2refLocs: A list of the same length as qlocs where each element is an integer vector containing the "reference-based locations" corresponding to the "query-based locations" passed in the corresponding element in qlocs.

Author(s)
Hervé Pagès & P. Aboyoun

References
http://samtools.sourceforge.net/
See Also

- The `sequenceLayer` function in the `GenomicAlignments` package for laying the query sequences alongside the "reference" or "pairwise" spaces.
- The `GAlignments` container for storing a set of genomic alignments.
- The `IRanges, IRangesList, and RleList` classes in the `IRanges` package.
- The `coverage` generic and methods for computing the coverage across a set of ranges or genomic ranges.

Examples

```r
### ---------------------------------------------------------------------
### A. CIGAR_OPS, explodeCigarOps(), explodeCigarOpLengths(),
###    cigarToRleList(), and cigarOpTable()
### ---------------------------------------------------------------------
### Supported CIGAR operations:
### CIGAR_OPS
### Transform CIGARs into other useful representations:
### cigar1 <- "3H15M55N4M210N25M6S"
### cigar2 <- c("40M2I9M", cigar1, "2S10M2000N15M", "3H33M5H")
### explodeCigarOps(cigar2)
### explodeCigarOpLengths(cigar2)
### explodeCigarOpLengths(cigar2, ops=c("I", "S"))
### cigarToRleList(cigar2)
### Summarize CIGARs:
### cigarOpTable(cigar2)
### ---------------------------------------------------------------------
### B. From CIGARs to ranges and to sequence lengths
### ---------------------------------------------------------------------
### CIGAR ranges along the "reference" space:
### cigarRangesAlongReferenceSpace(cigar1, with.ops=TRUE)[[1]]
### cigarRangesAlongReferenceSpace(cigar1, with.ops=TRUE)[[1]]
### ops <- setdiff(CIGAR_OPS, "N")
### cigarRangesAlongReferenceSpace(cigar1, ops=ops, with.ops=TRUE)[[1]]
### cigarRangesAlongReferenceSpace(cigar1, ops=ops, reduce.ranges=TRUE, with.ops=TRUE)[[1]]
### ops <- setdiff(CIGAR_OPS, c("D", "N"))
### cigarRangesAlongReferenceSpace(cigar1, ops=ops, with.ops=TRUE)[[1]]
### cigarWidthAlongReferenceSpace(cigar1)
### pos2 <- c(1, 1001, 1, 351)
```
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```r
cigarRangesAlongReferenceSpace(cigar2, pos=pos2, with.ops=TRUE)
res1a <- extractAlignmentRangesOnReference(cigar2, pos=pos2)
res1b <- cigarRangesAlongReferenceSpace(cigar2,
pos=pos2,
ops=setdiff(CIGAR_OPS, "N"),
reduce.ranges=TRUE)
stopifnot(identical(res1a, res1b))
res2a <- extractAlignmentRangesOnReference(cigar2, pos=pos2,
drop.D.ranges=TRUE)
res2b <- cigarRangesAlongReferenceSpace(cigar2,
pos=pos2,
ops=setdiff(CIGAR_OPS, c("D", "N")),
reduce.ranges=TRUE)
stopifnot(identical(res2a, res2b))
seqnames <- factor(c("chr6", "chr6", "chr2", "chr6"),
levels=c("chr2", "chr6"))
extractAlignmentRangesOnReference(cigar2, pos=pos2, f=seqnames)
## CIGAR ranges along the "query" space:
cigarRangesAlongQuerySpace(cigar2, with.ops=TRUE)
cigarWidthAlongQuerySpace(cigar1)
cigarWidthAlongQuerySpace(cigar1, before.hard.clipping=TRUE)
## CIGAR ranges along the "pairwise" space:
cigarRangesAlongPairwiseSpace(cigar2, with.ops=TRUE)
cigarRangesAlongPairwiseSpace(cigar2, dense=TRUE, with.ops=TRUE)
```

---

## C. COMPUTE THE COVERAGE OF THE READS STORED IN A BAM FILE

The information stored in a BAM file can be used to compute the "coverage" of the mapped reads i.e. the number of reads that hit any given position in the reference genome.

The following function takes the path to a BAM file and returns an object representing the coverage of the mapped reads that are stored in the file. The returned object is an RleList object named with the names of the reference sequences that actually receive some coverage.

```r
flag0 <- scanBamFlag(isUnmappedQuery=FALSE, isDuplicate=FALSE)
extractCoverageFromBAM <- function(bamfile)
{
  stopifnot(is(bamfile, "BamFile"))
  ## This ScanBamParam object allows us to load only the necessary
  ## information from the file.
  param <- ScanBamParam(flag=flag0, what=c("rname", "pos", "cigar"))
  bam <- scanBam(bamfile, param=param)[[1]]
  ## Note that unmapped reads and reads that are PCR/optical duplicates
  ## have already been filtered out by using the ScanBamParam object
  ## above.
  f <- factor(bam$rname, levels=seqlevels(bamfile))
  irl <- extractAlignmentRangesOnReference(bam$cigar, pos=bam$pos, f=f)
  coverage(irl, width=seqlengths(bamfile))
}
```
library(Rsamtools)
f1 <- system.file("extdata", "ex1.bam", package="Rsamtools")
cvg <- extractCoverageFromBAM(BamFile(f1))

## extractCoverageFromBAM() is equivalent but slightly more efficient
## than loading a GAlignments object and computing its coverage:
cvg2 <- coverage(readGAlignments(f1, param=ScanBamParam(flag=flag0)))
stopifnot(identical(cvg, cvg2))

## D. cigarNarrow() and cigarQNarrow()
## ---------------------------------------------------------------------

## cigarNarrow():
cigarNarrow(cigar1) # only drops the soft/hard clipping
       cigarNarrow(cigar1, start=10)
cigarNarrow(cigar1, start=15)
cigarNarrow(cigar1, start=15, width=57)
cigarNarrow(cigar1, start=16)
#cigarNarrow(cigar1, start=16, width=55) # ERROR! (empty cigar)
cigarNarrow(cigar1, start=71)
cigarNarrow(cigar1, start=72)
cigarNarrow(cigar1, start=75)

## cigarQNarrow():
cigarQNarrow(cigar1, start=4, end=-3)
cigarQNarrow(cigar1, start=10)
cigarQNarrow(cigar1, start=19)
cigarQNarrow(cigar1, start=24)

## E. PERFORMANCE
## ---------------------------------------------------------------------

if (interactive()) {
## We simulate 20 millions aligned reads, all 40-mers. 95% of them
## align with no indels. 5% align with a big deletion in the
## reference. In the context of an RNAseq experiment, those 5% would
## be suspected to be "junction reads".
set.seed(123)
nreads <- 20000000L
njunctionreads <- nreads * 5L / 100L
cigar3 <- character(nreads)
cigar3[] <- "40M"
junctioncigars <- paste(
    paste(10:30, "M", sep=""),
    paste(sample(80:8000, njunctionreads, replace=TRUE), "M", sep=""),
    paste(30:10, "M", sep=""), sep="")
cigar3[sample(nreads, njunctionreads)] <- junctioncigars
some_fake_rnames <- paste("chr", c(1:6, "X"), sep="")
    rname <- factor(sample(some_fake_rnames, nreads, replace=TRUE),
        levels=some_fake_rnames)
pos <- sample(80000000L, nreads, replace=TRUE)

## The following takes < 3 sec. to complete:
system.time(irl1 <- extractAlignmentRangesOnReference(cigar3, pos=pos))
## The following takes < 4 sec. to complete:
```
system.time(irl2 <- extractAlignmentRangesOnReference(cigar3, pos=pos, f=rname))
```

## The sizes of the resulting objects are about 240M and 160M, respectively:
```
object.size(irl1)
object.size(irl2)
```

---

**coverage-methods**

### Description

`coverage` methods for `GAlignments`, `GAlignmentPairs`, `GAlignmentsList`, and `BamFile` objects.

NOTE: The `coverage` generic function and methods for `Ranges` and `RangesList` objects are defined and documented in the `IRanges` package. Methods for `GRanges` and `GRangesList` objects are defined and documented in the `GenomicRanges` package.

### Usage

```
## S4 method for signature 'GAlignments'
coverage(x, shift=0L, width=NULL, weight=1L, 
    method=c("auto", "sort", "hash"), drop.D.ranges=FALSE)

## S4 method for signature 'GAlignmentPairs'
coverage(x, shift=0L, width=NULL, weight=1L, 
    method=c("auto", "sort", "hash"), drop.D.ranges=FALSE)

## S4 method for signature 'GAlignmentsList'
coverage(x, shift=0L, width=NULL, weight=1L, ...)

## S4 method for signature 'BamFile'
coverage(x, shift=0L, width=NULL, weight=1L, ..., 
    param=ScanBamParam())

## S4 method for signature 'character'
coverage(x, shift=0L, width=NULL, weight=1L, ..., 
    yieldSize=2500000L)
```

### Arguments

- **x**
  - A `GAlignments`, `GAlignmentPairs`, `GAlignmentsList`, or `BamFile` object, or the path to a BAM file.
- **shift, width, weight**
  - See `coverage` method for `GRanges` objects in the `GenomicRanges` package.
- **method**
  - See `?coverage` in the `IRanges` package for a description of this argument.
Whether the coverage calculation should ignore ranges corresponding to D (deletion) in the CIGAR string.

Additional arguments passed to the coverage method for GAlignments objects.

An optional ScanBamParam object passed to readGAlignments.

An optional argument controlling how many records are input when iterating through a BamFile.

The methods for GAlignments and GAlignmentPairs objects do:

\[
\text{coverage}(\text{grglist}(x, \text{drop.D.ranges}=\text{drop.D.ranges}), \ldots)
\]

The method for GAlignmentsList objects does:

\[
\text{coverage}(\text{unlist}(x), \ldots)
\]

The method for BamFile objects iterates through a BAM file, reading \text{yieldSize}(x) records (or all records, if is.na(yieldSize(x))) and calculating:

\[
\text{gal} \leftarrow \text{readGAlignments}(x, \text{param} = \text{param})
\]

\[
\text{coverage}(\text{gal}, \text{shift}=\text{shift}, \text{width}=\text{width}, \text{weight}=\text{weight}, \ldots)
\]

The method for character vectors of length 1 creates a BamFile object from \(x\) and performs the calculation for \text{coverage,BamFile-method}.

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

See Also

- \text{coverage} in the IRanges package.
- \text{coverage-methods} in the GenomicRanges package.
- RleList objects in the IRanges package.
- GAlignments and GAlignmentPairs objects.
- \text{readGAlignments}.
- BamFile objects in the Rsamtools package.

Examples

```r
## A. EXAMPLE WITH TOY DATA

ex1_file <- system.file("extdata", "ex1.bam", package="Rsamtools")

## Coverage of a GAlignments object:

gal <- readGAlignments(ex1_file)
cvg1 <- coverage(gal)
cvg1
```
## Coverage of a GAlignmentPairs object:

galp <- readGAlignmentPairs(ex1_file)
cvg2 <- coverage(galp)
cvg2

## Coverage of a GAlignmentsList object:

galist <- readGAlignmentsList(ex1_file)
cvg3 <- coverage(galist)
cvg3

table(mcols(galist)$mate_status)
mated_idx <- which(mcols(galist)$mate_status == "mated")
mated_galist <- galist[mated_idx]
mated_cvg3 <- coverage(mated_galist)
mated_cvg3

## Sanity checks:

stopifnot(identical(cvg1, cvg3))
stopifnot(identical(cvg2, mated_cvg3))

## B. EXAMPLE WITH REAL DATA

library(pasillaBamSubset)

## See 'pasillaBamSubset' for more information about the 2 BAM files included in this package.

reads <- readGAlignments(untreated3_chr4())
table(njunc(reads)) # data contains junction reads

## Junctions do NOT contribute to the coverage:

read1 <- reads[which(njunc(reads) != 0L)[1]] # 1st read with a junction
read1 # cigar shows a "skipped region" of length 15306
grglist(read1)[[1]] # the junction is between pos 4500 and 19807
coverage(read1)$chr4 # junction is not covered

## Sanity checks:

cvg <- coverage(reads)
read_chunks <- unlist(grglist(reads), use.names=FALSE)
read_chunks_per_chrom <- split(read_chunks, seqnames(read_chunks))
stopifnot(identical(sum(cvg), sum(width(read_chunks_per_chrom))))
galist <- readGAlignmentsList(untreated3_chr4())
stopifnot(identical(cvg, coverage(galist)))

---

**encodeOverlaps-methods**

*Encode the overlaps between RNA-seq reads and the transcripts of a gene model*

**Description**

In the context of an RNA-seq experiment, encoding the overlaps between the aligned reads and the transcripts of a given gene model can be used for detecting those overlaps that are compatible with the splicing of the transcript.
The central tool for this is the `encodeOverlaps` method for `GRangesList` objects, which computes the "overlap encodings" between a query and a subject, both list-like objects with list elements containing multiple ranges.

Other related utilities are also documented in this man page.

### Usage

```r
encodeOverlaps(query, subject, hits=NULL, ...)
```

#### S4 method for signature 'GRangesList,GRangesList'

```r
codeOverlaps(query, subject, hits=NULL,
             flip.query.if.wrong.strand=FALSE)
```

#### Related utilities:

- `flipQuery(x, i)`
- `selectEncodingWithCompatibleStrand(ovencA, ovencB, query.strand, subject.strand, hits=NULL)`
- `isCompatibleWithSplicing(x)`
- `isCompatibleWithSkippedExons(x, max.skipped.exons=NA)`
- `extractSteppedExonRanks(x, for.query.right.end=FALSE)`
- `extractSpannedExonRanks(x, for.query.right.end=FALSE)`
- `extractSkippedExonRanks(x, for.query.right.end=FALSE)`
- `extractQueryStartInTranscript(query, subject, hits=NULL, ovenc=NULL, flip.query.if.wrong.strand=FALSE, for.query.right.end=FALSE)`

### Arguments

- `query, subject` Typically `GRangesList` objects representing the aligned reads and the transcripts of a given gene model, respectively. If the 2 objects don’t have the same length, and if the `hits` argument is not supplied, then the shortest is recycled to the length of the longest (the standard recycling rules apply).
- `hits` An optional `Hits` object typically obtained from a previous call to `findOverlaps(query, subject)`. Strictly speaking, `hits` only needs to be compatible with `query` and `subject`, that is, `queryLength(hits)` and `subjectLength(hits)` must be equal to `length(query)` and `length(subject)`, respectively.
- `...` Additional arguments for methods.
- `flip.query.if.wrong.strand` See the "OverlapEncodings" vignette located in this package (GenomicAlignments).
For flipQuery: a GRangesList object.

For isCompatibleWithSplicing, isCompatibleWithSkippedExons, extractSteppedExonRanks, extractSpannedExonRanks, and extractSkippedExonRanks: an OverlapEncodings object, a factor, or a character vector.

Subscript specifying the elements in x to flip. If missing, all the elements are flipped.

OverlapEncodings objects.

Vector-like objects containing the strand of the query and subject, respectively.

Not supported yet. If NA (the default), the number of skipped exons must be 1 or more (there is no max).

If TRUE, then the information reported in the output is for the right ends of the paired-end reads. Using for.query.right.end=TRUE with single-end reads is an error.

See ?OverlapEncodings for a short introduction to "overlap encodings". The topic of working with overlap encodings is covered in details in the "OverlapEncodings" vignette located this package (GenomicAlignments) and accessible with vignette("OverlapEncodings").

For encodeOverlaps: An OverlapEncodings object. If hits is not supplied, this object is parallel to the longest of query and subject, that is, it has the length of the longest and the i-th encoding in it corresponds to the i-th element in the longest. If hits is supplied, then the returned object is parallel to it, that is, it has one encoding per hit.

For flipQuery: TODO
For selectEncodingWithCompatibleStrand: TODO
For isCompatibleWithSplicing and isCompatibleWithSkippedExons: A logical vector parallel to x.
For extractSteppedExonRanks, extractSpannedExonRanks, and extractSkippedExonRanks: TODO
For extractQueryStartInTranscript: TODO

The OverlapEncodings class for a brief introduction to "overlap encodings".

The Hits class defined and documented in the S4Vectors package.

The "OverlapEncodings" vignette in this package.

findCompatibleOverlaps for a specialized version of findOverlaps that uses encodeOverlaps internally to keep only the hits where the junctions in the aligned read are compatible with the splicing of the annotated transcript.
The `GRangesList` class defined and documented in the `GenomicRanges` package.

The `findOverlaps` generic function defined in the `IRanges` package.

**Examples**

```r
## A. BETWEEN 2 RangesList OBJECTS
## In the context of an RNA-seq experiment, encoding the overlaps
## between 2 GRangesList objects, one containing the reads (the query),
## and one containing the transcripts (the subject), can be used for
## detecting hits between reads and transcripts that are "compatible"
## with the splicing of the transcript. Here we illustrate this with 2
## RangesList objects, in order to keep things simple:

## 4 aligned reads in the query:
read1 <- IRanges(c(7, 15, 22), c(9, 19, 23)) # 2 junctions
read2 <- IRanges(c(5, 15), c(9, 17)) # 1 junction
read3 <- IRanges(c(16, 22), c(19, 24)) # 1 junction
read4 <- IRanges(c(16, 23), c(19, 24)) # 1 junction
query <- IRangesList(read1, read2, read3, read4)

## 1 transcript in the subject:
tx <- IRanges(c(1, 4, 15, 22, 38), c(2, 9, 19, 25, 47)) # 5 exons
subject <- IRangesList(tx)

## Encode the overlaps:
ovenc <- encodeOverlaps(query, subject)
encoding(ovenc)

## Reads that are "compatible" with the transcript can be detected with
## a regular expression (the regular expression below assumes that
## reads have at most 2 junctions):
regex0 <- "(:[fgij]:|:[jg].:..[gf]:|:[jg].:.g.:..[gf]:)"
grepl(regex0, encoding(ovenc)) # read4 is NOT "compatible"

## This was for illustration purpose only. In practise you don't need
## (and should not) use this regular expression, but use instead the
## isCompatibleWithSplicing() utility function:
isCompatibleWithSplicing(ovenc)
```

```
## B. BETWEEN 2 GRangesList OBJECTS
## With real RNA-seq data, the reads and transcripts will typically be
## stored in GRangesList objects. Please refer to the "OverlapEncodings"
## vignette in this package for realistic examples.
```

**findCompatibleOverlaps-methods**

Finding hits between reads and transcripts that are compatible with
the splicing of the transcript
findCompatibleOverlaps-methods

Description
In the context of an RNA-seq experiment, findCompatibleOverlaps (or countCompatibleOverlaps) can be used for finding (or counting) hits between reads and transcripts that are compatible with the splicing of the transcript.

Usage
findCompatibleOverlaps(query, subject)
countCompatibleOverlaps(query, subject)

Arguments
query A GAlignments or GAlignmentPairs object representing the aligned reads.
subject A GRangesList object representing the transcripts.

Details
findCompatibleOverlaps is a specialized version of findOverlaps that uses encodeOverlaps internally to keep only the hits where the junctions in the aligned read are compatible with the splicing of the annotated transcript.

The topic of working with overlap encodings is covered in details in the "OverlapEncodings" vignette located this package (GenomicAlignments) and accessible with vignette("OverlapEncodings").

Value
A Hits object for findCompatibleOverlaps.
An integer vector parallel to (i.e. same length as) query for countCompatibleOverlaps.

Author(s)
Hervé Pagès

See Also
• The findOverlaps generic function defined in the IRanges package.
• The encodeOverlaps generic function and OverlapEncodings class.
• The "OverlapEncodings" vignette in this package.
• GAlignments and GAlignmentPairs objects.
• GRangesList objects in the GenomicRanges package.

Examples
## Here we only show a simple example illustrating the use of
## countCompatibleOverlaps() on a very small data set. Please
## refer to the "OverlapEncodings" vignette in the GenomicAlignments
## package for a comprehensive presentation of "overlap
## encodings" and related tools/concepts (e.g. "compatible"
## overlaps, "almost compatible" overlaps etc...), and for more
## examples.

## sm_treated1.bam contains a small subset of treated1.bam, a BAM
## file containing single-end reads from the "Pasilla" experiment
findMateAlignment

Pairing the elements of a GAlignments object

Description

Utilities for pairing the elements of a GAlignments object.

NOTE: Until BioC 2.13, findMateAlignment was the power horse used by readGAlignmentPairs for pairing the records loaded from a BAM file containing aligned paired-end reads. Starting with BioC 2.14, readGAlignmentPairs relies on scanBam(BamFile(asMates=TRUE), ...) for the pairing.

Usage

findMateAlignment(x)
makeGAlignmentPairs(x, use.names=FALSE, use.mcols=FALSE, strandMode=1)

## Related low-level utilities:
getDumpedAlignments()
countDumpedAlignments()
flushDumpedAlignments()
Arguments

x A named GAlignments object with metadata columns flag, mrnm, and mpos. Typically obtained by loading aligned paired-end reads from a BAM file with:

```r
param <- ScanBamParam(what=c("flag", "mrnm", "mpos"))
x <- readGAlignments(..., use.names=TRUE, param=param)
```

use.names Whether the names on the input object should be propagated to the returned object or not.

use.mcols Names of the metadata columns to propagate to the returned GAlignmentPairs object.

strandMode Strand mode to set on the returned GAlignmentPairs object. See ?strandMode for more information.

Details

Pairing algorithm used by findMateAlignment: findMateAlignment is the power horse used by makeGAlignmentPairs for pairing the records loaded from a BAM file containing aligned paired-end reads.

It implements the following pairing algorithm:

- First, only records with flag bit 0x1 (multiple segments) set to 1, flag bit 0x4 (segment unmapped) set to 0, and flag bit 0x8 (next segment in the template unmapped) set to 0, are candidates for pairing (see the SAM Spec for a description of flag bits and fields). findMateAlignment will ignore any other record. That is, records that correspond to single-end reads, or records that correspond to paired-end reads where one or both ends are unmapped, are discarded.

- Then the algorithm looks at the following fields and flag bits:
  - (A) QNAME
  - (B) RNAME, RNEXT
  - (C) POS, PNEXT
  - (D) Flag bits 0x10 (segment aligned to minus strand) and 0x20 (next segment aligned to minus strand)
  - (E) Flag bits 0x40 (first segment in template) and 0x80 (last segment in template)
  - (F) Flag bit 0x2 (proper pair)
  - (G) Flag bit 0x100 (secondary alignment)

2 records rec1 and rec2 are considered mates if all the following conditions are satisfied:

- (A) QNAME(rec1) == QNAME(rec2)
- (B) RNEXT(rec1) == RNAME(rec2) and RNEXT(rec2) == RNAME(rec1)
- (C) PNEXT(rec1) == POS(rec2) and PNEX(T(rec2) == POS(rec1)
- (D) Flag bit 0x20 of rec1 == Flag bit 0x10 of rec2 and Flag bit 0x20 of rec2 == Flag bit 0x10 of rec1
- (E) rec1 corresponds to the first segment in the template and rec2 corresponds to the last segment in the template, OR, rec2 corresponds to the first segment in the template and rec1 corresponds to the last segment in the template
- (F) rec1 and rec2 have same flag bit 0x2
- (G) rec1 and rec2 have same flag bit 0x100

Timing and memory requirement of the pairing algorithm: The estimated timings and memory requirements on a modern Linux system are (those numbers may vary depending on your hardware and OS):
### findMateAlignment

<table>
<thead>
<tr>
<th>nb of alignments</th>
<th>time</th>
<th>required memory</th>
</tr>
</thead>
<tbody>
<tr>
<td>8 millions</td>
<td>28 sec</td>
<td>1.4 GB</td>
</tr>
<tr>
<td>16 millions</td>
<td>58 sec</td>
<td>2.8 GB</td>
</tr>
<tr>
<td>32 millions</td>
<td>2 min</td>
<td>5.6 GB</td>
</tr>
<tr>
<td>64 millions</td>
<td>4 min 30 sec</td>
<td>11.2 GB</td>
</tr>
</tbody>
</table>

This is for a GAlignments object coming from a file with an "average nb of records per unique QNAME" of 2.04. A value of 2 (which means the file contains only primary reads) is optimal for the pairing algorithm. A greater value, say > 3, will significantly degrade its performance. An easy way to avoid this degradation is to load only primary alignments by setting the isSecondaryAlignment flag to FALSE in ScanBamParam(). See examples in `?readGAlignmentPairs` for how to do this.

**Ambiguous pairing:** The above algorithm will find almost all pairs unambiguously, even when the same pair of reads maps to several places in the genome. Note that, when a given pair maps to a single place in the genome, looking at (A) is enough to pair the 2 corresponding records. The additional conditions (B), (C), (D), (E), (F), and (G), are only here to help in the situation where more than 2 records share the same QNAME. And that works most of the times. Unfortunately there are still situations where this is not enough to solve the pairing problem unambiguously.

For example, here are 4 records (loaded in a GAlignments object) that cannot be paired with the above algorithm:

**Showing the 4 records as a GAlignments object of length 4:**

```
<table>
<thead>
<tr>
<th>seqnames</th>
<th>strand</th>
<th>cigar</th>
<th>qwidth</th>
<th>start</th>
<th>end</th>
</tr>
</thead>
<tbody>
<tr>
<td>SRR031714.2658602</td>
<td>chr2R</td>
<td>+ 21M384N16M</td>
<td>37</td>
<td>6983850</td>
<td>6984270</td>
</tr>
<tr>
<td>SRR031714.2658602</td>
<td>chr2R</td>
<td>+ 21M384N16M</td>
<td>37</td>
<td>6983850</td>
<td>6984270</td>
</tr>
<tr>
<td>SRR031714.2658602</td>
<td>chr2R</td>
<td>- 13M372N24M</td>
<td>37</td>
<td>6983858</td>
<td>6984266</td>
</tr>
<tr>
<td>SRR031714.2658602</td>
<td>chr2R</td>
<td>- 13M378N24M</td>
<td>37</td>
<td>6983858</td>
<td>6984272</td>
</tr>
</tbody>
</table>
```

Note that the BAM fields show up in the following columns:

- **QNAME:** the names of the GAlignments object (unnamed col)
- **RNAME:** the seqnames col
- **POS:** the start col
- **RNEXT:** the mrnm col
- **PNEXT:** the mpos col

As you can see, the aligner has aligned the same pair to the same location twice! The only difference between the 2 aligned pairs is in the CIGAR i.e. one end of the pair is aligned twice to the same location with exactly the same CIGAR while the other end of the pair is aligned twice to the same location but with slightly different CIGARs.

Now showing the corresponding flag bits:

```
isPaired isProperPair isUnmappedQuery hasUnmappedMate isMinusStrand
[1,] 1 1 0 0 0
[2,] 1 1 0 0 0
```
As you can see, rec(1) and rec(2) are second mates, rec(3) and rec(4) are both first mates. But looking at (A), (B), (C), (D), (E), (F), and (G), the pairs could be rec(1) <-> rec(3) and rec(2) <-> rec(4), or they could be rec(1) <-> rec(4) and rec(2) <-> rec(3). There is no way to disambiguate!

So `findMateAlignment` is just ignoring (with a warning) those alignments with ambiguous pairing, and dumping them in a place from which they can be retrieved later (i.e. after `findMateAlignment` has returned) for further examination (see "Dumped alignments" subsection below for the details). In other words, alignments that cannot be paired unambiguously are not paired at all. Concretely, this means that `readGAlignmentPairs` is guaranteed to return a `GAlignmentPairs` object where every pair was formed in an non-ambiguous way. Note that, in practice, this approach doesn’t seem to leave aside a lot of records because ambiguous pairing events seem pretty rare.

### Dumped alignments:
Alignments with ambiguous pairing are dumped in a place ("the dump environment") from which they can be retrieved with `getDumpedAlignments()` after `findMateAlignment` has returned.

Two additional utilities are provided for manipulation of the dumped alignments: `countDumpedAlignments` for counting them (a fast equivalent to `length(getDumpedAlignments())`), and `flushDumpedAlignments` to flush "the dump environment". Note that "the dump environment" is automatically flushed at the beginning of a call to `findMateAlignment`.

### Value

- **For `findMateAlignment`**: An integer vector of the same length as `x`, containing only positive or NA values, where the i-th element is interpreted as follow:
  - An NA value means that no mate or more than 1 mate was found for `x[i]`.
  - A non-NA value j gives the index in `x` of `x[i]`'s mate.

- **For `makeGAlignmentPairs`**: A `GAlignmentPairs` object where the pairs are formed internally by calling `findMateAlignment` on `x`.

- **For `getDumpedAlignments`**: NULL or a `GAlignments` object containing the dumped alignments. See "Dumped alignments" subsection in the "Details" section above for the details.

- **For `countDumpedAlignments`**: The number of dumped alignments.

- **Nothing** for `flushDumpedAlignments`.

### Author(s)

Hervé Pagès
findOverlaps-methods

Finding overlapping genomic alignments

Description

Finds range overlaps between a GAlignments, GAlignmentPairs, or GAlignmentsList object, and another range-based object.

NOTE: The findOverlaps generic function and methods for Ranges and RangesList objects are defined and documented in the IRanges package. The methods for GRanges and GRangesList objects are defined and documented in the GenomicRanges package.

GAlignments, GAlignmentPairs, and GAlignmentsList objects also support countOverlaps, overlapsAny, and subsetByOverlaps thanks to the default methods defined in the IRanges package and to the findOverlaps method defined in this package and documented below.

Usage

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

Arguments

query, subject A GAlignments, GAlignmentPairs, or GAlignmentsList object for either query or subject. A vector-like object containing ranges for the other one.

maxgap, minoverlap, type, select
See findOverlaps in the IRanges package for a description of these arguments.

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

Examples

bamfile <- system.file("extdata", "ex1.bam", package="Rsamtools",
  mustWork=TRUE)
param <- ScanBamParam(what=c("flag", "mrnm", "mpos"))
x <- readGAlignments(bamfile, use.names=TRUE, param=param)
mate <- findMateAlignment(x)
head(mate)
table(is.na(mate))
galp <- makeGAlignmentPairs(x)
galp
colnames(mcols(galp))
colnames(mcols(first(galp)))
colnames(mcols(last(galp)))
findOverlaps-methods

Details

When the query or the subject (or both) is a GAlignments object, it is first turned into a GRangesList object (with as( , "GRangesList")) and then the rules described previously apply. GAlignmentsList objects are coerced to GAlignments then to a GRangesList. Feature indices are mapped back to the original GAlignmentsList list elements.

When the query is a GAlignmentPairs object, it is first turned into a GRangesList object (with as( , "GRangesList")) and then the rules described previously apply.

Value

A Hits object when select="all" or an integer vector otherwise.

See Also

- findOverlaps.
- Hits-class.
- GRanges-class.
- GRangesList-class.
- GAlignments-class.
- GAlignmentPairs-class.
- GAlignmentsList-class.

Examples

```r
ex1_file <- system.file("extdata", "ex1.bam", package="Rsamtools")
galn <- readGAlignments(ex1_file)

subject <- granges(galn)[1]

## Note the absence of query no. 9 (i.e. 'galn[9]') in this result:
as.matrix(findOverlaps(galn, subject))

## This is because, by default, findOverlaps()/countOverlaps() are
## strand specific:
galn[8:10]
countOverlaps(galn[8:10], subject)
countOverlaps(galn[8:10], subject, ignore.strand=TRUE)

## Count alignments in 'galn' that DO overlap with 'subject' vs those
## that do NOT:
table(overlapsAny(galn, subject))
## Extract those that DO:
subsetByOverlaps(galn, subject)

## GAlignmentsList
galist <- GAlignmentsList(galn[8:10], galn[3000:3002])
gr <- GRanges(c("seq1", "seq1", "seq2"),
              IRanges(c(15, 18, 1233), width=1),
              strand=c("-", "+", ""))

countOverlaps(galist, gr)
countOverlaps(galist, gr, ignore.strand=TRUE)
findOverlaps(galist, gr)
findOverlaps(galist, gr, ignore.strand=TRUE)
```
findSpliceOverlaps-methods

Classify ranges (reads) as compatible with existing genomic annotations or as having novel splice events

Description

The `findSpliceOverlaps` function identifies ranges (reads) that are compatible with a specific transcript isoform. The non-compatible ranges are analyzed for the presence of novel splice events.

Usage

```r
findSpliceOverlaps(query, subject, ignore.strand=FALSE, ...)  
## S4 method for signature 'GRangesList,GRangesList'
findSpliceOverlaps(query, subject, ignore.strand=FALSE, ..., cds=NULL)

## S4 method for signature 'GAlignments,GRangesList'
findSpliceOverlaps(query, subject, ignore.strand=FALSE, ..., cds=NULL)

## S4 method for signature 'GAlignmentPairs,GRangesList'
findSpliceOverlaps(query, subject, ignore.strand=FALSE, ..., cds=NULL)

## S4 method for signature 'BamFile,ANY'
findSpliceOverlaps(query, subject, ignore.strand=FALSE, ...,  
  param=ScanBamParam(), singleEnd=TRUE)
```

Arguments

- **query**: A `GRangesList`, `GAlignments`, `GAlignmentPairs`, or `BamFile` object containing the reads. Can also be a single string containing the path to a BAM file. Single or paired-end reads are specified with the `singleEnd` argument (default `FALSE`). Paired-end reads can be supplied in a BAM file or `GAlignmentPairs` object. Single-end are expected to be in a BAM file, `GAlignments` or `GRanges` object.

- **subject**: A `GRangesList` containing the annotations. This list is expected to contain exons grouped by transcripts.

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

- **...**: Additional arguments such as `param` and `singleEnd` used in the method for `BamFile` objects. See below.

- **cds**: Optional `GRangesList` of coding regions for each transcript in the `subject`. If provided, the "coding" output column will be a logical vector indicating if the read falls in a coding region. When not provided, the "coding" output is `NA`.

- **param**: An optional `ScanBamParam` instance to further influence scanning, counting, or filtering.

- **singleEnd**: A logical value indicating if reads are single or paired-end. See `summarizeOverlaps` for more information.
findSpliceOverlaps-methods

Details

When a read maps compatibly and uniquely to a transcript isoform we can quantify the expression and look for shifts in the balance of isoform expression. If a read does not map in compatible way, novel splice events such as splice junctions, novel exons or retentions can be quantified and compared across samples.

findSpliceOverlaps detects which reads (query) match to transcripts (subject) in a compatible fashion. Compatibility is based on both the transcript bounds and splicing pattern. Assessing the splicing pattern involves comparison of the read splices (i.e., the N operations in the CIGAR) with the transcript introns. For paired-end reads, the inter-read gap is not considered a splice junction. The analysis of non-compatible reads for novel splice events is under construction.

Value

The output is a Hits object with the metadata columns defined below. Each column is a logical indicating if the read (query) met the criteria.

- compatible: Every splice (N) in a read alignment matches an intron in an annotated transcript. The read does not extend into an intron or outside the transcript bounds.
- unique: The read is compatible with only one annotated transcript.
- strandSpecific: The query (read) was stranded.

Author(s)

Michael Lawrence and Valerie Obenchain <vobencha@fredhutch.org>

See Also

- GRangesList objects in the GenomicRanges package.
- GAlignments and GAlignmentPairs objects.
- BamFile objects in the Rsamtools package.

Examples

```r
## Isoform expression:
## findSpliceOverlaps() can assist in quantifying isoform expression by identifying reads that map compatibly and uniquely to a transcript isoform.
library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
library(pasillaBamSubset)
se <- untreated1_chr4()  ## single-end reads
txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
exbytx <- exonsBy(txdb, "tx")
cdsbytx <- cdsBy(txdb, "tx")
param <- ScanBamParam(which=GRanges("chr4", IRanges(1e5,3e5)))
sehits <- findSpliceOverlaps(se, exbytx, cds=cdsbytx, param=param)

## Tally the reads by category to get an idea of read distribution.
lst <- lapply(mcols(sehits), table)
nms <- names(lst)
tbl <- do.call(rbind, lst[nms])
tbl
```
## Reads compatible with one or more transcript isoforms.

rnms <- rownames(tbl)
tbl[rnms == "compatible","TRUE"]/sum(tbl[rnms == "compatible",])

## Reads compatible with a single isoform.

tbl[rnms == "unique","TRUE"]/sum(tbl[rnms == "unique",])

## All reads fall in a coding region as defined by
## the txdb annotation.

lst["coding"]

## Check: Total number of reads should be the same across categories.
lapply(lst, sum)

## Paired-end reads:

pe <- untreated3_chr4()

hits2 <- findSpliceOverlaps(pe, exbytx, singleEnd=FALSE, param=param)

## In addition to BAM files, paired-end reads can be supplied in a
## GAlignmentPairs object.

genes <- GRangesList(
  GRanges("chr1", IRanges(c(5, 20), c(10, 25)), "+"),
  GRanges("chr1", IRanges(c(5, 22), c(15, 25)), "+"))
galp <- GAlignmentPairs(
  GAlignments("chr1", 5L, "11M4N6M", strand("+")),
  GAlignments("chr1", 50L, "6M", strand("-")))

findSpliceOverlaps(galp, genes)

---

### GAlignmentPairs-class

#### GAlignmentPairs objects

**Description**

The GAlignmentPairs class is a container for storing *pairs of genomic alignments*. These pairs are typically obtained by aligning paired-end reads to a reference genome or transcriptome.

**Details**

A GAlignmentPairs object is a list-like object where each list element represents a pair of genomic alignment.

An *alignment pair* is made of a "first" and a "last"/"second" alignment, and is formally represented by a GAlignments object of length 2. In most applications, an *alignment pair* will represent an aligned paired-end read. In that case, the "first" member of the pair represents the alignment of the first end of the read (aka "first segment in the template", using SAM Spec terminology), and the "last" member of the pair represents the alignment of the second end of the read (aka "last segment in the template", using SAM Spec terminology).

In general, a GAlignmentPairs object will be created by loading records from a BAM (or SAM) file containing aligned paired-end reads, using the readGAlignmentPairs function (see below). Each element in the returned object will be obtained by pairing 2 records.
GA
ingmentPairs-class

Constructor

GA
ingmentPairs(first, last, strandMode=1, isProperPair=TRUE, names=NULL):

Low-level GAlignmentPairs constructor. Generally not used directly.

Accessors

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

strandMode(x), strandMode(x) <- value: The strand mode is a per-object switch on GAlign-
mentPairs objects that controls the behavior of the strand getter. More precisely, it indicates
how the strand of a pair should be inferred from the strand of the first and last alignments in
the pair:

• 0: strand of the pair is always *.
• 1: strand of the pair is strand of its first alignment. This mode should be used when the
paired-end data was generated using one of the following stranded protocols: Directional
Illumina (Ligation), Standard SOLiD.
• 2: strand of the pair is strand of its last alignment. This mode should be used when
the paired-end data was generated using one of the following stranded protocols: dUTP,
NSR, NNSR, Illumina stranded TruSeq PE protocol.

These modes are equivalent to strandSpecific equal 0, 1, and 2, respectively, for the featureCounts
function defined in the Rsubread package.

Note that, by default, the readGAlignmentPairs function sets the strand mode to 1 on the
returned GAlignmentPairs object. The function has a strandMode argument to let the user set
different strand mode. The strand mode can also be changed any time with the strandMode
setter or with invertStrand.

Also note that 3rd party programs TopHat2 and Cufflinks have a --library-type option to let
the user specify which protocol was used. Please refer to the documentation of these programs
for more information.

length(x): Return the number of alignment pairs in x.

names(x), names(x) <- value: Get or set the names on x. See readGAlignmentPairs for how
to automatically extract and set the names when reading the alignments from a file.

first(x, real.strand=FALSE), last(x, real.strand=FALSE), second(x, real.strand=FALSE):
Get the “first” or “last”/“second” alignment for each alignment pair in x. The result is a
GAlignments object of the same length as x.

If real.strand=TRUE, then the strand is inverted on-the-fly according to the strand mode
currently set on the object (see strandMode(x) above). More precisely, if strandMode(x)
is 0, then the strand is set to * for the GAlignments object returned by both, first() and
last(). If strandMode(x) is 1, then the strand of the object returned by last() is inverted.
If strandMode(x) is 2, then the strand of the object returned by first() is inverted.

seqnames(x): Get the sequence names of the pairs in x i.e. the name of the reference sequence
for each alignment pair in x. The sequence name of a pair is the sequence name of the 2 align-
ments in the pair if they are the same (concordant seqnames), or NA if they differ (discordant
seqnames).

The sequence names are returned in a factor-Rle object that is parallel to x, i.e. the i-th element
in the returned object is the sequence name of the i-th pair in x.

strand(x): Get the strand for each alignment pair in x. Obey strandMode(x) above to infer the
strand of a pair. Return * for pairs with discordant strand, or for all pairs if strandMode(x)
is 0.

njunc(x): Equivalent to njunc(first(x)) + njunc(last(x)).
isProperPair(x): Get the "isProperPair" flag bit (bit 0x2 in SAM Spec) set by the aligner for each alignment pair in \(x\).

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

seqlevels(x), seqlevels(x) <- 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 GAlignmentPairs 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.

geno(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.

seqnameStyle(x): Get or set the seqname style for \(x\). Note that this information is not stored in \(x\) but inferred by looking up seqnames(x) against a seqname style database stored in the seqnames.db metadata package (required). seqnameStyle(x) is equivalent to seqnameStyle(seqinfo(x)) and can return more than 1 seqname style (with a warning) in case the style cannot be determined unambiguously.

**Vector methods**

In the code snippets below, \(x\) is a GAlignmentPairs object.

\(x[i]\): Return a new GAlignmentPairs object made of the selected alignment pairs.

**List methods**

In the code snippets below, \(x\) is a GAlignmentPairs object.

\(x[[i]]\): Extract the \(i\)-th alignment pair as a GAlignments object of length 2. As expected \(x[[i]][1]\) and \(x[[i]][2]\) are respectively the "first" and "last" alignments in the pair.

unlist(x, use.names=TRUE): Return the GAlignments object conceptually defined by c(x[[1]], x[[2]], ..., x[[length(x)]]). use.names determines whether \(x\) names should be propagated to the result or not.

**Coercion**

In the code snippets below, \(x\) is a GAlignmentPairs object.

granges(x, use.names=TRUE, use.mcols=FALSE, on.discordant.seqnames="error", ranges(x, use.names=TRUE, use.mcols=FALSE, on.discordant.seqnames="error")

Return a GRanges object (for granges()) or IRanges) object (for ranges()). If \(x\) contains no pairs with discordant seqnames, the operation is guaranteed to be successful and to return an object parallel to \(x\), that is, an object where the i-th element is the range of the genomic region spanned by the i-th alignment in \(x\) (all gaps in the region are ignored).

If \(x\) contains pairs with discordant seqnames, then an error is raised, unless the on.discordant.seqnames argument is set to "drop" or "split", in which case the pairs with discordant seqnames are either dropped or represented with 2 genomic ranges (or 2 ranges for ranges()) in the returned object. In that case, the returned object is NOT parallel to \(x\).
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.

grglist(x, use.mcols=FALSE, drop.D.ranges=FALSE):

Return a GRangesList object of length length(x) where the i-th element represents the ranges (with respect to the reference) of the i-th alignment pair in x. The strand of the returned ranges obeys the strand mode currently set on the object (see strandMode(x) above). More precisely, if grl1 and grl2 are grglist(first(x, real.strand=TRUE), order.as.in.query=TRUE) and grglist(last(x, real.strand=TRUE), order.as.in.query=TRUE), respectively, then the i-th element in the returned GRangesList object is c(grl1[[i]], grl2[[i]]), if strandMode(x) is 1, or c(grl2[[i]], grl1[[i]]), if strandMode(x) is 2.

Note that this results in the ranges being always ordered consistently with the original "query template", that is, being in the order defined by walking the "query template" from the beginning to the end.

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.

If drop.D.ranges is TRUE, then deletions (Ds in the CIGAR) are treated like junctions (Ns in the CIGAR), that is, the ranges corresponding to deletions are dropped.

as(x, "GRanges"), as(x, "Ranges"), as(x, "GRangesList"): Alternate ways of doing granges(x, use.names=TRUE, use.mcols=TRUE), ranges(x, use.names=TRUE, use.mcols=TRUE), and grglist(x, use.names=TRUE, use.mcols=TRUE), respectively.

as(x, "GAlignments"): Equivalent of unlist(x, use.names=TRUE).

Other methods

In the code snippets below, x is a GAlignmentPairs 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 GRanges and GAlignments objects, as well as other objects defined in the IRanges and Biostrings packages (e.g. Ranges and XStringSet objects).

Author(s)

Hervé Pagès

See Also

- readGAlignmentPairs for reading aligned paired-end reads from a file (typically a BAM file) into a GAlignmentPairs object.
- GAlignments objects for handling aligned single-end reads.
- makeGAlignmentPairs for pairing the elements of a GAlignments object into a GAlignmentPairs object.
- junctions-methods for extracting and summarizing junctions from a GAlignmentPairs object.
- coverage-methods for computing the coverage of a GAlignmentPairs object.
- findOverlaps-methods for finding range overlaps between a GAlignmentPairs object and another range-based object.
• seqinfo in the GenomeInfoDb package for getting/setting/modifying the sequence information stored in an object.

• The GRanges and GRangesList classes defined and documented in the GenomicRanges package.

Examples

library(Rsamtools) # for the ex1.bam file
ex1_file <- system.file("extdata", "ex1.bam", package="Rsamtools")
galp <- readGAlignmentPairs(ex1_file, use.names=TRUE, strandMode=1)
galp

length(galp)
head(galp)
head(names(galp))

first(galp)
last(galp)
# or
second(galp)

strandMode(galp)
first(galp, real.strand=TRUE)
last(galp, real.strand=TRUE)
strand(galp)

strandMode(galp) <- 2
first(galp, real.strand=TRUE)
last(galp, real.strand=TRUE)
strand(galp)

seqnames(galp)

head(njunc(galp))
table(isProperPair(galp))
seqlevels(galp)

## Rename the reference sequences:
seqlevels(galp) <- sub("seq", "chr", seqlevels(galp))
seqlevels(galp)

galp[[1]]
unlist(galp)
grglist(galp) # a GRangesList object

strandMode(galp) <- 1
grglist(galp)

## Alternatively the strand mode can be changed with invertStrand():
invertStrand(galp)

stopifnot(identical(unname(elementNROWS(grglist(galp))), njunc(galp) + 2L))
granges(galp) # a GRanges object
GAlignments-class

GAlignments objects

Description

The GAlignments class is a simple container which purpose is to store a set of genomic alignments that will hold just enough information for supporting the operations described below.

Details

A GAlignments object is a vector-like object where each element describes a genomic alignment i.e. how a given sequence (called "query" or "read", typically short) aligns to a reference sequence (typically long).

Typically, a GAlignments object will be created by loading records from a BAM (or SAM) file and each element in the resulting object will correspond to a record. BAM/SAM records generally contain a lot of information but only part of that information is loaded in the GAlignments object. In particular, we discard the query sequences (SEQ field), the query qualities (QUAL), the mapping qualities (MAPQ) and any other information that is not needed in order to support the operations or methods described below.

This means that multi-reads (i.e. reads with multiple hits in the reference) won’t receive any special treatment i.e. the various SAM/BAM records corresponding to a multi-read will show up in the GAlignments object as if they were coming from different/unrelated queries. Also paired-end reads will be treated as single-end reads and the pairing information will be lost (see ?GAlignmentPairs for how to handle aligned paired-end reads).

Each element of a GAlignments object consists of:

- The name of the reference sequence. (This is the RNAME field in a SAM/BAM record.)
- The strand in the reference sequence to which the query is aligned. (This information is stored in the FLAG field in a SAM/BAM record.)
- The CIGAR string in the "Extended CIGAR format" (see the SAM Format Specifications for the details).
- The 1-based leftmost position/coordinate of the clipped query relative to the reference sequence. We will refer to it as the "start" of the query. (This is the POS field in a SAM/BAM record.)
- The 1-based rightmost position/coordinate of the clipped query relative to the reference sequence. We will refer to it as the "end" of the query. (This is NOT explicitly stored in a SAM/BAM record but can be inferred from the POS and CIGAR fields.) Note that all positions/coordinates are always relative to the first base at the 5’ end of the plus strand of the reference sequence, even when the query is aligned to the minus strand.
- The genomic intervals between the "start" and "end" of the query that are "covered" by the alignment. Saying that the full [start,end] interval is covered is the same as saying that the alignment contains no junction (no N in the CIGAR). It is then considered to be a simple alignment. Note that a simple alignment can have mismatches or deletions (in the reference). In other words, a deletion (encoded with a D in the CIGAR) is NOT considered to introduce a gap in the coverage, but a junction is.

Note that the last 2 items are not explicitly stored in the GAlignments object: they are inferred on-the-fly from the CIGAR and the "start".
Optionally, a GAlignments object can have names (accessed thru the names generic function) which will be coming from the QNAME field of the SAM/BAM records.

The rest of this man page will focus on describing how to:

- Access the information stored in a GAlignments object in a way that is independent from how the data are actually stored internally.
- How to create and manipulate a GAlignments object.

**Constructor**

GAlignments(seqnames=Rle(factor()), pos=integer(0),
            cigar=character(0),
            strand=NULL, names=NULL, seqlengths=NULL, ...)

Low-level GAlignments constructor. Generally not used directly. Named arguments in ... are used as metadata columns.

**Accessors**

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

length(x): Return the number of alignments in x.

names(x), names(x) <- value: Get or set the names on x. See readGAlignments for how to automatically extract and set the names from a file.

seqnames(x), seqnames(x) <- value: Get or set the name of the reference sequence for each alignment in x (see Details section above for more information about the RNAME field of a SAM/BAM file). value can be a factor, or a 'factor' Rle, or a character vector.

rname(x), rname(x) <- value: Same as seqnames(x) and seqnames(x) <- value.

strand(x), strand(x) <- value: Get or set the strand for each alignment in x (see Details section above for more information about the strand of an alignment). value can be a factor (with levels +, - and *), or a 'factor' Rle, or a character vector.

cigar(x): Returns a character vector of length length(x) containing the CIGAR string for each alignment.

qwidth(x): Returns an integer vector of length length(x) containing the length of the query "after" hard clipping (i.e. the length of the query sequence that is stored in the corresponding SAM/BAM record).

start(x), end(x): Returns an integer vector of length length(x) containing the "start" and "end" (respectively) of the query for each alignment. See Details section above for the exact definitions of the "start" and "end" of a query. Note that start(x) and end(x) are equivalent to start(granges(x)) and end(granges(x)), respectively (or, alternatively, to min(rglist(x)) and max(rglist(x)), respectively).

width(x): Equivalent to width(granges(x)) (or, alternatively, to end(x) - start(x) + 1L). Note that this is generally different from qwidth(x) except for alignments with a trivial CIGAR string (i.e. a string of the form "<n>M" where <n> is a number).

njunc(x): Returns an integer vector of the same length as x containing the number of junctions (i.e. N operations in the CIGAR) in each alignment. Equivalent to unname(elementNROWS(rglist(x))) - 1L.

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

seqlevels(x), seqlevels(x) <- 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 GAlignments 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.

seqnameStyle(x): Get or set the seqname style for x. Note that this information is not stored in x but inferred by looking up seqnames(x) against a seqname style database stored in the seqnames.db metadata package (required). seqnameStyle(x) is equivalent to seqnameStyle(seqinfo(x)) and can return more than 1 seqname style (with a warning) in case the style cannot be determined unambiguously.

Coercion

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

granges(x, use.names=TRUE, use.mcols=FALSE), ranges(x, use.names=TRUE, use.mcols=FALSE): Return a GRanges object (for granges()) or IRanges object (for ranges()) parallel to x where the i-th element is the range of the genomic region spanned by the i-th alignment in x. All gaps in the region are ignored.

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.

grglist(x, use.names=TRUE, use.mcols=FALSE, order.as.in.query=FALSE, drop.D.ranges=FALSE), rglist(x, use.names=TRUE, use.mcols=FALSE, order.as.in.query=FALSE, drop.D.ranges=FALSE): Return either a GRangesList or a RangesList object of length length(x) where the i-th element represents the ranges (with respect to the reference) of the i-th alignment in x. More precisely, the RangesList object returned by rglist(x) is a CompressedIRangesList object.

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.

The order.as.in.query toggle affects the order of the ranges within each top-level element of the returned object.

If FALSE (the default), then the ranges are ordered from 5’ to 3’ in elements associated with the plus strand (i.e. corresponding to alignments located on the plus strand), and from 3’ to 5’ in elements associated with the minus strand. So, whatever the strand is, the ranges are in ascending order (i.e. left-to-right).

If TRUE, then the order of the ranges in elements associated with the minus strand is reversed. So they end up being ordered from 5’ to 3’ too, which means that they are now in descending order (i.e. right-to-left). It also means that, when order.as.in.query=TRUE is used, the ranges are always ordered consistently with the original “query template”, that is, in the order defined by walking the “query template” from the beginning to the end.

If drop.D.ranges is TRUE, then deletions (D operations in the CIGAR) are treated like junctions (N operations in the CIGAR), that is, the ranges corresponding to deletions are dropped. See Details section above for more information.
as(x, "GRanges"), as(x, "Ranges"), as(x, "GRangesList"), as(x, "RangesList"): Alternate ways of doing granges(x, use.names=TRUE, use.mcols=TRUE), ranges(x, use.names=TRUE, use.mcols=TRUE), grglist(x, use.names=TRUE, use.mcols=TRUE), and rglist(x, use.names=TRUE, use.mcols=TRUE), respectively.

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

as(from, "GAlignments"): Creates a GAlignments object from a GRanges object. The metadata columns are propagated. cigar values are created from the sequence width unless a "cigar" metadata column already exists in from.

Subsetting and related operations

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

x[i]: Return a new GAlignments object made of the selected alignments. i can be a numeric or logical vector.

Combining

c(...): Concatenates the GAlignments objects in ....

Other methods

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

Author(s)

Hervé Pagès and P. Aboyoun

References

http://samtools.sourceforge.net/

See Also

• readGAlignments for reading genomic alignments from a file (typically a BAM file) into a GAlignments object.
• GAlignmentPairs objects for handling aligned paired-end reads.
• junctions-methods for extracting and summarizing junctions from a GAlignments object.
• coverage-methods for computing the coverage of a GAlignments object.
• findOverlaps-methods for finding overlapping genomic alignments.
• seqinfo in the GenomeInfoDb package for getting/settting/modifying the sequence information stored in an object.
• The GRanges and GRangesList classes defined and documented in the GenomicRanges package.
• The CompressedIRangesList class defined and documented in the IRanges package.
Examples

library(Rsamtools)  # for the ex1.bam file
ex1_file <- system.file("extdata", "ex1.bam", package="Rsamtools")
gal <- readGAlignments(ex1_file, param=ScanBamParam(what="flag"))
gal

## A. BASIC MANIPULATION
length(gal)
head(gal)
names(gal)  # no names by default
seqnames(gal)
strand(gal)
head(cigar(gal))
head(qwidth(gal))
table(qwidth(gal))
head(start(gal))
head(end(gal))
head(width(gal))
head(njunc(gal))
seqlevels(gal)

## Invert the strand:
invertStrand(gal)

## Rename the reference sequences:
seqlevels(gal) <- sub("seq", "chr", seqlevels(gal))
seqlevels(gal)

grglist(gal)  # a GRangesList object
stopifnot(identical(unname(elementNROWS(grglist(gal)))), njunc(gal) + 1L)
granges(gal)  # a GRanges object
rglist(gal)  # a CompressedIRangesList object
stopifnot(identical(unname(elementNROWS(rglist(gal)))), njunc(gal) + 1L)
ranges(gal)  # an IRanges object

## Modify the number of lines in 'show'
options(showHeadLines=3)
options(showTailLines=2)
gal

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

## B. SUBSETTING
##
## A confirmation that none of the alignments contains junctions (in
## other words, each alignment can be represented by a single genomic
## range on the reference):
stopifnot(all(njunc(gal) == 0))

## Different ways to subset:
gal[[6]] # a GAlignments object of length 1
grglist(gal)[[6]] # a GRanges object of length 1
rglist(gal)[[6]] # a NormalIRanges object of length 1

## Unlike N operations, D operations don’t introduce gaps:
ii <- grep("D", cigar(gal), fixed=TRUE)
gal[ii]
njunc(gal[ii])
grglist(gal[ii])

## qwidth() vs width():
gal[qwidth(gal) != width(gal)]

## This MUST return an empty object:
gal[cigar(gal) == "35M" & qwidth(gal) != 35]
## but this doesn’t have too:
gal[cigar(gal) != "35M" & qwidth(gal) == 35]

GAlignmentsList-class  GAlignmentsList objects

Description

The GAlignmentsList class is a container for storing a collection of GAlignments objects.

Details

A GAlignmentsList object contains a list of GAlignments objects. The majority of operations on this page are described in more detail on the GAlignments man page, see ?GAlignments.

Constructor

GAlignmentsList(...): Creates a GAlignmentsList from a list of GAlignments objects.

Accessors

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

length(x): Return the number of elements in x.
names(x), names(x) <- value: Get or set the names of the elements of x.
seqnames(x), seqnames(x) <- value: Get or set the name of the reference sequences of the alignments in each element of x.
rname(x), rname(x) <- value: Same as seqnames(x) and seqnames(x) <- value.
strand(x), strand(x) <- value: Get or set the strand of the alignments in each element of x.
cigar(x): Returns a character list of length length(x) containing the CIGAR string for the alignments in each element of x.
qwidth(x): Returns an integer list of length length(x) containing the length of the alignments in each element of x *after* hard clipping (i.e. the length of the query sequence that is stored in the corresponding SAM/BAM record).
GAlignmentsList-class

start(x), end(x): Returns an integer list of length length(x) containing the "start" and "end" (respectively) of the alignments in each element of x.

width(x): Returns an integer list of length length(x) containing the "width" of the alignments in each element of x.

njunc(x): Returns an integer list of length x containing the number of junctions (i.e. N operations in the CIGAR) for the alignments in each element of x.

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

seqlevels(x), seqlevels(x) <- value: Get or set the sequence levels of the alignments in each element of x.

seqlengths(x), seqlengths(x) <- value: Get or set the sequence lengths for each element of x. 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 for the alignments in each element in x. value must be a named logical list eventually with NAs.

genome(x), genome(x) <- value: Get or set the genome identifier or assembly name for the alignments in each element of x. value must be a named character list eventually with NAs.

seqnameStyle(x): Get or set the seqname style for alignments in each element of x.

Coercion

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

granges(x, use.names=TRUE, use.mcols=FALSE, ignore.strand=FALSE), ranges(x, use.names=TRUE, use.mcols=FALSE)

Return either a GRanges or a IRanges object of length length(x). Note this coercion IGNORES the cigar information. The resulting ranges span the entire range, including any junctions or spaces between paired-end reads.

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.

granges coercion supports ignore.strand to allow ranges of opposite strand to be combined (see examples). All ranges in the resulting GRanges will have strand ".*".

grglist(x, use.names=TRUE, use.mcols=FALSE, ignore.strand=FALSE), rglist(x, use.names=TRUE, use.mcols=FALSE)

Return either a GRangesList or an IRangesList object of length length(x). This coercion RESPECTS the cigar information. The resulting ranges are fragments of the original ranges that do not include junctions or spaces between paired-end reads.

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.

grglist coercion supports ignore.strand to allow ranges of opposite strand to be combined (see examples). When ignore.strand is TRUE all ranges in the resulting GRangesList have strand ".*".

as(x, "GRanges"), as(x, "Ranges"), as(x, "GRangesList"), as(x, "RangesList"): Alternate ways of doing granges(x, use.names=TRUE, use.mcols=TRUE), ranges(x, use.names=TRUE, use.mcols=TRUE), and rglist(x, use.names=TRUE, use.mcols=TRUE) respectively.

as.data.frame(x, row.names = NULL, optional = FALSE, ..., value.name = "value", use.outer.mcols = FALSE)

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

as(x, "GAlignmentsList"): Here x is a GAlignmentPairs object. Return a GAlignmentsList object of length length(x) where the i-th list element represents the ranges of the i-th alignment pair in x.
Subsetting and related operations

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

x[i], x[i] <- value: Get or set list elements i. i can be a numeric or logical vector. value must be a GAlignments.

x[[i]], x[[i]] <- value: Same as x[i], x[i] <- value.

x[i, j], x[i, j] <- value: Get or set list elements i with optional metadata columns j. i can be a numeric, logical or missing. value must be a GAlignments.

Combining

c(...): Concatenates the GAlignmentsList objects in ....

Author(s)

Valerie Obenchain <vobencha@fredhutch.org

References

http://samtools.sourceforge.net/

See Also

• readGAlignmentsList for reading genomic alignments from a file (typically a BAM file) into a GAlignmentsList object.

• GAlignments and GAlignmentPairs objects for handling aligned single- and paired-end reads, respectively.

• junctions-methods for extracting and summarizing junctions from a GAlignmentsList object.

• findOverlaps-methods for finding range overlaps between a GAlignmentsList object and another range-based object.

• seqinfo in the GenomeInfoDb package for getting/setting/modifying the sequence information stored in an object.

• The GRanges and GRangesList classes defined and documented in the GenomicRanges package.

Examples

gal1 <- GAlignments(
  sequences=Rle(factor(c("chr1", "chr2", "chr1", "chr3")), c(1, 3, 2, 4)),
  pos=1:10, cigar=paste0(10:1, "M"),
  strand=Rle(strand(c("-", "+", "+", "-")), c(1, 2, 3, 2)),
  names=head(letters, 10), score=1:10)

gal2 <- GAlignments(
  sequences=Rle(factor(c("chr2", "chr4")), c(3, 4)), pos=1:7,
  cigar=c("5M", "3M2N3M2N3M", "5M", "10M", "5M1N4M", "8M2N1M", "5M"),
  strand=Rle(strand(c("-", "+")), c(4, 3)),
  names=tail(letters, 7), score=1:7)

galist <- GAlignmentsList(noGaps=gal1, Gaps=gal2)
A. BASIC MANIPULATION

length(galist)
names(galist)
seqnames(galist)
strand(galist)
head(cigar(galist))
head(qwidth(galist))
head(start(galist))
head(end(galist))
head(width(galist))
head(njunc(galist))
seqlevels(galist)

## Rename the reference sequences:
seqlevels(galist) <- sub("chr", "seq", seqlevels(galist))
seqlevels(galist)
grglist(galist) # a GRangesList object
rglist(galist) # an IRangesList object

B. SUBSETTING

galist[strand(galist) == "-"]
has_junctions <- sapply(galist,
    function(x) any(grepl("N", cigar(x), fixed=TRUE)))
galist[has_junctions]

## Different ways to subset:
galist[2] # a GAlignments object of length 1
galist[[2]] # a GAlignments object of length 1
grglist(galist[2]) # a GRangesList object of length 1
rglist(galist[2]) # a NormalIRangesList object of length 1

C. mcols()/elementMetadata()

## Metadata can be defined on the individual GAlignment elements
## and the overall GAlignmentsList object. By default, 'level=between'
## extracts the GAlignmentsList metadata. Using 'level=within'
## will extract the metadata on the individual GAlignments objects.
mcols(galist) # no metadata on the GAlignmentsList object
mcols(galist, level="within")

D. readGAlignmentsList()

library(pasillaBamSubset)
fl <- untreated3_chr4()
galist1 <- readGAlignmentsList(fl)
galist1[1:3]
length(galist1)
table(elementNROWS(galist1))

When 'file' is a BamFile, 'asMates' must be TRUE. If FALSE, the data are treated as single-end and each list element of the GAlignmentsList will be of length 1. For single-end data use readGAlignments() instead of readGAlignmentsList().

bf <- BamFile(fl, yieldSize=3, asMates=TRUE)
readGAlignmentsList(bf)

Use a 'param' to fine tune the results.

param <- ScanBamParam(flag=scanBamFlag(isProperPair=TRUE))
galist2 <- readGAlignmentsList(fl, param=param)
length(galist2)

---

The granges() and grlist() coercions support 'ignore.strand' to allow ranges from different strands to be combined. In this example paired-end reads aligned to opposite strands were read into a GAlignmentsList. If the desired operation is to combine these ranges, regardless of junctions or the space between pairs, 'ignore.strand' must be TRUE.

granges(galist1[1])
granges(galist1[1], ignore.strand=TRUE)

grglist()
galist <- GAlignmentsList(noGaps=gal1, Gaps=gal2)
grglist(galist)
grglist(galist, ignore.strand=TRUE)

---

GappedReads-class (Legacy) GappedReads objects

Description

The GappedReads class extends the GAlignments class.

A GappedReads object contains all the information contained in a GAlignments object plus the sequences of the queries. Those sequences can be accessed via the qseq accessor.

Constructor

GappedReads objects are typically created when reading a file containing aligned reads with the readGappedReads function.
Accessors

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

qseq(x): Extracts the sequences of the queries as a DNAStringSet object.

Author(s)

Hervé Pagès

References

http://samtools.sourceforge.net/

See Also

• GAlignments objects.
  • readGappedReads.

Examples

```r
greads_file <- system.file("extdata", "ex1.bam", package="Rsamtools")
greads <- readGappedReads(greads_file)
greads
qseq(greads)
```

**Description**

This man page documents intra range transformations of a GAlignments or GAlignmentsList 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 GRanges and GRangesList objects are defined and documented in the GenomicRanges package.

Usage

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

## S4 method for signature 'GAlignments'
qnarrow(x, start=NA, end=NA, width=NA)
## S4 method for signature 'GAlignmentsList'
qnarrow(x, start=NA, end=NA, width=NA)
```
Arguments

- **x**: A `GAAlignments` or `GAAlignmentsList` object.
- **start, end, width**: Vectors of integers. NAs and negative values are accepted and "solved" according to the rules of the SEW (Start/End/Width) interface (see `?solveUserSEW` for more information about the SEW interface). See `?intra-range-methods` for more information about the start, end, and width arguments.
- **use.names**: See `?intra-range-methods`.

Details

- **() narrow** on a `GAAlignments` object behaves like on a `Ranges` object. See `?intra-range-methods` for the details.
  - A major difference though is that it returns a `GAAlignments` object instead of a `Ranges` object.
  - Unlike with `qnarrow` (see below), the start/end/width arguments here describe the narrowing on the reference side, not the query side.
- **() qnarrow** on a `GAAlignments` object behaves like `narrow` except that the start/end/width arguments here specify the narrowing with respect to the query sequences.
  - `qnarrow` on a `GAAlignmentsList` object returns a `GAAlignmentsList` object.

Value

An object of the same class as, and parallel to (i.e. same length and names as), the original object `x`.

Note

There is no difference between `narrow` and `qnarrow` when all the alignments have a simple CIGAR (i.e. no indels or junctions).

Author(s)

Hervé Pagès and V. Obenchain <vobencha@fredhutch.org>

See Also

- `GAAlignments` and `GAAlignmentsList` objects.
- The `intra-range-methods` man page in the `IRanges` package.
- The `intra-range-methods` man page in the `GenomicRanges` package.

Examples

```r
# A. ON A GAAlignments OBJECT
ex1_file <- system.file("extdata", "ex1.bam", package="Rsamtools")
param <- ScanBamParam(what=c("seq", "qual"))
gal <- readGAlignments(ex1_file, param=param)
gal

# This trims 3 nucleotides on the left and 5 nucleotides on the right
```
## of each alignment:
```r
gal2 <- qnarrow(gal, start=4, end=-6)
gal2
```
## Note that the 'start' and 'end' values are relative to the query sequence and specify the query substring that must be kept for each alignment. Negative values are relative to the right end of the query sequence.
## Also note that the metadata columns on 'gal' are propagated as-is so the "seq" and "qual" metadata columns must be adjusted "by hand" with narrow();
```r
mcols(gal2)$seq <- narrow(mcols(gal)$seq, start=4, end=-6)
mcols(gal2)$qual <- narrow(mcols(gal)$qual, start=4, end=-6)
gal2
```
## Sanity checks:
```r
stopifnot(identical(qwidth(gal2), width(mcols(gal2)$seq)))
stopifnot(identical(qwidth(gal2), width(mcols(gal2)$qual)))
```
### B. ON A GAlignmentsList OBJECT
```r
gal1 <- GAlignments(  seqnames=Rle(factor(c("chr1", "chr2", "chr1", "chr3")),  
  c(1, 3, 2, 4)),  
  pos=1:10, cigar=paste0(10:1, "M"),  
  strand=Rle(strand(c("-", "+", "#", "+", "-")), c(1, 2, 3, 2)),  
  names=tail(letters, 10), score=1:10)
gal2 <- GAlignments(  seqnames=Rle(factor(c("chr2", "chr4")), c(3, 4)),  
  pos=1:7,  
  cigar=c("5M", "3M2N3M2N", "5M", "5M1N4M", "8M3N1M", "5M"),  
  strand=Rle(strand(c("-", "+")), c(4, 3)),  
  names=tail(letters, 7), score=1:7)
galist <- GAlignmentsList(noGaps=gal1, Gaps=gal2)
galist
```  
### Extract junctions from genomic alignments

**Description**

Given an object \( x \) containing genomic alignments (e.g. a \( \text{GAlignments} \), \( \text{GAlignmentPairs} \), or \( \text{GAlignmentsList} \) object), \( \text{junctions}(x) \) extracts the junctions from it and \( \text{summarizeJunctions}(x) \) extracts and summarizes them.

\( \text{readTopHatJunctions} \) and \( \text{readSTARJunctions} \) are utilities for importing the junction file generated by the TopHat and STAR aligners, respectively.
Usage

## junctions() generic and methods
## -----------------------------------------------

junctions(x, use.mcols=FALSE, ...)

## S4 method for signature 'GAlignments'
junctions(x, use.mcols=FALSE)

## S4 method for signature 'GAlignmentPairs'
junctions(x, use.mcols=FALSE)

## S4 method for signature 'GAlignmentsList'
junctions(x, use.mcols=FALSE, ignore.strand=FALSE)

## summarizeJunctions() and NATURAL_INTRON_MOTIFS
## -----------------------------------------------

summarizeJunctions(x, with.revmap=FALSE, genome=NULL)

NATURAL_INTRON_MOTIFS

## Utilities for importing the junction file generated by some aligners
## ----------------------------------------------------------------------

readTopHatJunctions(file, file.is.raw.juncs=FALSE)

readSTARJunctions(file)

Arguments

x    A GAlignments, GAlignmentPairs, or GAlignmentsList object.
use.mcols TRUE or FALSE (the default). Whether the metadata columns on x (accessible with mcols(x)) should be propagated to the returned object or not.
...  Additional arguments, for use in specific methods.
ignore.strand TRUE or FALSE (the default). If set to TRUE, then the strand of x is set to "*" prior to any computation.
with.revmap TRUE or FALSE (the default). If set to TRUE, then a revmap metadata column is added to the output of summarizeJunctions. This metadata column is an IntegerList object representing the mapping from each element in the output (i.e. each junction) to the corresponding elements in the input x.
genome NULL (the default), or a BSgenome object containing the sequences of the reference genome that was used to align the reads, or the name of this reference genome specified in a way that is accepted by the getBSgenome function defined in the BSgenome software package. In that case the corresponding BSgenome data package needs to be already installed (see ?getBSgenome in the BSgenome package for the details).

If genome is supplied, then the intron_motif and intron_strand metadata columns are computed (based on the dinucleotides found at the intron boundaries) and added to the output of summarizeJunctions. See the Value section below for a description of these metadata columns.
file The path (or a connection) to the junction file generated by the aligner. This file should be the junctions.bed or new_list.juncs file for readTopHatJunctions, and the SJ.out.tab file for readSTARJunctions.

file.is.raw.juncs TRUE or FALSE (the default). If set to TRUE, then the input file is assumed to be a TopHat .juncs file instead of the junctions.bed file generated by TopHat. A TopHat .juncs file can be obtained by passing the junctions.bed file thru TopHat’s bed_to_juncs script. See the TopHat manual at http://tophat.cbcb.umd.edu/manual.shtml for more information.

Details

An N operation in the CIGAR of a genomic alignment is interpreted as a junction. junctions(x) will return the genomic ranges of all junctions found in x.

More precisely, on a GAlignments object x, junctions(x) is equivalent to:

\[
\text{psetdiff(granges(x), grglist(x, order.as.in.query=TRUE))}
\]

On a GAlignmentPairs object x, it’s equivalent to (but faster than):

\[
\text{mendoapply(c, junctions(first(x, real.strand=TRUE)),}
\text{junctions(last(x, real.strand=TRUE)))}
\]

Note that starting with BioC 3.2, the behavior of junctions on a GAlignmentPairs object has been slightly modified so that the returned ranges now have the real strand set on them. See the documentation of the real.strand argument in the man page of GAlignmentPairs objects for more information.

NATURAL_INTRON_MOTIFS is a predefined character vector containing the 5 natural intron motifs described at http://www.ncbi.nlm.nih.gov/pmc/articles/PMC84117/.

Value

junctions(x) returns the genomic ranges of the junctions in a GRangesList object parallel to x (i.e. with 1 list element per element in x). If x has names on it, they’re propagated to the returned object. If use.mcols is TRUE and x has metadata columns on it (accessible with mcols(x)), they’re propagated to the returned object.

summarizeJunctions returns the genomic ranges of the unique junctions in x in an unstranded GRanges object with the following metadata columns:

- score: The total number of alignments crossing each junction, i.e. that have the junction encoded in their CIGAR.
- plus_score and minus_score: The strand-specific number of alignments crossing each junction.
- revmap: [Only if with.revmap was set to TRUE.] An IntegerList object representing the mapping from each element in the output (i.e. each junction) to the corresponding elements in input x.
- intron_motif and intron_strand: [Only if genome was supplied.] The intron motif and strand for each junction, based on the dinucleotides found in the genome sequences at the intron boundaries. The intron_motif metadata column is a factor whose levels are the 5 natural intron motifs stored in predefined character vector NATURAL_INTRON_MOTIFS. If the dinucleotides found at the intron boundaries don’t match any of these natural intron motifs, then intron_motif and intron_strand are set to NA and *, respectively.
readTopHatJunctions and readSTARJunctions return the junctions reported in the input file in a stranded GRanges object. With the following metadata columns for readTopHatJunctions (when reading in the junctions.bed file):

- **name**: An id assigned by TopHat to each junction. This id is of the form JUNC00000017 and is unique within the junctions.bed file.
- **score**: The total number of alignments crossing each junction.

With the following metadata columns for readSTARJunctions:

- **intron_motif** and **intron_strand**: The intron motif and strand for each junction, based on the code found in the input file (0: non-canonical, 1: GT/AG, 2: CT/AC, 3: GC/AG, 4: CT/GC, 5: AT/AC, 6: GT/AT). Note that of the 5 natural intron motifs stored in predefined character vector NATURAL_INTRON_MOTIFS, only the first 3 are assigned codes by the STAR software (2 codes per motif, one if the intron is on the plus strand and one if it’s on the minus strand). Thus the intron_motif metadata column is a factor with only 3 levels. If code is 0, then intron_motif and intron_strand are set to NA and *, respectively.
- **um_reads**: The number of uniquely mapping reads crossing the junction (a pair where the 2 alignments cross the same junction is counted only once).
- **mm_reads**: The number of multi-mapping reads crossing the junction (a pair where the 2 alignments cross the same junction is counted only once).


**Author(s)**

Hervé Pagès

**References**

http://www.ncbi.nlm.nih.gov/pmc/articles/PMC84117/ for the 5 natural intron motifs stored in predefined character vector NATURAL_INTRON_MOTIFS.

TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions

- TopHat2 paper: http://genomebiology.com/2013/14/4/r36
- TopHat2 software and manual: http://tophat.cbcb.umd.edu/

STAR: ultrafast universal RNA-seq aligner

- STAR paper: http://bioinformatics.oxfordjournals.org/content/early/2012/10/25/bioinformatics.bts635
- STAR software and manual: https://code.google.com/p/rna-star/

**See Also**

- The readGAlignments and readGAlignmentPairs functions for reading genomic alignments from a BAM file.
- GAlignments, GAlignmentPairs, and GAlignmentsList objects.
- GRanges and GRangesList objects implemented and documented in the GenomicRanges package.
- IntegerList objects implemented and documented in the IRanges package.
• The `getBSgenome` function in the `BSgenome` package, for searching the installed BSgenome data packages for the specified genome and returning it as a `BSgenome` object.

• The `extractList` function in the `IRanges` package, for extracting groups of elements from a vector-like object and returning them into a `List` object.

**Examples**

```r
library(RNAseqData.HNRNPC.bam.chr14)
bamfile <- RNAseqData.HNRNPC.bam.chr14_BAMFILES[1]

# A. junctions()

# readGAlignments(bamfile)
table(njunc(gal))  # some alignments have 3 junctions!

# Read the alignments and extract the junctions
juncs <- junctions(gal)
juncs

stopifnot(identical(unname(elementNROWS(juncs)), njunc(gal)))

# readGAlignmentPairs(bamfile)
juncs <- junctions(galp)
juncs

stopifnot(identical(unname(elementNROWS(juncs)), njunc(galp)))

# B. summarizeJunctions()

# By default, only the "score", "plus_score", and "minus_score" metadata columns are returned:
junc_summary <- summarizeJunctions(gal)
junc_summary

# The "score" metadata column reports the total number of alignments crossing each junction, i.e., that have the junction encoded in their CIGAR:
median(mcols(junc_summary)$score)

# The "plus_score" and "minus_score" metadata columns report the strand-specific number of alignments crossing each junction:
stopifnot(identical(mcols(junc_summary)$score,
    mcols(junc_summary)$plus_score +
    mcols(junc_summary)$minus_score))

# If 'with.revmap' is TRUE, the "revmap" metadata column is added to the output. This metadata column is an IntegerList object representing the mapping from each element in the output (i.e., a junction) to the corresponding elements in the input 'x'. Here we're going to use this to compute a 'score2' for each junction. We obtain this score by summing the mapping qualities of the alignments crossing the junction:
gal <- readGAlignments(bamfile, param=ScanBamParam(what="mapq"))
junc_summary <- summarizeJunctions(gal, with.revmap=TRUE)
junc_score2 <- sum(extractList(mcols(gal)$mapq,
```
mcols(junc_summary)$revmap)

mcols(junc_summary)$score2 <- junc_score2

## If the name of the reference genome is specified thru the 'genome'
## argument (in which case the corresponding BSgenome data package needs
## to be installed), then summarizeJunctions() returns the intron motif
## and strand for each junction.
## Since the reads in RNAseqData.HNRNPC.bam.chr14 were aligned to
## the hg19 genome, the following requires that you have
## BSgenome.Hsapiens.UCSC.hg19 installed:
junc_summary <- summarizeJunctions(gal, with.revmap=TRUE, genome="hg19")
mcols(junc_summary)$score2 <- junc_score2 # putting 'score2' back

## The "intron_motif" metadata column is a factor whose levels are the
## 5 natural intron motifs stored in predefined character vector
## 'NATURAL_INTRON_MOTIFS':
table(mcols(junc_summary)$intron_motif)

## C. STRANDED RNA-seq PROTOCOL

## Here is a simple test for checking whether the RNA-seq protocol was
## stranded or not:
strandedTest <- function(plus_score, minus_score)
  (sum(plus_score ^ 2) + sum(minus_score ^ 2)) / 
  sum((plus_score + minus_score) ^ 2)

## The result of this test is guaranteed to be >= 0.5 and <= 1.
## If, for each junction, the strand of the crossing alignments looks
## random (i.e. "plus_score" and "minus_score" are close), then
## strandedTest() will return a value close to 0.5. If it doesn’t look
## random (i.e. for each junction, one of "plus_score" and "minus_score"
## is much bigger than the other), then strandedTest() will return a
## value close to 1.
## If the reads are single-end, the test is meaningful when applied
## directly on 'junc_summary'. However, for the test to be meaningful
## on paired-end reads, it needs to be applied on the first and last
## alignments separately:
junc_summary1 <- summarizeJunctions(first(galp))
junc_summary2 <- summarizeJunctions(last(galp))
strandedTest(mcols(junc_summary1)$plus_score, 
            mcols(junc_summary1)$minus_score)
strandedTest(mcols(junc_summary2)$plus_score, 
            mcols(junc_summary2)$minus_score)

## Both values are close to 0.5 which suggests that the RNA-seq protocol
## used for this experiment was not stranded.

## D. UTILITIES FOR IMPORTING THE JUNCTION FILE GENERATED BY SOME
## ALIGNERS

## The TopHat aligner generates a junctions.bed file where it reports
## all the junctions satisfying some "quality" criteria (see the TopHat
## manual at http://tophat.cbcb.umd.edu/manual.shtml for more
## information). This file can be loaded with readTopHatJunctions():
runname <- names(RNaseqData.HNRNPC.bam.chr14_BAMFILES)[1]
junctions_file <- system.file("extdata", "tophat2_out", runname,
"junctions.bed",
package="RNaseqData.HNRNPC.bam.chr14")

th_junctions <- readTopHatJunctions(junctions_file)

## Comparing the "TopHat junctions" with the result of
## summarizeJunctions():
seqlevels(th_junctions14, force=TRUE) <- "chr14"
mcols(th_junctions14)$intron_strand <- strand(th_junctions14)
strand(th_junctions14) <- "*"

## All the "TopHat junctions" are in `junc_summary`:
stopifnot(all(th_junctions14 %in% junc_summary))

## But not all the junctions in `junc_summary` are reported by TopHat
## (that's because TopHat reports only junctions that satisfy some
## "quality" criteria):
is_in_th_junctions14 <- junc_summary %in% th_junctions14
table(is_in_th_junctions14) # 32 junctions are not in TopHat's
# junctions.bed file

junc_summary2 <- junc_summary[is_in_th_junctions14]

## `junc_summary2` and `th_junctions14` contain the same junctions in
## the same order:
stopifnot(all(junc_summary2 == th_junctions14))

## Let's merge their metadata columns. We use our own version of
## merge() for this, which is stricter (it checks that the common
## columns are the same in the 2 data frames to merge) and also
## simpler:
merge2 <- function(df1, df2)
{
  common_colnames <- intersect(colnames(df1), colnames(df2))
  lapply(common_colnames,
         function(colname)
           stopifnot(all(df1[, colname] == df2[, colname])))
  extra_mcolnames <- setdiff(colnames(df2), colnames(df1))
  cbind(df1, df2[, extra_mcolnames, drop=FALSE])
}
mcols(th_junctions14) <- merge2(mcols(th_junctions14),
mcols(junc_summary2))

## Here is a peculiar junction reported by TopHat:
idx0 <- which(mcols(th_junctions14)$score2 == 0L)
th_junctions14[idx0] gal[mcols(th_junctions14)$revmap[[idx0]]]

## The junction is crossed by 5 alignments (score is 5), all of which
## have a mapping quality of 0!
Description

Map range coordinates between reads (local) and genome (reference) space using the CIGAR in a GAlignments object.

See ?mapToTranscripts in the GenomicRanges package for mapping coordinates between features in the transcriptome and genome space.

Usage

```r
## S4 method for signature 'GenomicRanges,GAlignments'
mapToAlignments(x, alignments, ...)
## S4 method for signature 'GenomicRanges,GAlignments'
pmapToAlignments(x, alignments, ...)
## S4 method for signature 'GenomicRanges,GAlignments'
mapFromAlignments(x, alignments, ...)
## S4 method for signature 'GenomicRanges,GAlignments'
pmapFromAlignments(x, alignments, ...)
```

Arguments

- `x` GenomicRanges object of positions to be mapped. `x` must have names when mapping to the genome.
- `alignments` A GAlignments object that represents the alignment of `x` to the genome. The alignments object must have names. When mapping to the genome names are used to determine mapping pairs and in the reverse direction they are used as the seqlevels of the output object.
- `...` Arguments passed to other methods.

Details

These methods use a GAlignments object to represent the alignment between the ranges in `x` and the output. The following CIGAR operations in the "Extended CIGAR format" are used in the mapping algorithm:

- M, X, = Sequence match or mismatch
- I Insertion to the reference
- D Deletion from the reference
- N Skipped region from the reference
- S Soft clip on the read
- H Hard clip on the read
- P Silent deletion from the padded reference

- `mapToAlignments, pmapToAlignments` The CIGAR is used to map the genomic (reference) position `x` to local coordinates. The mapped position starts at

  \[ \text{start}(x) - \text{start}(\text{alignments}) + 1 \]

and is incremented or decremented as the algorithm walks the length of the CIGAR. A successful mapping in this direction requires that `x` fall within `alignments`. The seqlevels of the return object are taken from the `alignments` object and will be a name descriptive of the read or aligned region. In this direction, mapping is attempted between all elements of `x` and all elements of `alignments`. 
mapToAlignments

- `mapToAlignments`, `pmapToAlignments` The CIGAR is used to map the local position \( x \) to genomic (reference) coordinates. The mapped position starts at

\[
\text{start}(x) + \text{start}(\text{alignments}) - 1
\]

and is incremented or decremented as the algorithm walks the length of the CIGAR. A successful mapping in this direction requires that the width of `alignments` is \( \leq \) the width of `x`.

When mapping to the genome, name matching is used to determine the mapping pairs (vs attempting to match all possible pairs). Ranges in `x` are only mapped to ranges in `alignments` with the same name. Name matching is motivated by use cases such as differentially expressed regions where the expressed regions in `x` would only be related to a subset of regions in `alignments`, which may contains gene or transcript ranges.

- `element-wise versions pmapToAlignments` and `pmapFromAlignments` are element-wise (aka 'parallel') versions of `mapToAlignments` and `mapFromAlignments`. The i-th range in `x` is mapped to the i-th range in `alignments`; `x` and `alignments` must have the same length.

Ranges in `x` that do not map (out of bounds) are returned as zero-width ranges starting at 0. These ranges are given the special seqname of "UNMAPPED". Note the non-parallel methods do not return unmapped ranges so the "UNMAPPED" seqname is unique to `pmapToAlignments` and `pmapFromAlignments`.

- `strand` By SAM convention, the CIGAR string is reported for mapped reads on the forward genomic strand. There is no need to consider strand in these methods. The output of these methods will always be unstranded (i.e., "*").

**Value**

An object the same class as `x`.

Parallel methods return an object the same shape as `x`. Ranges that cannot be mapped (out of bounds) are returned as zero-width ranges starting at 0 with a seqname of "UNMAPPED".

Non-parallel methods return an object that varies in length similar to a `Hits` object. The result only contains mapped records, out of bound ranges are not returned. `xHits` and `alignmentsHits` metadata columns indicate the elements of `x` and `alignments` used in the mapping.

When present, names from `x` are propagated to the output. When mapping locally, the seqlevels of the output are the names on the `alignment` object. When mapping globally, the output seqlevels are the seqlevels of `alignment` which are usually chromosome names.

**Author(s)**

V. Obenchain, M. Lawrence and H. Pagès

**See Also**

- `?mapToTranscripts` in the `GenomicFeatures` package for methods mapping between transcriptome and genome space.

**Examples**

```r
## ---------------------------------------------------------------------
## A. Basic use
## ---------------------------------------------------------------------
```
## 1. Map to local space with mapToAlignments()
## ---------------------------------------------------------------------

## Mapping to local coordinates requires 'x' to be within 'alignments'.
## In this 'x', the second range is too long and can't be mapped.
alignments <- GAlignments("chr1", 10L, "11M", strand("x"), names="read_A")
x <- GRanges("chr1", IRanges(c(12, 12), width=c(6, 20)))
mapToAlignments(x, alignments)

## The element-wise version of the function returns unmapped ranges
## as zero-width ranges with a seqlevel of "UNMAPPED":
pmapToAlignments(x, c(alignments, alignments))

## Mapping the same range through different alignments demonstrates
## how the CIGAR operations affect the outcome.
ops <- c("no-op", "junction", "insertion", "deletion")
x <- GRanges(rep("chr1", 4), IRanges(rep(12, 4), width=rep(6, 4), names=ops))
alignments <- GAlignments(rep("chr1", 4), rep(10L, 4),
                          cigar = c("11M", "5M2N4M", "5M2I4M", "5M2D4M"),
                          strand = strand(rep("x", 4)),
                          names = paste0("region_", 1:4))
pmapToAlignments(x, alignments)

## 2. Map to genome space with mapFromAlignments()
## ---------------------------------------------------------------------

## One of the criteria when mapping to genomic coordinates is that the
## shifted 'x' range falls within 'alignments'. Here the first 'x'
## range has a shifted start value of 14 (5 + 10 - 1 = 14) with a width of
## 2 and so is successfully mapped. The second has a shifted start of 29
## (20 + 10 - 1 = 29) which is outside the range of 'alignments'.
x <- GRanges("chr1", IRanges(c(5, 20), width=2, names=rep("region_A", 2)))
alignments <- GAlignments("chr1", 10L, "11M", strand("x"), names="region_A")
mapFromAlignments(x, alignments)

## Another characteristic of mapping this direction is the name matching
## used to determine pairs. Mapping is only attempted between ranges in 'x'
## and 'alignments' with the same name. If we change the name of the first 'x'
## range, only the second will be mapped to 'alignment'. We know the second
## range fails to map so we get an empty result.
names(x) <- c("region_B", "region_A")
mapFromAlignments(x, alignments)

## CIGAR operations: insertions reduce the width of the output while
## junctions and deletions increase it.
ops <- c("no-op", "junction", "insertion", "deletion")
x <- GRanges(rep("chr1", 4), IRanges(rep(3, 4), width=rep(5, 4), names=ops))
alignments <- GAlignments(rep("chr1", 4), rep(10L, 4),
                          cigar = c("11M", "5M2N4M", "5M2I4M", "5M2D4M"),
                          strand = strand(rep("x", 4)))
pmapFromAlignments(x, alignments)

## B. TATA box motif: mapping from read -> genome -> transcript
## ---------------------------------------------------------------------
The TATA box motif is a conserved DNA sequence in the core promoter region. Many eukaryotic genes have a TATA box located approximately 25-35 base pairs upstream of the transcription start site. The motif is the binding site of general transcription factors or histones and plays a key role in transcription.

In this example, the position of the TATA box motif (if present) is located in the DNA sequence corresponding to read ranges. The local motif positions are mapped to genome coordinates and then mapped to gene features such as promoters regions.

Load reads from chromosome 4 of D. melanogaster (dm3):
library(pasillaBamSubset)
fl <- untreated1_chr4()
gal <- readGAlignments(fl)

Extract DNA sequences corresponding to the read ranges:
library(GenomicFeatures)
library(BSgenome.Dmelanogaster.UCSC.dm3)
dna <- extractTranscriptSeqs(BSgenome.Dmelanogaster.UCSC.dm3, grglist(gal))

Search for the consensus motif TATAAA in the sequences:
box <- vmatchPattern("TATAAA", dna)

Some sequences had more than one match:
table(elementNROWS(box))

The element-wise function we'll use for mapping to genome coordinates requires the two input argument to have the same length. We need to replicate the read ranges to match the number of motifs found.

Expand the read ranges to match motifs found:
motif <- elementNROWS(box) != 0
alignments <- rep(gal[motif], elementNROWS(box)[motif])

We make the IRanges into a GRanges object so the seqlevels can propagate to the output. Seqlevels are needed in the last mapping step.
readCoords <- GRanges(seqnames(alignments), unlist(box, use.names=FALSE))

Map the local position of the motif to genome coordinates:
genomeCoords <- pmapFromAlignments(readCoords, alignments)
genomeCoords

We are interested in the location of the TATA box motifs in the promoter regions. To perform the mapping we need the promoter ranges as a GRanges or GRangesList.

Extract promoter regions 50 bp upstream from the transcription start site:
library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
promoters <- promoters(txdb, upstream=50, downstream=0)

Map the genome coordinates to the promoters:
names(promoters) <- mcols(promoters)$tx_name  ## must be named
mapToTranscripts(genomeCoords, promoters)
OverlapEncodings-class

OverlapEncodings objects

Description

The OverlapEncodings class is a container for storing the "overlap encodings" returned by the `encodeOverlaps` function.

Usage

```r
## OverlapEncodings accessors:
## S4 method for signature 'OverlapEncodings'
length(x)
## S4 method for signature 'OverlapEncodings'
Loffset(x)
## S4 method for signature 'OverlapEncodings'
Roffset(x)
## S4 method for signature 'OverlapEncodings'
encoding(x)
## S4 method for signature 'OverlapEncodings'
levels(x)
## S4 method for signature 'OverlapEncodings'
flippedQuery(x)

## S4 method for signature 'OverlapEncodings'
Lencoding(x)
## S4 method for signature 'OverlapEncodings'
Rencoding(x)

## S4 method for signature 'OverlapEncodings'
junc(x)
## S4 method for signature 'OverlapEncodings'
Lnjunc(x)
## S4 method for signature 'OverlapEncodings'
Rnjunc(x)

## Coercing an OverlapEncodings object:
## S4 method for signature 'OverlapEncodings'
as.data.frame(x, row.names=NULL, optional=FALSE, ...)
```
Low-level related utilities:

S4 method for signature 'character'
Lencoding(x)

S4 method for signature 'character'
Rencoding(x)

S4 method for signature 'character'
njunc(x)

S4 method for signature 'character'
Lnjunc(x)

S4 method for signature 'character'
Rnjunc(x)

S4 method for signature 'factor'
Lencoding(x)

S4 method for signature 'factor'
Rencoding(x)

S4 method for signature 'factor'
njunc(x)

S4 method for signature 'factor'
Lnjunc(x)

S4 method for signature 'factor'
Rnjunc(x)

Arguments

x An OverlapEncodings object. For the low-level utilities, x can also be a character vector or factor containing encodings.

row.names NULL or a character vector.

optional, ... Ignored.

Details

Given a query and a subject of the same length, both list-like objects with top-level elements typically containing multiple ranges (e.g. RangesList objects), the "overlap encoding" of the i-th element in query and i-th element in subject is a character string describing how the ranges in query[[i]] are qualitatively positioned relatively to the ranges in subject[[i]].

The encodeOverlaps function computes those overlap encodings and returns them in an OverlapEncodings object of the same length as query and subject.

The topic of working with overlap encodings is covered in details in the "OverlapEncodings" vignette located this package (GenomicAlignments) and accessible with vignette("OverlapEncodings").

OverlapEncodings accessor

In the following code snippets, x is an OverlapEncodings object typically obtained by a call to encodeOverlaps(query, subject).

length(x): Get the number of elements (i.e. encodings) in x. This is equal to length(query) and length(subject).

Loffset(x), Roffset(x): Get the "left offsets" and "right offsets" of the encodings, respectively. Both are integer vectors of the same length as x.
Let's denote \( Q_i = \text{query}[i] \), \( S_i = \text{subject}[i] \), and \( [q_1, q_2] \) the range covered by \( Q_i \) i.e. \( q_1 = \min(\text{start}(Q_i)) \) and \( q_2 = \max(\text{end}(Q_i)) \), then \( \text{Loffset}(x)[i] \) is the number \( L \) of ranges at the head of \( S_i \) that are strictly to the left of all the ranges in \( Q_i \) i.e. \( L \) is the greatest value such that \( \text{end}(S_i)[k] < q_1 - 1 \) for all \( k \) in \( \text{seq_len}(L) \). Similarly, \( \text{Roffset}(x)[i] \) is the number \( R \) of ranges at the tail of \( S_i \) that are strictly to the right of all the ranges in \( Q_i \) i.e. \( R \) is the greatest value such that \( \text{start}(S_i)[\text{length}(S_i) + 1 - k] > q_2 + 1 \) for all \( k \) in \( \text{seq_len}(L) \).

**encoding(x)**: Factor of the same length as \( x \) where the \( i \)-th element is the encoding obtained by comparing each range in \( Q_i \) with all the ranges in \( tS_i = S_i[(1+L):(\text{length}(S_i)-R)] \) (\( tS_i \) stands for "trimmed \( S_i \)"). More precisely, here is how this encoding is obtained:

1. All the ranges in \( Q_i \) are compared with \( tS_i[1] \), then with \( tS_i[2] \), etc... At each step (one step per range in \( tS_i \)), comparing all the ranges in \( Q_i \) with \( tS_i[k] \) is done with \( \text{rangeComparisonCodeToLetter}(\text{compare}(Q_i, tS_i[k])) \). So at each step, we end up with a vector of \( M \) single letters (where \( M \) is \( \text{length}(Q_i) \)).
2. Each vector obtained previously (1 vector per range in \( tS_i \), all of them of length \( M \)) is turned into a single string (called "encoding block") by pasting its individual letters together.
3. All the encoding blocks (1 per range in \( tS_i \)) are pasted together into a single long string and separated by colons (":"). An additional colon is prepended to the long string and another one appended to it.
4. Finally, a special block containing the value of \( M \) is prepended to the long string. The final string is the encoding.

**levels(x)**: Equivalent to \( \text{levels(encoding}(x)) \).

**flippedQuery(x)**: Whether or not the top-level element in query used for computing the encoding was "flipped" before the encoding was computed. Note that this flipping generally affects the "left offset", "right offset", in addition to the encoding itself.

**Lencoding(x)**, **Rencoding(x)**: Extract the "left encodings" and "right encodings" of paired-end encodings.

Paired-end encodings are obtained by encoding paired-end overlaps i.e. overlaps between paired-end reads and transcripts (typically). The difference between a single-end encoding and a paired-end encoding is that all the blocks in the latter contain a "--" separator to mark the separation between the "left encoding" and the "right encoding". See the "Overlap encodings" vignette located in this package for examples of paired-end encodings.

**njunc(x)**, **Lnjunc(x)**, **Rnjunc(x)**: Extract the number of junctions in each encoding by looking at their first block (aka special block). If an element \( x_i \) in \( x \) is a paired-end encoding, then \( \text{Lnjunc}(x_i), \text{Rnjunc}(x_i), \) and \( \text{njunc}(x_i) \), return \( \text{njunc}(\text{Lencoding}(x_i)), \text{njunc}(\text{Rencoding}(x_i)), \) and \( \text{Lnjunc}(x_i) + \text{Rnjunc}(x_i) \), respectively.

**Coercing an OverlapEncodings object**

In the following code snippets, \( x \) is an OverlapEncodings object.

**as.data.frame(x)**: Return \( x \) as a data frame with columns "Loffset", "Roffset" and "encoding".

**Author(s)**

Hervé Pagès
pileLettersAt

See Also

- The "OverlapEncodings" vignette in this package.
- The `encodeOverlaps` function for computing "overlap encodings".
- The `compare` function in the `IRanges` package for the interpretation of the strings returned by encoding.
- The `GRangesList` class defined and documented in the `GenomicRanges` package.

Examples

element(encodeOverlaps)  # to generate the 'ovenc' object

length(ovenc)
Loffset(ovenc)
Roffset(ovenc)
encoding(ovenc)
levels(ovenc)
nlevels(ovenc)
flippedQuery(ovenc)
njunc(ovenc)

as.data.frame(ovenc)
njunc(levels(ovenc))

pileLettersAt(x, seqnames, pos, cigar, at)

Description

`pileLettersAt` extracts the letters/nucleotides of a set of reads that align to a set of genomic positions of interest. The extracted letters are returned as "piles of letters" (one per genomic position of interest) stored in an `XStringSet` (typically `DNAStringSet`) object.

Usage

`pileLettersAt(x, seqnames, pos, cigar, at)`

Arguments

- `x`: An `XStringSet` (typically `DNAStringSet`) object containing `N` unaligned read sequences (a.k.a. the query sequences) reported with respect to the + strand.
- `seqnames`: A factor-Rle parallel to `x`. For each `i`, `seqnames[i]` must be the name of the reference sequence of the `i`-th alignment.
- `pos`: An integer vector parallel to `x`. For each `i`, `pos[i]` must be the 1-based position on the reference sequence of the first aligned letter in `x[[i]]`.
- `cigar`: A character vector parallel to `x`. Contains the extended CIGAR strings of the alignments.
At: A GPos object containing the genomic positions of interest. seqlevels(at) must be identical to levels(seqnames).

If at is not a GPos object, pileLettersAt will first try to turn it into one by calling the GPos() constructor function on it. So for example at can be a GRanges object (or any other GenomicRanges derivative), and, in that case, each range in it will be interpreted as a run of adjacent genomic positions. See ?GPos in the GenomicRanges package for more information.

Details

x, seqnames, pos, cigar must be 4 parallel vectors describing N aligned reads.

Value

An XStringSet (typically DNAStringSet) object parallel to at (i.e. with 1 string per genomic position).

Author(s)

Hervé Pagès

See Also

• The pileup and applyPileups functions defined in the Rsamtools package, as well as the SAMtools mpileup command (available at http://samtools.sourceforge.net/ as part of the SAMtools project), for more powerful flexible alternatives.
• The stackStringsFromBam function for stacking the read sequences (or their quality strings) stored in a BAM file on a region of interest.
• DNAStringSet objects in the Biostrings package.
• GPos objects in the GenomicRanges package.
• GAlignments objects.
• cigar-utils for the CIGAR utility functions used internally by pileLettersAt.

Examples

## Input

### - A BAM file:
bamfile <- BamFile(system.file("extdata", "ex1.bam", package="Rsamtools"))
seqinfo(bamfile) # to see the seqlevels and seqlengths
stackStringsFromBam(bamfile, param="seq1:1-21") # a quick look at the reads

### - A GPos object containing Genomic Positions Of Interest:
my_GPOI <- GPos(c("seq1:1-5", "seq1:21-21", "seq1:1575-1575", "seq2:1513-1514"))

### Some preliminary massage on 'my_GPOI'

seqinfo(my_GPOI) <- merge(seqinfo(my_GPOI), seqinfo(bamfile))
seqlevels(my_GPOI) <- seqlevelsInUse(my_GPOI)

### Load the BAM file in a GAlignments object. Note that we load only
## Description

Read genomic alignments from a file (typically a BAM file) into a `GAlignments`, `GAlignmentPairs`, `GAlignmentsList`, or `GappedReads` object.

## Usage

```r
readGAlignments(file, index=file, use.names=FALSE, param=NULL, with.which_label=FALSE)
```
readGAlignmentPairs(file, index=file, use.names=FALSE, param=NULL,
    with.which_label=FALSE, strandMode=1)

readGAlignmentsList(file, index=file, use.names=FALSE,
    param=ScanBamParam(), with.which_label=FALSE)

readGappedReads(file, index=file, use.names=FALSE, param=NULL,
    with.which_label=FALSE)

Arguments

file          The path to the file to read or a BamFile object. Can also be a BamViews object for readGAlignments.
index         The path to the index file of the BAM file to read. Must be given without the '.bai' extension. See scanBam in the Rsamtools packages for more information.
use.names     TRUE or FALSE. By default (i.e. use.names=FALSE), the resulting object has no names. If use.names is TRUE, then the names are constructed from the query template names (QNAME field in a SAM/BAM file). Note that the 2 records in a pair (when using readGAlignmentPairs or the records in a group (when using readGAlignmentsList) have the same QNAME.
param         NULL or a ScanBamParam object. Like for scanBam, this influences what fields and which records are imported. However, note that the fields specified thru this ScanBamParam object will be loaded in addition to any field required for generating the returned object (GAlignments, GAlignmentPairs, or GappedReads object), but only the fields requested by the user will actually be kept as metadata columns of the object.

By default (i.e. param=NULL or param=ScanBamParam()), no additional field is loaded. The flag used is scanBamFlag(isUnmappedQuery=FALSE) for readGAlignments, readGAlignmentsList, and readGappedReads. (i.e. only records corresponding to mapped reads are loaded), and scanBamFlag(isUnmappedQuery=FALSE, isPaired=TRUE, for readGAlignmentPairs (i.e. only records corresponding to paired-end reads with both ends mapped are loaded).

with.which_label

TRUE or FALSE (the default). If TRUE and if param has a which component, a "which_label" metadata column is added to the returned GAlignments or GappedReads object, or to the first and last components of the returned GAlignmentPairs object. In the case of readGAlignmentsList, it’s added as an inner metadata column, that is, the metadata column is placed on the GAlignments object obtained by unlisting the returned GAlignmentsList object.

The purpose of this metadata column is to unambiguously identify the range in which where each element in the returned object originates from. The labels used to identify the ranges are normally of the form "seq1:12250-246500", that is, they’re the same as the names found on the outer list that scanBam would return if called with the same param argument. If some ranges are duplicated, then the labels are made unique by appending a unique suffix to all of them. The "which_label" metadata column is represented as a factor-Rle.

strandMode    Strand mode to set on the returned GAlignmentPairs object. See ?strandMode for more information.
Details

- `readGAlignments` reads a file containing aligned reads as a `GAlignments` object. See ?`GAlignments` for a description of `GAlignments` objects.

  When file is a `BamViews` object, `readGAlignments` visits each path in `bamPaths(file)`, returning the result of `readGAlignments` applied to the specified path. When index is missing, it is set equal to `bamIndices(file)`. Only reads in `bamRanges(file)` are returned (if `param` is supplied, `bamRanges(file)` takes precedence over `bamWhich(param)`). The return value is a `SimpleList` object, with elements of the list corresponding to each path. `bamSamples(file)` is available as metadata columns (accessed with `mcols`) of the returned `SimpleList` object.


- `readGAlignmentsList` reads a file containing aligned reads as a `GAlignmentsList` object. See ?`GAlignmentsList` for a description of `GAlignmentsList` objects.

  `readGAlignmentsList` pairs records into mates according to the pairing criteria described below. The 1st mate will always be 1st in the `GAlignmentsList` list elements that have `mate_status` set to "mated", and the 2nd mate will always be 2nd.

  A `GAlignmentsList` is returned with a 'mate_status' metadata column on the outer list elements. `mate_status` is a factor with 3 levels indicating mate status, 'mated', 'ambiguous' or 'unmated':
  - mated: primary or non-primary pairs
  - ambiguous: multiple segments matching to the same location (indistinguishable)
  - unmated: mate does not exist or is unmapped

  When the 'file' argument is a `BamFile`, 'asMates=TRUE' must be set, otherwise the data are treated as single-end reads. See the 'asMates' section of ?`BamFile` in the `Rsamtools` package for details.


For all these functions, flags, tags and ranges may be specified in the supplied `ScanBamParam` object for fine tuning of results.

Value

A `GAlignments` object for `readGAlignments`.

A `GAlignmentPairs` object for `readGAlignmentPairs`. Note that a BAM (or SAM) file can in theory contain a mix of single-end and paired-end reads, but in practise it seems that single-end and paired-end are not mixed. In other words, the value of flag bit 0x1 (`isPaired`) is the same for all the records in a file. So if `readGAlignmentPairs` returns a `GAlignmentPairs` object of length zero, this almost always means that the BAM (or SAM) file contains alignments for single-end reads (although it could also mean that the user-supplied `ScanBamParam` is filtering out everything, or that the file is empty, or that all the records in the file correspond to unmapped reads).

A `GAlignmentsList` object for `readGAlignmentsList`. When the list contains paired-end reads a metadata data column of `mate_status` is added to the object. See details in the 'Bam specific back-ends' section on this man page.

A `GappedReads` object for `readGappedReads`.

Pairing criteria

This section describes the pairing criteria used by `readGAlignmentsList` and `readGAlignmentPairs`. 
• First, only records with flag bit 0x1 (multiple segments) set to 1, flag bit 0x4 (segment unmapped) set to 0, and flag bit 0x8 (next segment in the template unmapped) set to 0, are candidates for pairing (see the SAM Spec for a description of flag bits and fields). Records that correspond to single-end reads, or records that correspond to paired-end reads where one or both ends are unmapped, will remain unmated.

• Then the following fields and flag bits are considered:
  - (A) QNAME
  - (B) RNAME, RNEXT
  - (C) POS, PNEXT
  - (D) Flag bits 0x10 (segment aligned to minus strand) and 0x20 (next segment aligned to minus strand)
  - (E) Flag bits 0x40 (first segment in template) and 0x80 (last segment in template)
  - (F) Flag bit 0x2 (proper pair)
  - (G) Flag bit 0x100 (secondary alignment)

2 records rec1 and rec2 are considered mates iff all the following conditions are satisfied:
  - (A) QNAME(rec1) == QNAME(rec2)
  - (B) RNEXT(rec1) == RNAME(rec2) and RNEXT(rec2) == RNAME(rec1)
  - (C) PNEXT(rec1) == POS(rec2) and PNEXT(rec2) == POS(rec1)
  - (D) Flag bit 0x20 of rec1 == Flag bit 0x10 of rec2 and Flag bit 0x20 of rec2 == Flag bit 0x10 of rec1
  - (E) rec1 corresponds to the first segment in the template and rec2 corresponds to the last segment in the template, OR, rec2 corresponds to the first segment in the template and rec1 corresponds to the last segment in the template
  - (F) rec1 and rec2 have same flag bit 0x2
  - (G) rec1 and rec2 have same flag bit 0x100

Note that this is actually the pairing criteria used by scanBam (when the BamFile passed to it has the asMates toggle set to TRUE), which readGAlignmentsList and readGAlignmentPairs call behind the scene. It is also the pairing criteria used by findMateAlignment.

Note

BAM records corresponding to unmapped reads are always ignored.

Starting with Rsamtools 1.7.1 (BioC 2.10), PCR or optical duplicates are loaded by default (use scanBamFlag(isDuplicate=FALSE) to drop them).

Author(s)

Hervé Pagès <hpages@fredhutch.org> and Valerie Obenchain <vobencha@fredhutch.org>

See Also

• scanBam and ScanBamParam in the Rsamtools package.
• GAlignments, GAlignmentPairs, GAlignmentsList, and GappedReads objects.
• RangesList objects (used in the examples below to specify the which regions) in the IRanges package.
Examples

## Examples

---

### A. readGAlignments()

```r
# Simple use:
bamfile <- system.file("extdata", "ex1.bam", package="Rsamtools",
                   mustWork=TRUE)
gal1 <- readGAlignments(bamfile)
gal1
names(gal1)

# Using the 'use.names' arg:
gal2 <- readGAlignments(bamfile, use.names=TRUE)
gal2
head(names(gal2))

# Using the 'param' arg to drop PCR or optical duplicates as well as
# secondary alignments, and to load additional BAM fields:
param <- ScanBamParam(flag=scanBamFlag(isDuplicate=FALSE,
                                    isSecondaryAlignment=FALSE),
                      what=c("qual", "flag"))
gal3 <- readGAlignments(bamfile, param=param)
gal3
mcols(gal3)

# Using the 'param' arg to load alignments from particular regions.
which <- RangesList(seq1=IRanges(1000, 1100),
                    seq2=IRanges(c(1546, 1555, 1567), width=10))
param <- ScanBamParam(which=which)
gal4 <- readGAlignments(bamfile, use.names=TRUE, param=param)
gal4

# IMPORTANT NOTE: A given record is loaded one time for each region
# it overlaps with. We call this "duplicated record selection" (this
# is a scanBam() feature, readGAlignments() is based on scanBam()):
which <- RangesList(seq1=rep(IRanges(1000, 1100), 2),
                    seq2=IRanges(c(1546, 1555, 1567), width=10))
param <- ScanBamParam(which=which)
gal5b <- readGAlignments(bamfile, use.names=TRUE, param=param)
length(gal5b) # > length(gal4), because all the records overlapping
```

---

This becomes clearer if we use 'with.which_label=TRUE' to identify
the region in 'which' where each element in 'gal5' originates from.
gal5 <- readGAlignments(bamfile, use.names=TRUE, param=param,
                        with.which_label=TRUE)
gal5

# Not surprisingly, we also get "duplicated record selection" when
# 'which' contains repeated or overlapping regions. Using the same
# regions as we did for 'gal4' above, except that now we're
# repeating the region on seq1:
which <- RangesList(seq1=rep(IRanges(1000, 1100), 2),
                    seq2=IRanges(c(1546, 1555, 1567), width=10))
param <- ScanBamParam(which=which)
gal4b <- readGAlignments(bamfile, use.names=TRUE, param=param)
length(gal4b) # > length(gal4), because all the records overlapping
# with bases 1000 to 1100 on seq1 are now duplicated

## The "duplicated record selection" will artificially increase the ## coverage or affect other downstream results. It can be mitigated ## (but not completely eliminated) by first "reducing" the set of ## regions:
which <- reduce(which)
which
param <- ScanBamParam(which=which)
gal4c <- readGAlignments(bamfile, use.names=TRUE, param=param)
length(gal4c) # < length(gal4), because the 2 first original regions # on seq2 were merged into a single one

## Note that reducing the set of regions didn't completely eliminate ## "duplicated record selection". Records that overlap the 2 reduced ## regions on seq2 (which$seq2) are loaded twice (like for 'gal5' ## above). See example D. below for how to completely eliminate ## "duplicated record selection".

## Using the 'param' arg to load tags. Except for MF and Aq, the tags ## specified below are predefined tags (see the SAM Spec for the list ## of predefined tags and their meaning).
param <- ScanBamParam(tag=c("MF", "Aq", "NM", "UQ", "H0", "H1"), what="isize")
gal6 <- readGAlignments(bamfile, param=param)
mcols(gal6) # "tag" cols always after "what" cols

## With a BamViews object:
fls <- system.file("extdata", "ex1.bam", package="Rsamtools", mustWork=TRUE)
bv <- BamViews(fls, 
  bamSamples=DataFrame(info="test", row.names="ex1"),
  auto.range=TRUE)

## Note that the "readGAlignments" method for BamViews objects ## requires the ShortRead package to be installed.

## B. readGAlignmentPairs()

## Here we use the 'param' arg to filter by proper pair, drop PCR / ## optical duplicates, and drop secondary alignments. Filtering by ## proper pair and dropping secondary alignments can help make the ## pairing algorithm run significantly faster:
param <- ScanBamParam(flag=scanBamFlag(isProperPair=TRUE, 
  isDuplicate=FALSE, 
  isSecondaryAlignment=FALSE))
galp2 <- readGAlignmentPairs(bamfile, use.names=TRUE, param=param)
galp2
readGAlignments

## C. readGAlignmentsList()

```r
library(pasillaBamSubset)

# 'file' as character.
bam <- untreated3_chr4()
galist1 <- readGAlignmentsList(bam)
galist1[1:3]
length(galist1)
table(elementNROWS(galist1))
```

## When 'file' is a BamFile, 'asMates' must be TRUE. If FALSE, the data are treated as single-end and each list element of the # GAlignmentsList will be of length 1. For single-end data # use readGAlignments().
bamfile <- BamFile(bam, yieldSize=3, asMates=TRUE)
readGAlignmentsList(bamfile)

## Use a 'param' to fine tune the results.
param <- ScanBamParam(flag=scanBamFlag(isProperPair=TRUE))
galist2 <- readGAlignmentsList(bam, param=param)
length(galist2)

## D. COMPARING 4 STRATEGIES FOR LOADING THE ALIGNMENTS THAT OVERLAP WITH THE EXONIC REGIONS ON FLY CHROMOSOME 4

```r
library(pasillaBamSubset)
bam <- untreated1_chr4()

library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
ex <- exons(txdb)
seqlevels(ex, force=TRUE) <- "chr4"
length(ex)

# Some of the exons overlap with each other:
isDisjoint(ex) # FALSE
exonic_regions <- reduce(ex)
isDisjoint(exonic_regions) # no more overlaps
length(exonic_regions)
```

## Strategy #1: slow and loads a lot of records more than once (see "duplicated record selection" in example A. above).
```
param1 <- ScanBamParam(which=ex)
gal1 <- readGAlignments(bam, param=param1)
length(gal1) # many "duplicated records"
```

## Strategy #2: faster and generates less duplicated records but doesn't eliminate them.
```
param2 <- ScanBamParam(which=exonic_regions)
gal2 <- readGAlignments(bam, param=param2)
length(gal2) # less "duplicated records"
```
## Strategy #3: fast and completely eliminates duplicated records.

```r
gal0 <- readGAlignments(bam)
gal3 <- subsetByOverlaps(gal0, exonic_regions, ignore.strand=TRUE)
length(gal3) # no "duplicated records"
```

## Note that, in this case using 'exonic_regions' or 'ex' makes no difference:

```r
gal3b <- subsetByOverlaps(gal0, ex, ignore.strand=TRUE)
stopifnot(identical(gal3, gal3b))
```

## Strategy #4: strategy #3 however can require a lot of memory if the file is big because we load all the alignments into memory before we select those that overlap with the exonic regions. Strategy #4 addresses this by loading the file by chunks.

```r
bamfile <- BamFile(bam, yieldSize=50000)
open(bamfile)
while (length(chunk0 <- readGAlignments(bamfile))) {
  chunk <- subsetByOverlaps(chunk0, ex, ignore.strand=TRUE)
  cat("chunk0:", length(chunk0), "- chunk:", length(chunk), "\n")
  ## ... do something with 'chunk' ... 
}
close(bamfile)
```

## E. readGappedReads()

```r
greads1 <- readGappedReads(bamfile)
greads1
names(greads1)
qseq(greads1)
greads2 <- readGappedReads(bamfile, use.names=TRUE)
head(greads2)
head(names(greads2))
```

---

### sequenceLayer

**Lay read sequences alongside the reference space, using their CIGARs**

**Description**

The `sequenceLayer` function can lay strings that belong to a given space (e.g. the "query" space) alongside another space (e.g. the "reference" space) by removing/injecting substrings from/into them, using the supplied CIGARs.

Its primary use case is to lay the read sequences stored in a BAM file (which are considered to belong to the "query" space) alongside the "reference" space. It can also be used to remove the parts of the read sequences that correspond to soft-clipping. More generally it can lay strings that belong to any supported space alongside any other supported space. See the Details section below for the list of supported spaces.

**Usage**

```r
sequenceLayer(x, cigar, from="query", to="reference",
    D.letter="-", N.letter=".",
    I.letter="-", S.letter="+", H.letter="+")
```
sequenceLayer

Arguments

\textbf{x} \quad \text{An XStringSet object containing strings that belong to a given space.}

\textbf{cigar} \quad \text{A character vector or factor of the same length as x containing the extended CIGAR strings (one per element in x).}

\textbf{from, to} \quad \text{A single string specifying one of the 8 supported spaces listed in the Details section below. from must be the current space (i.e. the space the strings in x belong to) and to is the space alongside which to lay the strings in x.}

\textbf{D.letter, N.letter, I.letter, S.letter, H.letter} \quad \text{A single letter used as a filler for injections. More on this in the Details section below.}

Details


Each space can be characterized by the extended CIGAR operations that are \textit{visible} in it. A CIGAR operation is said to be \textit{visible} in a given space if it "runs along it", that is, if it’s associated with a block of contiguous positions in that space (the size of the block being the length of the operation). For example, the M/=X operations are \textit{visible} in all spaces, the D/N operations are \textit{visible} in the "reference" space but not in the "query" space, the S operation is \textit{visible} in the "query" space but not in the "reference" or in the "query-after-soft-clipping" space, etc...

Here are the extended CIGAR operations that are \textit{visible} in each space:

1. reference: M, D, N, =, X
2. reference-N-regions-removed: M, D, =, X
3. query: M, I, S, =, X
5. query-after-soft-clipping: M, I, =, X
6. pairwise: M, I, D, N, =, X
7. pairwise-N-regions-removed: M, I, D, =, X
8. pairwise-dense: M, =, X

sequenceLayer lays a string that belongs to one space alongside another by (1) removing the substrings associated with operations that are not \textit{visible} anymore in the new space, and (2) injecting substrings associated with operations that become \textit{visible} in the new space. Each injected substring has the length of the operation associated with it, and its content is controlled via the corresponding \textit{*.letter} argument.

For example, when going from the "query" space to the "reference" space (the default), the I- and S-substrings (i.e. the substrings associated with I/S operations) are removed, and substrings associated with D/N operations are injected. More precisely, the D-substrings are filled with the letter specified in D.letter, and the N-substrings with the letter specified in N.letter. The other \textit{*.letter} arguments are ignored in that case.

Value

An XStringSet object of the same class and length as \textit{x}.

Author(s)

Hervé Pagès
sequenceLayer

See Also

- The `stackStringsFromBam` function for stacking the read sequences (or their quality strings) stored in a BAM file on a region of interest.
- The `readGAlignments` function for loading read sequences from a BAM file (via a `GAlignments` object).
- The `extractAt` and `replaceAt` functions in the `Biostrings` package for extracting/replacing arbitrary substrings from/in a string or set of strings.
- `cigar-utils` for the CIGAR utility functions used internally by `sequenceLayer`.

Examples

```r
## A. FROM "query" TO "reference" SPACE
## ---------------------------------------------------------------------
## Load read sequences from a BAM file (they will be returned in a
## GAlignments object):
## Load read sequences from a BAM file (they will be returned in a
bamfile <- system.file("extdata", "ex1.bam", package="Rsamtools")
param <- ScanBamParam(what="seq")
gal <- readGAlignments(bamfile, param=param)
qseq <- mcols(gal)$seq  # the read sequences (aka query sequences)

## Lay the query sequences alongside the reference space. This will
## remove the substrings associated with insertions to the reference
## (I operations) and soft clipping (S operations), and will inject new
## substrings (filled with "-") where deletions from the reference (D
## operations) and skipped regions from the reference (N operations)
## occurred during the alignment process:
qseq_on_ref <- sequenceLayer(qseq, cigar(gal))

## A typical use case for doing the above is to compute 1 consensus
## sequence per chromosome. The code below shows how this can be done
## in 2 extra steps.

## Step 1: Compute one consensus matrix per chromosome.
qseq_on_ref_by_chrom <- splitAsList(qseq_on_ref, seqnames(gal))
pos_by_chrom <- splitAsList(start(gal), seqnames(gal))

cm_by_chrom <- lapply(names(pos_by_chrom),
  function(seqname)
    consensusMatrix(qseq_on_ref_by_chrom[[seqname]],
      as.prob=TRUE,
      shift=pos_by_chrom[[seqname]]-1,
      width=seqlengths(gal)[[seqname]]))
names(cm_by_chrom) <- names(pos_by_chrom)

'cm_by_chrom' is a list of consensus matrices. Each matrix has 17
## rows (1 per letter in the DNA alphabet) and 1 column per chromosome
## position.

## Step 2: Compute the consensus string from each consensus matrix.
## We'll put "*" in the strings wherever there is no coverage for that
## position, and "N" where there is coverage but no consensus.
cs_by_chrom <- lapply(cm_by_chrom,
  function(cm) {
```
```
## Because consensusString() doesn't like consensus matrices
## with columns that contain only zeroes (and you will have
## columns like that for chromosome positions that don't
## receive any coverage), we need to "fix" cm' first.
idx <- colSums(cm) == 0
cm["+", idx] <- 1
DNAString(consensusString(cm, ambiguityMap="N"))

## consensusString() provides some flexibility to let you extract
## the consensus in different ways. See ?consensusString in the
## Biostrings package for the details.

## Finally, note that the read quality strings can also be used as
## input for sequenceLayer():
param <- ScanBamParam(what="qual")
gal <- readGAlignments(bamfile, param=param)
qual <- mcols(gal)$qual # the read quality strings
qual_on_ref <- sequenceLayer(qual, cigar(gal))

## Note that since the "-" letter is a valid quality code, there is
## no way to distinguish it from the "-" letters inserted by
## sequenceLayer().

## B. FROM "query" TO "query-after-soft-clipping" SPACE
## Going from "query" to "query-after-soft-clipping" simply removes
## the substrings associated with soft clipping (S operations):
qseq <- DNAStringSet(c("AAAGTTCGAA", "TTACGATTAN", "GGATAATTTT"))
cigar <- c("3H10M", "2S7M1S2H", "2M1I1M3D2M4S")
clipped_qseq <- sequenceLayer(qseq, cigar,
from="query", to="query-after-soft-clipping")

sequenceLayer(clipped_qseq, cigar,
from="query-after-soft-clipping", to="query")

## C. BRING QUERY AND REFERENCE SEQUENCES TO THE "pairwise" or
## "pairwise-dense" SPACE
## Load read sequences from a BAM file:
library(RNaseqData.HNRNPC.bam.chr14)
bamfile <- RNaseqData.HNRNPC.bam.chr14_BAMFILES[1]
param <- ScanBamParam(what="seq",
which=GRanges("chr14", IRanges(1, 25000000)))
gal <- readGAlignments(bamfile, param=param)
qseq <- mcols(gal)$seq # the read sequences (aka query sequences)

Load the corresponding reference sequences from the appropriate
BSgenome package (the reads in RNaseqData.HNRNPC.bam.chr14 were
aligned to hg19):
library(BSgenome.Hsapiens.UCSC.hg19)
rseq <- getSeq(Hsapiens, as(gal, "GRanges")) # the reference sequences

## Bring 'qseq' and 'rseq' to the "pairwise" space.
## For 'qseq', this will remove the substrings associated with soft
## clipping (S operations) and inject substrings (filled with "-")
## associated with deletions from the reference (D operations) and
## skipped regions from the reference (N operations). For 'rseq', this
## will inject substrings (filled with "-") associated with insertions
## to the reference (I operations).
qseq2 <- sequenceLayer(qseq, cigar(gal),
                     from="query", to="pairwise")
rseq2 <- sequenceLayer(rseq, cigar(gal),
                     from="reference", to="pairwise")

## Sanity check: 'qseq2' and 'rseq2' should have the same shape.
stopifnot(identical(elementNROWS(qseq2), elementNROWS(rseq2)))

## A closer look at reads with insertions and deletions:
cigar_op_table <- cigarOpTable(cigar(gal))
head(cigar_op_table)

I_idx <- which(cigar_op_table[, "I"] >= 2) # at least 2 insertions
qseq2[I_idx]
rseq2[I_idx]

D_idx <- which(cigar_op_table[, "D"] >= 2) # at least 2 deletions
qseq2[D_idx]
rseq2[D_idx]

## A closer look at reads with skipped regions:
N_idx <- which(cigar_op_table[, "N"] != 0)
qseq2[N_idx]
rseq2[N_idx]

## A variant of the "pairwise" space is the "pairwise-dense" space.
## In that space, all indels and skipped regions are removed from 'qseq'
## and 'rseq'.
qseq3 <- sequenceLayer(qseq, cigar(gal),
                     from="query", to="pairwise-dense")
rseq3 <- sequenceLayer(rseq, cigar(gal),
                     from="reference", to="pairwise-dense")

## Sanity check: 'qseq3' and 'rseq3' should have the same shape.
stopifnot(identical(elementNROWS(qseq3), elementNROWS(rseq3)))

## Insertions were removed:
qseq3[I_idx]
rseq3[I_idx]

## Deletions were removed:
qseq3[D_idx]
rseq3[D_idx]

## Skipped regions were removed:
qseq3[N_idx]
rseq3[N_idx]
## D. SANITY CHECKS

```r
cigarWidth <- list(
function(cigar) cigarWidthAlongReferenceSpace(cigar),
function(cigar) cigarWidthAlongReferenceSpace(cigar, N.regions.removed=TRUE),
function(cigar) cigarWidthAlongQuerySpace(cigar),
function(cigar) cigarWidthAlongQuerySpace(cigar, before.hard.clipping=TRUE),
function(cigar) cigarWidthAlongQuerySpace(cigar, after.soft.clipping=TRUE),
function(cigar) cigarWidthAlongPairwiseSpace(cigar),
function(cigar) cigarWidthAlongPairwiseSpace(cigar, N.regions.removed=TRUE),
function(cigar) cigarWidthAlongPairwiseSpace(cigar, dense=TRUE)
)
cigar <- c("3H2S4M1D2M2I1M5N3M6H", "5M1I3M2D4M2S")
seq <- list(
BStringSet(c(A="AAAA-BBC.....DDD", B="AAAAABBB--CCCC")),
BStringSet(c(A="AAAA--BCDODD", B="AAAAABBB--CCCC")),
BStringSet(c(A="++AAAABBiiCDDD", B="AAAAAiBBBCCCC++")),
BStringSet(c(A="++++AAAAABBBiiCDDD++++++", B="AAAAAiBBBCCCC++")),
BStringSet(c(A="AAAABBBiiCDDD", B="AAAAAiBBBCCCC")),
BStringSet(c(A="AAAA-BBBiiC......DDD", B="AAAAAiBBB--CCCC")),
BStringSet(c(A="AAAA-BBBiiCDCDDD", B="AAAAAiBBB--CCCC")),
BStringSet(c(A="AAAAABBBiCDCDDD", B="AAAAABBBCCCC"))
)
stopifnot(all(sapply(1:8, function(i) identical(width(seq[[i]]), cigarWidth[[i]](cigar)))))
sequenceLayer2 <- function(x, cigar, from, to)
    sequenceLayer(x, cigar, from=from, to=to, I.letter="i")
identical_XStringSet <- function(target, current)
{
    ok1 <- identical(class(target), class(current))
    ok2 <- identical(names(target), names(current))
    ok3 <- all(target == current)
    ok1 && ok2 && ok3
}
res <- sapply(1:8, function(i) {
    ...
}
```
```r
tsapply(1:8, function(j) {
  target <- seq[[j]]
  current <- sequenceLayer2(seq[[i]], cigar,
                            from=SPACES[i], to=SPACES[j])
  identical_XStringSet(target, current)
})
```

Description

Perform set operations on `GAlignments` objects.

NOTE: The `pintersect` generic function and method for `Ranges` objects is defined and documented in the `IRanges` package. Methods for `GRanges` and `GRangesList` objects are defined and documented in the `GenomicRanges` package.

Usage

```r
## S4 method for signature 'GAlignments,GRanges'
pintersect(x, y, ...)
## S4 method for signature 'GRanges,GAlignments'
pintersect(x, y, ...)
```

Arguments

- `x, y` A `GAlignments` object and a `GRanges` object. They must have the same length.
- `...` Further arguments to be passed to or from other methods.

Value

A `GAlignments` object parallel to (i.e. same length as) `x` and `y`.

See Also

- The `GAlignments` class.
- The `setops-methods` man page in the `GenomicRanges` package.

Examples

```r
## Parallel intersection of a GAlignments and a GRanges object:
nsys <- system.file("extdata", "ex1.bam", package="Rsamtools")
gal <- readGAlignments(nsys)
pintersect(gal, shift(as(gal, "GRanges"), 6))
```
**stackStringsFromBam**  
*Stack the read sequences stored in a BAM file on a region of interest*

**Description**

`stackStringsFromBam` stacks the read sequences (or their quality strings) stored in a BAM file over a user-specified region.

`alphabetFrequencyFromBam` computes the alphabet frequency of the reads over a user-specified region.

Both functions take into account the CIGAR of each read to "lay" the read sequence (or its quality string) alongside the reference space. This step ensures that each nucleotide in a read is associated with the correct position on the reference sequence.

**Usage**

```r
stackStringsFromBam(file, index=file, param,
                    what="seq", use.names=FALSE,
                    D.letter="-", N.letter=".",
                    Lpadding.letter="+", Rpadding.letter="+")

alphabetFrequencyFromBam(file, index=file, param, what="seq", ...)
```

**Arguments**

- `file, index`  
  The path to the BAM file to read, and to the index file of the BAM file to read, respectively. The latter is given without the `.bai` extension. See `scanBam` for more information.

- `param`  
  A `ScanBamParam` object containing exactly 1 genomic region (i.e. `unlist(bamWhich(param))` must have length 1). Alternatively, `param` can be a `GRanges` or `RangesList` object containing exactly 1 genomic region (the strand will be ignored in case of a `GRanges` object), or a character string specifying a single genomic region (in the `"chr14:5201-5300"` format).

- `what`  
  A single string. Either "seq" or "qual". If "seq" (the default), the read sequences will be stacked. If "qual", the read quality strings will be stacked.

- `use.names`  
  Use the query template names (QNAME field) as the names of the returned object? If not (the default), then the returned object has no names.

- `D.letter, N.letter`  
  A single letter used as a filler for injections. The 2 arguments are passed down to the `sequenceLayer` function. See `?sequenceLayer` for more details.

- `Lpadding.letter, Rpadding.letter`  
  A single letter to use for padding the sequences on the left, and another one to use for padding on the right. The 2 arguments are passed down to the `stackStrings` function defined in the `Biostrings` package. See `?stackStrings` in the `Biostrings` package for more details.

- `...`  
  Further arguments to be passed to `alphabetFrequency`.
Details

`stackStringsFromBam` performs the 3 following steps:

1. Load the read sequences (or their quality strings) from the BAM file. Only the read sequences that overlap with the specified region are loaded. This is done with the `readGAlignments` function. Note that if the file contains paired-end reads, the pairing is ignored.
2. Lay the sequences alongside the reference space, using their CIGARs. This is done with the `sequenceLayer` function.
3. Stack them on the specified region. This is done with the `stackStrings` function defined in the `Biostrings` package.

`alphabetFrequencyFromBam` also performs steps 1. and 2. but, instead of stacking the sequences at step 3., it computes the nucleotide frequencies for each genomic position in the specified region.

Value

For `stackStringsFromBam`: A rectangular (i.e. constant-width) `DNAStringSet` object (if what is "seq") or `BStringSet` object (if what is "qual").

For `alphabetFrequencyFromBam`: By default a matrix like one returned by `alphabetFrequency`. The matrix has 1 row per nucleotide position in the specified region.

Note

TWO IMPORTANT CAVEATS ABOUT `stackStringsFromBam`:

Specifying a big genomic region, say >= 100000 bp, can require a lot of memory (especially with high coverage reads) and is not recommended. See the `pileLettersAt` function for piling the read letters on top of a set of genomic positions, which is more flexible and more memory efficient.

Paired-end reads are treated as single-end reads (i.e. they’re not paired).

Author(s)

Hervé Pagès

See Also

- The `pileLettersAt` function for piling the letters of a set of aligned reads on top of a set of genomic positions.
- The `readGAlignments` function for loading read sequences (or their quality strings) from a BAM file (via a `GAlignments` object).
- The `sequenceLayer` function for laying read sequences alongside the reference space, using their CIGARs.
- The `stackStrings` function in the `Biostrings` package for stacking an arbitrary `XStringSet` object.
- The `alphabetFrequency` function in the `Biostrings` package.
Examples

```r
## A. EXAMPLE WITH TOY DATA

bamfile1 <- BamFile(system.file("extdata", "ex1.bam", package="Rsamtools"))
region1 <- GRanges("seq1", IRanges(1, 60))  # region of interest

## Stack the read sequences:
stackStringsFromBam(bamfile1, param=region1)

## Compute the "consensus matrix" (1 column per nucleotide position
## in the region of interest):
af <- alphabetFrequencyFromBam(bamfile1, param=region1, baseOnly=TRUE)
af <- t(af[, DNA_BASES])

## Stack their quality strings:
stackStringsFromBam(bamfile1, param=region1, what="qual")

## Control the number of reads to display:
options(showHeadLines=18)
options(showTailLines=6)
stackStringsFromBam(bamfile1, param=GRanges("seq1", IRanges(61, 120)))

## Region of interest:
region2 <- GRanges("chr14", IRanges(19650095, 19650159))

## Stack the read sequences:
stackStringsFromBam(bamfile1, param=region2)

## Compute the "consensus matrix" (1 column per nucleotide position
## in the region of interest):
af <- alphabetFrequencyFromBam(bamfile1, param=region2, baseOnly=TRUE)
af <- t(af[, DNA_BASES])

## Stack their quality strings:
stackStringsFromBam(bamfile1, param=region2, what="qual")
```

## B. EXAMPLE WITH REAL DATA

```r
library(RNAseqData.HNRNPC.bam.chr14)
bamfile2 <- BamFile(RNAseqData.HNRNPC.bam.chr14_BAMFILES[1])

## Region of interest:
region2 <- GRanges("chr14", IRanges(19650095, 19650159))

## Stack the read sequences:
stackStringsFromBam(bamfile2, param=region2)

## Compute the "consensus matrix" (1 column per nucleotide position
## in the region of interest):
af <- alphabetFrequencyFromBam(bamfile2, param=region2, baseOnly=TRUE)
af <- t(af[, DNA_BASES])
```

## C. COMPUTE READ CONSENSUS SEQUENCE FOR REGION OF INTEREST

Let's write our own little naive function to go from consensus matrix to consensus sequence. For each nucleotide position in the region of interest (i.e. each column in the matrix), we select the letter with highest frequency. We also use special letter "*" at positions where there is a tie, and special letter "." at positions where all the frequencies are 0 (a particular type of tie):

```r
cm_to_cs <- function(cm) {
    stopifnot(is.matrix(cm))
    nr <- nrow(cm)
    rnames <- rownames(cm)
    stopifnot(!is.null(rnames) && all(nchar(rnames) == 1L))
    selection <- apply(cm, 2, function(x) {
        i <- which.max(x)
        if (x[i] == 0L)
            return(nr + 1L)
        if (sum(x == x[i]) != 1L)
            return(nr + 2L)
        i
    })
    paste0(c(rnames, ".", "*" )[selection], collapse="")
}
```

```r
cm_to_cs(cm1a)
cm_to_cs(cm1b)
cm_to_cs(cm2)
```

## Note that the consensus sequences we obtain are relative to the plus strand of the reference sequence.

---

**summarizeOverlaps-methods**

*Perform overlap queries between reads and genomic features*

### Description

`summarizeOverlaps` extends `findOverlaps` by providing options to resolve reads that overlap multiple features.

### Usage

```r
## S4 method for signature 'GRanges,GAlignments'
summarizeOverlaps(
    features, reads, mode=Union,
    ignore.strand=FALSE, inter.feature=TRUE, preprocess.reads=NULL, ...)
```

```r
## S4 method for signature 'GRangesList,GAlignments'
summarizeOverlaps(
    features, reads, mode=Union,
    ignore.strand=FALSE, inter.feature=TRUE, preprocess.reads=NULL, ...)
```
summarizeOverlaps-methods

ignore.strand=FALSE, inter.feature=TRUE, preprocess.reads=NULL, ...)

## S4 method for signature 'GRanges,GRanges'
summarizeOverlaps(
  features, reads, mode=Union,
  ignore.strand=FALSE, inter.feature=TRUE, preprocess.reads=NULL, ...)

## S4 method for signature 'GRangesList,GRanges'
summarizeOverlaps(
  features, reads, mode=Union,
  ignore.strand=FALSE, inter.feature=TRUE, preprocess.reads=NULL, ...)

## S4 method for signature 'GRanges,GAlignmentPairs'
summarizeOverlaps(
  features, reads, mode=Union,
  ignore.strand=FALSE, inter.feature=TRUE, preprocess.reads=NULL, ...)

## mode functions
Union(features, reads, ignore.strand=FALSE,
      inter.feature=TRUE)
IntersectionStrict(features, reads, ignore.strand=FALSE,
                   inter.feature=TRUE)
IntersectionNotEmpty(features, reads, ignore.strand=FALSE,
                     inter.feature=TRUE)

## S4 method for signature 'GRanges,BamFile'
summarizeOverlaps(
  features, reads, mode=Union,
  ignore.strand=FALSE, inter.feature=TRUE, singleEnd=TRUE,
  fragments=FALSE, param=ScanBamParam(), preprocess.reads=NULL, ...)

## S4 method for signature 'BamViews,missing'
summarizeOverlaps(
  features, reads, mode=Union,
  ignore.strand=FALSE, inter.feature=TRUE, singleEnd=TRUE,
  fragments=FALSE, param=ScanBamParam(), preprocess.reads=NULL, ...)

Arguments

- **features**: A `GRanges` or a `GRangesList` object of genomic regions of interest. When a `GRanges` is supplied, each row is considered a feature. When a `GRangesList` is supplied, each higher list-level is considered a feature. This distinction is important when defining overlaps. When `features` is a `BamViews` the `reads` argument is missing. Features are extracted from the `bamRanges` and the reads from `bamPaths`. Metadata from `bamPaths` and `bamSamples` are stored in the colData of the resulting `RangedSummarizedExperiment` object. `bamExperiment` metadata are stored in the metadata slot.
summarizeOverlaps-methods

reads
A GRanges, GRangesList GAlignments, GAlignmentsList, GAlignmentPairs, BamViews or BamFileList object that represents the data to be counted by summarizeOverlaps. reads is missing when a BamViews object is the only argument supplied to summarizeOverlaps. reads are the files specified in bamPaths of the BamViews object.

mode
mode can be one of the pre-defined count methods such as "Union", "IntersectionStrict", or "IntersectionNotEmpty" or it a user supplied count function. For a custom count function, the input arguments must match those of the pre-defined options and the function must return a vector of counts the same length as the annotation (’features’ argument). See examples for details.

The pre-defined options are designed after the counting modes available in the HTSeq package by Simon Anders (see references).

• "Union" : (Default) Reads that overlap any portion of exactly one feature are counted. Reads that overlap multiple features are discarded. This is the most conservative of the 3 modes.

• "IntersectionStrict" : A read must fall completely "within" the feature to be counted. If a read overlaps multiple features but falls "within" only one, the read is counted for that feature. If the read is "within" multiple features, the read is discarded.

• "IntersectionNotEmpty" : A read must fall in a unique disjoint region of a feature to be counted. When a read overlaps multiple features, the features are partitioned into disjoint intervals. Regions that are shared between the features are discarded leaving only the unique disjoint regions. If the read overlaps one of these remaining regions, it is assigned to the feature the unique disjoint region came from.

• user supplied function : A function can be supplied as the mode argument. It must (1) have arguments that correspond to features, reads, ignore.strand and inter.feature arguments (as in the defined mode functions) and (2) return a vector of counts the same length as features.

ignore.strand
A logical indicating if strand should be considered when matching.

inter.feature
(Default TRUE) A logical indicating if the counting mode should be aware of overlapping features. When TRUE (default), reads mapping to multiple features are dropped (i.e., not counted). When FALSE, these reads are retained and a count is assigned to each feature they map to.

There are 6 possible combinations of the mode and inter.feature arguments. When inter.feature=FALSE the behavior of modes 'Union' and 'IntersectionStrict' are essentially 'countOverlaps' with 'type=any' and type=within, respectively. 'IntersectionNotEmpty' does not reduce to a simple countOverlaps because common (shared) regions of the annotation are removed before counting.

preprocess.reads
A function applied to the reads before counting. The first argument should be reads and the return value should be an object compatible with the reads argument to the counting modes, Union, IntersectionStrict and IntersectionNotEmpty.

The distinction between a user-defined 'mode' and user-defined 'preprocess.reads' function is that in the first case the user defines how to count; in the second case the reads are preprocessed before counting with a pre-defined mode. See examples.
Additional arguments passed to functions or methods called from within `summarizeOverlaps`. For BAM file methods arguments may include `singleEnd`, `fragments` or `param` which apply to reading records from a file (see below). Providing `count.mapped.reads=TRUE` include additional passes through the BAM file to collect statistics similar to those from `countBam`.

A `BPPARAM` argument can be passed down to the `bplapply` called by `summarizeOverlaps`. The argument can be `MulticoreParam()`, `SnowParam()`, `BatchJobsParam()` or `DoparParam()`. See the BioCParallel package for details in specifying the params.

### `singleEnd`

(Default TRUE) A logical indicating if reads are single or paired-end. In Bioconductor > 2.12 it is not necessary to sort paired-end BAM files by `qname`. When counting with `summarizeOverlaps`, setting `singleEnd=FALSE` will trigger paired-end reading and counting. It is fine to also set `asMates=TRUE` in the `BamFile` but is not necessary when `singleEnd=FALSE`.

### `fragments`

(Default FALSE) A logical; applied to paired-end data only. `fragments` controls which function is used to read the data which subsequently affects which records are included in counting.

When `fragments=FALSE`, data are read with `readGAlignmentPairs` and returned in a `GAlignmentPairs` class. In this case, singletons, reads with unmapped pairs, and other fragments, are dropped.

When `fragments=TRUE`, data are read with `readGAlignmentsList` and returned in a `GAlignmentsList` class. This class holds 'mated pairs' as well as same-strand pairs, singletons, reads with unmapped pairs and other fragments. Because more records are kept, generally counts will be higher when `fragments=TRUE`. The term 'mated pairs' refers to records paired with the algorithm described on the `?readGAlignmentsList` man page.

### `param`

An optional `ScanBamParam` instance to further influence scanning, counting, or filtering. See `?BamFile` for details of how records are returned when both `yieldSize` is specified in a `BamFile` and which is defined in a `ScanBamParam`.

### Details

`summarizeOverlaps` offers counting modes to resolve reads that overlap multiple features. The `mode` argument defines a set of rules to resolve the read to a single feature such that each read is counted a maximum of once. New to GenomicRanges >= 1.13.9 is the `inter.feature` argument which allows reads to be counted for each feature they overlap. When `inter.feature=TRUE` the counting modes are aware of feature overlap; reads that overlap multiple features are dropped and not counted. When `inter.feature=FALSE` multiple feature overlap is ignored and reads are counted once for each feature they map to. This essentially reduces modes ‘Union’ and ‘IntersectionStrict’ to `countOverlaps` with `type="any"`, and `type="within"`, respectively. ‘IntersectionNotEmpty’ is not reduced to a derivative of `countOverlaps` because the shared regions are removed before counting.

The `BamViews`, `BamFile` and `BamFileList` methods summarize overlaps across one or several files. The latter uses `bplapply`; control parallel evaluation using the `register` interface in the BioCParallel package.

### features

A ‘feature’ can be any portion of a genomic region such as a gene, transcript, exon etc. When the `features` argument is a `GRanges` the rows define the features. The result will be the same length as the `GRanges`. When `features` is a `GRangesList` the highest list-level defines the features and the result will be the same length as the `GRangesList`.

When `inter.feature=TRUE`, each count mode attempts to assign a read that overlaps multiple features to a single feature. If there are ranges that should be considered together (e.g., exons
by transcript or cds regions by gene) the `GRangesList` would be appropriate. If there is no
grouping in the data then a `GRanges` would be appropriate.

**paired-end reads** : Paired-end reads are counted as a single hit if one or both parts of the pair are
overlapped. Paired-end records can be counted in a `GAlignmentPairs` container or BAM file.

Counting pairs in BAM files:
- The `singleEnd` argument should be `FALSE`.
- When `reads` are supplied as a `BamFile` or `BamFileList`, the `asMates` argument to the
  `BamFile` should be `TRUE`.
- When `fragments` is `FALSE`, a `GAlignmentPairs` object is used in counting (pairs only).
- When `fragments` is `TRUE`, a `GAlignmentsList` object is used in counting (pairs, single-
  tons, unmapped mates, etc.)

**Value**

A `RangedSummarizedExperiment` object. The assays slot holds the counts, rowRanges holds the
annotation from features.

When `reads` is a `BamFile` or `BamFileList` `colData` is an empty DataFrame with a single row
named 'counts'. If `count.mapped.reads=TRUE`, `colData` holds the output of `countBam` in 3 columns
named 'records' (total records), 'nucleotides' and 'mapped' (mapped records).

When `features` is a `BamViews` `colData` includes 2 columns named `bamSamples` and `bamIndices`.
In all other cases, `colData` has columns of 'object' (class of reads) and 'records' (length of `reads`).

**Author(s)**

Valerie Obenchain <vobencha@fredhutch.org>

**References**

HTSeq : [http://www-huber.embl.de/users/anders/HTSeq/doc/overview.html](http://www-huber.embl.de/users/anders/HTSeq/doc/overview.html)

**See Also**

- The `DESeq2`, `DEXSeq` and `edgeR` packages.
- The `RangedSummarizedExperiment` class defined in the `SummarizedExperiment` package.
- The `GAlignments` and `GAlignmentPairs` classes.
- The `BamFileList` and `BamViews` classes in the `Rsamtools` package.
- The `readGAlignments` and `readGAlignmentPairs` functions.

**Examples**

```r
reads <- GAlignments(
  names = c("a","b","c","d","e","f","g"),
  seqnames = Rle(c(rep(c("chr1", "chr2"), 3), "chr1")),
  pos = as.integer(c(1400, 2700, 3400, 7100, 4000, 3100, 5200)),
  cigar = c("500M", "100M", "300M", "500M", "300M",
            "50M200N50M", "50M150N50M"),
  strand = strand(rep("+", 7)))

gr <- GRanges(
  seqnames = c(rep("chr1", 7), rep("chr2", 4)), strand = "+",
```
ranges <- IRanges(c(1000, 3000, 3600, 4000, 4000, 5000, 5400, 2000, 3000, 7000, 7500),
                  width = c(500, 500, 300, 500, 900, 500, 500, 900, 500, 600, 300),
                  names=c("A", "B", "C1", "C2", "D1", "D2", "E", "F",
                        "G", "H1", "H2"))
groups <- factor(c(1,2,3,3,4,4,5,6,7,8,8))
grl <- splitAsList(gr, groups)
names(grl) <- LETTERS[seq_along(grl)]

## ---------------------------------------------------------------------
## Counting modes.
## ---------------------------------------------------------------------
## First count with a GRanges as the 'features'. 'Union' is the
## most conservative counting mode followed by 'IntersectionStrict'
## then 'IntersectionNotEmpty'.

counts1 <-
data.frame(union=assays(summarizeOverlaps(gr, reads))$counts,
            intStrict=assays(summarizeOverlaps(gr, reads,
                        mode="IntersectionStrict"))$counts,
            intNotEmpty=assays(summarizeOverlaps(gr, reads,
                        mode="IntersectionNotEmpty"))$counts)

colSums(counts1)

## Split the 'features' into a GRangesList and count again.

counts2 <-
data.frame(union=assays(summarizeOverlaps(grl, reads))$counts,
            intStrict=assays(summarizeOverlaps(grl, reads,
                        mode="IntersectionStrict"))$counts,
            intNotEmpty=assays(summarizeOverlaps(grl, reads,
                        mode="IntersectionNotEmpty"))$counts)

colSums(counts2)

## The GRangesList ('grl' object) has 8 features whereas the GRanges
## ('gr' object) has 11. The affect on counting can be seen by looking
## at feature 'H' with mode 'Union'. In the GRanges this feature is
## represented by ranges 'H1' and 'H2',
## gr[c("H1", "H2")]
## and by list element 'H' in the GRangesList,
## grl["H"]
## Read "d" hits both 'H1' and 'H2'. This is considered a multi-hit when
## using a GRanges (each range is a separate feature) so the read was
## dropped and not counted.
## counts1[c("H1", "H2"), ]

## When using a GRangesList, each list element is considered a feature.
## The read hits multiple ranges within list element 'H' but only one
## list element. This is not considered a multi-hit so the read is counted.
## counts2["H", ]

## Counting multi-hit reads.
## ---------------------------------------------------------------------
The goal of the counting modes is to provide a set of rules that resolve reads hitting multiple features so each read is counted a maximum of once. However, sometimes it may be desirable to count a read for each feature it overlaps. This can be accomplished by setting `inter.feature` to `FALSE`.

When `inter.feature=FALSE`, modes `Union` and `IntersectionStrict` essentially reduce to `countOverlaps()` with `type="any"` and `type="within"`, respectively.

When `inter.feature=TRUE` only features "A", "F" and "G" have counts.

```r
se1 <- summarizeOverlaps(gr, reads, mode="Union", inter.feature=TRUE)
assays(se1)$counts
```

When `inter.feature=FALSE` all 11 features have a count. There are 7 total reads so one or more reads were counted more than once.

```r
table(assays(se2)$counts)
```

Counting BAM files.

```r
library(pasillaBamSubset)
library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
exbygene <- exonsBy(TxDb.Dmelanogaster.UCSC.dm3.ensGene, "gene")
```

(i) Single-end:

Large files can be iterated over in chunks by setting a `yieldSize` on the BamFile.

```r
bf_s <- BamFile(untreated1_chr4(), yieldSize=50000)
```

```r
se_s <- summarizeOverlaps(exbygene, bf_s, singleEnd=TRUE)
table(assays(se_s)$counts > 0)
```

When a character (file name) is provided as `reads` instead of a BamFile object `summarizeOverlaps()` will create a BamFile and set a reasonable default `yieldSize`.

(ii) Paired-end:

A paired-end file may contain singletons, reads with unmapped pairs or reads with more than two fragments. When `fragments=FALSE` only reads paired by the algorithm are included in the counting.

```r
nofrag <- summarizeOverlaps(exbygene, untreated3_chr4(), singleEnd=FALSE, fragments=FALSE)
table(assays(nofrag)$counts > 0)
```

When `fragments=TRUE` all singletons, reads with unmapped pairs and other fragments will be included in the counting.

```r
bf <- BamFile(untreated3_chr4(), asMates=TRUE)
frag <- summarizeOverlaps(exbygene, bf, singleEnd=FALSE, fragments=TRUE)
table(assays(frag)$counts > 0)
```

As expected, using `fragments=TRUE` results in a larger number of total counts because singletons, unmapped pairs etc. are
## included in the counting.

## Total reads in the file:
`countBam(untreated3_chr4())`

## Reads counted with 'fragments=FALSE':
`sum(assays(nofrag)$counts)`

## Reads counted with 'fragments=TRUE':
`sum(assays(frag)$counts)`

Use output of summarizeOverlaps() for differential expression analysis
with DESeq2 or edgeR.

```r
fls <- list.files(system.file("extdata", package="GenomicAlignments"),
recursive=TRUE, pattern="*bam$", full=TRUE)
names(fls) <- basename(fls)
bf <- BamFileList(fls, index=character(), yieldSize=1000)
genes <- GRanges(
  seqnames = c(rep("chr2L", 4), rep("chr2R", 5), rep("chr3L", 2)),
  ranges = IRanges(c(1000, 3000, 4000, 7000, 2000, 3000, 3600,
                    4000, 7500, 5000, 5400),
                     width=c(rep(500, 3), 600, 900, 500, 300, 900,
                           300, 500, 500)))
se <- summarizeOverlaps(genes, bf)
```

When the reads are BAM files, the 'colData' contains summary
information from a call to countBam().

```r
colData(se)
```

Start differential expression analysis with the DESeq2 or edgeR
package:

```r
library(DESeq2)
deseq <- DESeqDataSet(se, design=~1)
library(edgeR)
edger <- DGEList(assays(se)$counts, group=rownames(colData(se)))
```

Filter records by map quality before counting.

```r
mapq_filter <- function(features, reads, ignore.strand, inter.feature)
{
  require(GenomicAlignments) # needed for parallel evaluation
  Union(features, reads[mcols(reads)$mapq >= 20],
        ignore.strand, inter.feature)
}
```

```r
genes <- GRanges("seq1", IRanges(seq(1, 1500, by=200), width=100))
```
param <- ScanBamParam(what="mapq")
fl <- system.file("extdata", "ex1.bam", package="Rsamtools")
se <- summarizeOverlaps(genes, fl, mode=mapq_filter, param=param)
assays(se)$counts

## The count function can be completely custom (i.e., not use the
## pre-defined count functions at all). Requirements are that
## the input arguments match the pre-defined modes and the output
## is a vector of counts the same length as 'features'.

my_count <- function(features, reads, ignore.strand, inter.feature) {
  ## perform filtering, or subsetting etc.
  require(GenomicAlignments) # needed for parallel evaluation
  countOverlaps(features, reads)
}

## Preprocessing reads before counting with a standard count mode.
## (user-supplied 'preprocess.reads' function)

## The 'preprocess.reads' argument takes a function that is
## applied to the reads before counting with a pre-defined mode.

ResizeReads <- function(reads, width=1, fix="start", ...) {
  reads <- as(reads, "GRanges")
  stopifnot(all(strand(reads) != "*"))
  resize(reads, width=width, fix=fix, ...)
}

## By default ResizeReads() counts reads that overlap on the 5' end:
summarizeOverlaps(grl, reads, mode=Union, preprocess.reads=ResizeReads)

## Count reads that overlap on the 3' end by passing new values
## for 'width' and 'fix':
summarizeOverlaps(grl, reads, mode=Union, preprocess.reads=ResizeReads,
                   width=1, fix="end")

## summarizeOverlaps() with BamViews.

## bamSamples and bamPaths metadata are included in the colData.
## BamExperiment metadata is put into the metadata slot.
fl <- system.file("extdata", "ex1.bam", package="Rsamtools", mustWork=TRUE)
rngs <- GRanges(c("seq1", "seq2"), IRanges(1, c(1575, 1584)))
samp <- DataFrame(info="test", row.names="ex1")
view <- BamViews(fl, bamSamples=samp, bamRanges=rngs)
se <- summarizeOverlaps(view, mode=Union, ignore.strand=TRUE)
colData(se)
metadata(se)
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