Package ‘SummarizedExperiment’

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Title SummarizedExperiment container

Description The SummarizedExperiment container contains one or more assays, each represented by a matrix-like object of numeric or other mode. The rows typically represent genomic ranges of interest and the columns represent samples.

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Collate Assays-class.R SummarizedExperiment-class.R 
RangedSummarizedExperiment-class.R intra-range-methods.R 
inter-range-methods.R coverage-methods.R findOverlaps-methods.R 
nearest-methods.R makeSummarizedExperimentFromExpressionSet.R 
makeSummarizedExperimentFromDataFrame.R 
makeSummarizedExperimentFromLoom.R readKallisto.R zzz.R

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The Assays virtual class and its methods provide a formal abstraction of the assays slot of SummarizedExperiment objects.

SimpleAssays and ShallowSimpleListAssays are concrete subclasses of Assays with the former being currently the default implementation of Assays objects. Other implementations (e.g. disk-based) could easily be added.

Note that these classes are not meant to be used directly by the end user and the material in this man page is aimed at package developers.

Details

Assays objects have a list-like semantics with elements having matrix- or array-like semantics (e.g., dim, dimnames).

The Assays API consists of:

- (a) The `Assays()` constructor function.
- (b) Lossless back and forth coercion from/to SimpleList. The coercion method from SimpleList doesn’t need (and should not) validate the returned object.
- (c) `length`, `names`, `\texttt{\textbackslash names<\texttt{\textbackslash}}, \texttt{getElement}, \texttt{setListElement}, \texttt{dim}, \texttt{[}, \texttt{[<\texttt{\textbackslash}}, \texttt{rbind}, \texttt{cbind}.

An Assays concrete subclass needs to implement (b) (required) plus, optionally any of the methods in (c).

IMPORTANT:

1. Nobody in the Assays hierarchy is allowed to inherit from SimpleList because of the conflicting semantic of `[`.
2. Methods that return a modified Assays object (a.k.a. endomorphisms), that is, \( \text{[]} \) as well as replacement methods \( \text{names} <- \), \( \text{setListElement} \), and \( \text{[]} <- \) must respect the *copy-on-change contract*. With objects that don’t make use of references internally, the developer doesn’t need to take any special action for that because it’s automatically taken care of by R itself. However, for objects that do make use of references internally (e.g. environments, external pointers, pointer to a file on disk, etc...), the developer needs to be careful to implement endomorphisms with copy-on-change semantics. This can easily be achieved (and is what the default methods for Assays objects do) by performing a full (deep) copy of the object before modifying it instead of trying to modify it in-place. However note that this full (deep) copy can be very expensive and is actually not necessary in order to achieve copy-on-change semantics: it’s enough (and often preferable for performance reasons) to copy only the parts of the object that need to be modified.

Assays has currently 3 implementations which are formalized by concrete subclasses SimpleAssays, ShallowSimpleListAssays, and AssaysInEnv. SimpleAssays is the default (prior to SummarizedExperiment 1.15.4, ShallowSimpleListAssays was the default). AssaysInEnv is a *broken* alternative to ShallowSimpleListAssays that does NOT respect the *copy-on-change contract*. It is only provided for illustration purposes (see source file Assays-class.R for the details).

A little more detail about ShallowSimpleListAssays: a small reference class hierarchy (not exported from the GenomicRanges name space) defines a reference class ShallowData with a single field data of type ANY, and a derived class ShallowSimpleListAssays that specializes the type of data as SimpleList, and contains=c("ShallowData","Assays"). The assays slot of a SummarizedExperiment object contains an instance of ShallowSimpleListAssays.

**Author(s)**

Martin Morgan and Hervé Pagès

**See Also**

* SummarizedExperiment objects.
* SimpleList objects in the S4Vectors package.

**Examples**

```r
## ---------------------------------------------------------------------
## DIRECT MANIPULATION OF Assays OBJECTS
## ---------------------------------------------------------------------

m1 <- matrix(runif(24), ncol=3)
m2 <- matrix(runif(24), ncol=3)
a <- Assays(SimpleList(m1, m2))
a
as(a, "SimpleList")

length(a)
getListElement(a, 2)
dim(a)

b <- a[-4, 2]
b
length(b)
getListElement(b, 2)
dim(b)
```
coverage-methods

 coverage-methods

  Coverage of a RangedSummarizedExperiment object

Description

This man page documents the coverage method for RangedSummarizedExperiment objects.

Usage

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

Arguments

  x
  A RangedSummarizedExperiment object.

  shift, width, weight, method

  See ?coverage in the GenomicRanges package.
Details

This method operates on the `rowRanges` component of the `RangedSummarizedExperiment` object, which can be a `GenomicRanges` or `GRangesList` object.

More precisely, on `RangedSummarizedExperiment` object `x`, `coverage(x,...)` is equivalent to `coverage(rowRanges(x),...)`.

See `?coverage` in the `GenomicRanges` package for the details of how `coverage` operates on a `GenomicRanges` or `GRangesList` object.

Value

See `?coverage` in the `GenomicRanges` package.

See Also

- `RangedSummarizedExperiment` objects.
- The `coverage` man page in the `GenomicRanges` package where the `coverage` methods for `GenomicRanges` and `GRangesList` objects are documented.

Examples

```r
nrows <- 20; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(5, 15)),
                      IRanges(sample(1000L, 20), width=100),
                      strand=Rle(c("+", "-"), c(12, 8)),
                      seqlengths=c(chr1=1800, chr2=1300))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                      row.names=LETTERS[1:6])
rse <- SummarizedExperiment(assays=SimpleList(counts=counts),
                            rowRanges=rowRanges, colData=colData)
cvg <- coverage(rse)
cvg
stopifnot(identical(cvg, coverage(rowRanges(rse)))))
```

Description

This man page documents the `findOverlaps` methods for `RangedSummarizedExperiment` objects. `RangedSummarizedExperiment` objects also support `countOverlaps`, `overlapsAny`, and `subsetByOverlaps` thanks to the default methods defined in the `IRanges` package and to the `findOverlaps` methods defined in this package and documented below.
Usage

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

Arguments

- `query`, `subject`: One of these two arguments must be a `RangedSummarizedExperiment` object.
- `maxgap`, `minoverlap`, `type`: See `?findOverlaps` in the `GenomicRanges` package.

Details

These methods operate on the `rowRanges` component of the `RangedSummarizedExperiment` object, which can be a `GenomicRanges` or `GRangesList` object.

More precisely, if any of the above functions is passed a `RangedSummarizedExperiment` object thru the `query` and/or `subject` argument, then it behaves as if `rowRanges(query)` and/or `rowRanges(subject)` had been passed instead.

See `?findOverlaps` in the `GenomicRanges` package for the details of how `findOverlaps` and family operate on `GenomicRanges` and `GRangesList` objects.

Value

See `?findOverlaps` in the `GenomicRanges` package.

See Also

- `RangedSummarizedExperiment` objects.
- The `findOverlaps` man page in the `GenomicRanges` package where the `findOverlaps` family of methods for `GenomicRanges` and `GRangesList` objects is documented.

Examples

```r
nrows <- 20; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(5, 15)),
IRanges(sample(100L, 20), width=100),
strand=Rle(c("+", "-"), c(12, 8))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
row.names=LETTERS[1:6])
rse0 <- SummarizedExperiment(assays=SimpleList(counts=counts),
```
inter-range-methods

rowRanges=rowRanges, colData=colData)

rse1 <- shift(rse0, 100)

hits <- findOverlaps(rse0, rse1)

hits

stopifnot(identical(hits, findOverlaps(rse0, rowRanges(rse1))))

stopifnot(identical(hits, findOverlaps(rowRanges(rse0), rse1)))

---

inter-range-methods  Inter range transformations of a RangedSummarizedExperiment object

Description

This man page documents the inter range transformations that are supported on RangedSummarizedExperiment objects.

Usage

## S4 method for signature 'RangedSummarizedExperiment'

isDisjoint(x, ignore.strand=FALSE)

## S4 method for signature 'RangedSummarizedExperiment'

disjointBins(x, ignore.strand=FALSE)

Arguments

x  A RangedSummarizedExperiment object.

ignore.strand  See ?isDisjoint in the GenomicRanges package.

Details

These transformations operate on the rowRanges component of the RangedSummarizedExperiment object, which can be a GenomicRanges or GRangesList object.

More precisely, any of the above functions performs the following transformation on RangedSummarizedExperiment object x:

\[ f(\text{rowRanges}(x), \ldots) \]

where \( f \) is the name of the function and \(...\) any additional arguments passed to it.

See ?isDisjoint in the GenomicRanges package for the details of how these transformations operate on a GenomicRanges or GRangesList object.

Value

See ?isDisjoint in the GenomicRanges package.

See Also

- RangedSummarizedExperiment objects.
- The isDisjoint man page in the GenomicRanges package where inter range transformations of a GenomicRanges or GRangesList object are documented.
Examples

nrows <- 20; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(5, 15)),
                      IRanges(sample(1000L, 20), width=100),
                      strand=Rle(c("+", "-"), c(12, 8)))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                      row.names=LETTERS[1:6])
rse0 <- SummarizedExperiment(assays=SimpleList(counts=counts),
                             rowRanges=rowRanges, colData=colData)
rse1 <- shift(rse0, 99*start(rse0))

isDisjoint(rse0) # FALSE
isDisjoint(rse1) # TRUE

bins0 <- disjointBins(rse0)
bins0
stopifnot(identical(bins0, disjointBins(rowRanges(rse0))))

bins1 <- disjointBins(rse1)
bins1
stopifnot(all(bins1 == bins1[1]))
restrict(x, start=NA, end=NA, keep.all.ranges=FALSE, use.names=TRUE)

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

Arguments

x  
A RangedSummarizedExperiment object.

shift, use.names  
See ?shift in the IRanges package.

start, end, width, fix  
See ?shift in the IRanges package.

ignore.strand, both  
See ?shift in the IRanges package.

upstream, downstream  
See ?shift in the IRanges package.

keep.all.ranges  
See ?shift in the IRanges package.

Details

These transformations operate on the rowRanges component of the RangedSummarizedExperiment object, which can be a GenomicRanges or GRangesList object.

More precisely, any of the above functions performs the following transformation on RangedSummarizedExperiment object x:

rowRanges(x) <- f(rowRanges(x), ...)

where f is the name of the function and ... any additional arguments passed to it.

See ?shift in the IRanges package for the details of how these transformations operate on a GenomicRanges or GRangesList object.

See Also

- RangedSummarizedExperiment objects.
- The shift man page in the IRanges package where intra range transformations of a GenomicRanges or GRangesList object are documented.

Examples

nrows <- 20; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(5, 15)),
                      IRanges(sample(1000L, 20), width=100),
                      strand=Rle(c("+", "-"), c(12, 8)))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                      row.names=LETTERS[1:6])
rse0 <- SummarizedExperiment(assays=SimpleList(counts=counts),
                             rowRanges=rowRanges, colData=colData)
rse1 <- shift(rse0, 1)
stopifnot(identical(
  rowRanges(rse1),
  shift(rowRanges(rse0), 1)
))

se2 <- narrow(rse0, start=10, end=-15)
stopifnot(identical(
  rowRanges(se2),
  narrow(rowRanges(rse0), start=10, end=-15)
))

se3 <- resize(rse0, width=75)
stopifnot(identical(
  rowRanges(se3),
  resize(rowRanges(rse0), width=75)
))

se4 <- flank(rse0, width=20)
stopifnot(identical(
  rowRanges(se4),
  flank(rowRanges(rse0), width=20)
))

se5 <- restrict(rse0, start=200, end=700, keep.all.ranges=TRUE)
stopifnot(identical(
  rowRanges(se5),
  restrict(rowRanges(rse0), start=200, end=700, keep.all.ranges=TRUE)
))

--

makeSummarizedExperimentFromDataFrame

Make a RangedSummarizedExperiment from a data.frame or DataFrame

Description

makeSummarizedExperimentFromDataFrame uses data.frame or DataFrame column names to create a GRanges object for the rowRanges of the resulting SummarizedExperiment object. It requires that non-range data columns be coercible into a numeric matrix for the SummarizedExperiment constructor. All columns that are not part of the row ranges attribute are assumed to be experiment data; thus, keeping metadata columns will not be supported. Note that this function only returns SummarizedExperiment objects with a single assay.

If metadata columns are to be kept, one can first construct the row ranges attribute by using the makeGRangesFromDataFrame function and subsequently creating the SummarizedExperiment.

Usage

makeSummarizedExperimentFromDataFrame(df,
                                      ..., seqinfo = NULL,
                                      starts.in.df.are.0based = FALSE)
makeSummarizedExperimentFromDataFrame

Arguments

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

...  
Additional arguments passed on to makeGRangesFromDataFrame

seqinfo  
Either NULL, or a Seqinfo object, or a character vector of seql levels, or a named numeric vector of sequence lengths. When not NULL, it must be compatible with the genomic ranges in df i.e. it must include at least the sequence levels represented in df.

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

Value

A RangedSummarizedExperiment object with rowRanges and a single assay

Author(s)

M. Ramos

See Also

• makeGRangesFromDataFrame

Examples

```r
# Note that rownames of the data.frame are also rownames of the result
df <- data.frame(chr="chr2", start = 11:15, end = 12:16,
    strand = c("+", "-", "+", "+", "."), expr0 = 3:7,
    expr1 = 8:12, expr2 = 12:16,
    row.names = paste0("GENE", letters[5:1]))

df
exRSE <- makeSummarizedExperimentFromDataFrame(df)

exRSE

assay(exRSE)

rowRanges(exRSE)
```
makeSummarizedExperimentFromExpressionSet

Make a RangedSummarizedExperiment object from an ExpressionSet and vice-versa

Description

Coercion between RangedSummarizedExperiment and ExpressionSet is supported in both directions.

For going from ExpressionSet to RangedSummarizedExperiment, the makeSummarizedExperimentFromExpressionSet function is also provided to let the user control how to map features to ranges.

Usage

makeSummarizedExperimentFromExpressionSet(from,
mapFun=naiveRangeMapper,
...
)

## range mapping functions
naiveRangeMapper(from)
probeRangeMapper(from)
geneRangeMapper(txDbPackage, key = "ENTREZID")

Arguments

- **from** An ExpressionSet object.
- **mapFun** A function which takes an ExpressionSet object and returns a GRanges, or GRangesList object which corresponds to the genomic ranges used in the ExpressionSet. The rownames of the returned GRanges are used to match the featureNames of the ExpressionSet. The naiveRangeMapper function is used by default.
- **...** Additional arguments passed to mapFun.
- **txDbPackage** A character string with the Transcript Database to use for the mapping.
- **key** A character string with the Gene key to use for the mapping.

Value

makeSummarizedExperimentFromExpressionSet takes an ExpressionSet object as input and a range mapping function that maps the features to ranges. It then returns a RangedSummarizedExperiment object that corresponds to the input.

The range mapping functions return a GRanges object, with the rownames corresponding to the featureNames of the ExpressionSet object.

Author(s)

Jim Hester, james.f.hestergmail.com
See Also

- RangedSummarizedExperiment objects.
- ExpressionSet objects in the Biobase package.
- TxDb objects in the GenomicFeatures package.

Examples

```r
## *---------------------------------------------------------------------
## GOING FROM ExpressionSet TO SummarizedExperiment
## *---------------------------------------------------------------------

data(sample.ExpressionSet, package="Biobase")

# naive coercion
makeSummarizedExperimentFromExpressionSet(sample.ExpressionSet)
as(sample.ExpressionSet, "RangedSummarizedExperiment")
as(sample.ExpressionSet, "SummarizedExperiment")

# using probe range mapper
makeSummarizedExperimentFromExpressionSet(sample.ExpressionSet, probeRangeMapper)

# using the gene range mapper
se <- makeSummarizedExperimentFromExpressionSet(
  sample.ExpressionSet,
  geneRangeMapper("TxDb.Hsapiens.UCSC.hg19.knownGene")
)
se
rowData(se) # duplicate row names

## *---------------------------------------------------------------------
## GOING FROM SummarizedExperiment TO ExpressionSet
## *---------------------------------------------------------------------

example(RangedSummarizedExperiment) # to create 'rse'
rse
as(rse, "ExpressionSet")
```

makeSummarizedExperimentFromLoom

Make a SummarizedExperiment from a `.loom` hdf5 file

Description

makeSummarizedExperimentFromLoom represents a `.loom` file as a SummarizedExperiment. The `/matrix` and `/layers` are represented as HDF5Array objects; row and column attributes are parsed to DataFrame. Optionally, row or column attributes can be specified as row and and column names.

Usage

```r
makeSummarizedExperimentFromLoom(file,
  rownames_attr = NULL,
  colnames_attr = NULL)
```
Arguments

file The path (as a single character string) to the HDF5 file where the dataset is located.
rownames_attr The name of the row attribute to be used as row names.
colnames_attr The name of the column attribute to be used as column names.

Value

A SummarizedExperiment object with row and column data and one or more assays.

Author(s)

Martin Morgan

See Also

http://loompy.org/loompy-docs/format/index.html for a specification of the .loom format.

Examples

## BASIC EXAMPLE
##

```r
file <- system.file(
  package="SummarizedExperiment", "extdata", "example.loom"
)
se <- makeSummarizedExperimentFromLoom(file)
se
assay(se)
metadata(se)
```

### nearest-methods

Finding the nearest range neighbor in RangedSummarizedExperiment objects

Description

This man page documents the nearest methods and family (i.e. precede, follow, distance, and distanceToNearest methods) for RangedSummarizedExperiment objects.

Usage

```r
## S4 method for signature 'RangedSummarizedExperiment,ANY'
precede(x, subject, select=c("arbitrary", "all"),
  ignore.strand=FALSE)
## S4 method for signature 'ANY,RangedSummarizedExperiment'
precede(x, subject, select=c("arbitrary", "all"),
  ignore.strand=FALSE)

## S4 method for signature 'RangedSummarizedExperiment,ANY'
follow(x, subject, select=c("arbitrary", "all"),
```
## S4 method for signature `'quotesingle.Var` RangedSummarizedExperiment,ANY`

#### Arguments

- **x**, **subject**
  One of these two arguments must be a RangedSummarizedExperiment object.

- **select**, **ignore.strand**
  See ?nearest in the GenomicRanges package.

- **y**
  For the distance methods, one of x or y must be a RangedSummarizedExperiment object.

- **...**
  Additional arguments for methods.

#### Details

These methods operate on the rowRanges component of the RangedSummarizedExperiment object, which can be a GenomicRanges or GRangesList object.

More precisely, if any of the above functions is passed a RangedSummarizedExperiment object thru the x, subject, and/or y argument, then it behaves as if rowRanges(x), rowRanges(subject), and/or rowRanges(y) had been passed instead.

See ?nearest in the GenomicRanges package for the details of how nearest and family operate on GenomicRanges and GRangesList objects.

#### Value

See ?nearest in the GenomicRanges package.

#### See Also

- RangedSummarizedExperiment objects.
- The nearest man page in the GenomicRanges package where the nearest family of methods for GenomicRanges and GRangesList objects is documented.
Examples

```r
nrows <- 20; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(5, 15)),
                      IRanges(sample(1000L, 20), width=100),
                      strand=Rle(c("+", "-"), c(12, 8))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                      row.names=LETTERS[1:6])
rse0 <- SummarizedExperiment(assays=SimpleList(counts=counts),
                             rowRanges=rowRanges, colData=colData)
rse1 <- shift(rse0, 100)
res <- nearest(rse0, rse1)
res
stopifnot(identical(res, nearest(rowRanges(rse0), rowRanges(rse1))))
stopifnot(identical(res, nearest(rse0, rowRanges(rse1))))
stopifnot(identical(res, nearest(rowRanges(rse0), rse1)))
res <- nearest(rse0) # missing subject
res
stopifnot(identical(res, nearest(rowRanges(rse0))))

hits <- nearest(rse0, rse1, select="all")
hits
stopifnot(identical(
  hits,
  nearest(rowRanges(rse0), rowRanges(rse1), select="all")
))
stopifnot(identical(
  hits,
  nearest(rse0, rowRanges(rse1), select="all")
))
stopifnot(identical(
  hits,
  nearest(rowRanges(rse0), rse1, select="all")
))
```

RangedSummarizedExperiment-class

RangedSummarizedExperiment objects

Description

The RangedSummarizedExperiment class is a matrix-like container where rows represent ranges of interest (as a GRanges or GRangesList object) and columns represent samples (with sample data summarized as a DataFrame). A RangedSummarizedExperiment contains one or more assays, each represented by a matrix-like object of numeric or other mode.

RangedSummarizedExperiment is a subclass of SummarizedExperiment and, as such, all the methods documented in ?SummarizedExperiment also work on a RangedSummarizedExperiment object. The methods documented below are additional methods that are specific to RangedSummarizedExperiment objects.
Usage

## Constructor

```r
SummarizedExperiment(assays=SimpleList(),
    rowData=NULL, rowRanges=GRangesList(),
    colData=DataFrame(),
    metadata=list())
```

## Accessors

```r
rowRanges(x, ...)
rowRanges(x, ...) <- value
```

## Subsetting

## S4 method for signature 'RangedSummarizedExperiment'

```r
subset(x, subset, select, ...)
```

## rowRanges access

## see 'GRanges compatibility', below

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>assays</td>
<td>A list or SimpleList of matrix-like elements, or a matrix-like object (e.g. an ordinary matrix, a data frame, a DataFrame object from the S4Vectors package, a sparseMatrix derivative from the Matrix package, a DelayedMatrix object from the DelayedArray package, etc...). All elements of the list must have the same dimensions, and dimension names (if present) must be consistent across elements and with the row names of rowRanges and colData.</td>
</tr>
<tr>
<td>rowData</td>
<td>A DataFrame object describing the rows. Row names, if present, become the row names of the SummarizedExperiment object. The number of rows of the DataFrame must equal the number of rows of the matrices in assays.</td>
</tr>
<tr>
<td>rowRanges</td>
<td>A GRanges or GRangesList object describing the ranges of interest. Names, if present, become the row names of the SummarizedExperiment object. The length of the GRanges or GRangesList must equal the number of rows of the matrices in assays. If rowRanges is missing, a SummarizedExperiment instance is returned.</td>
</tr>
<tr>
<td>colData</td>
<td>An optional DataFrame describing the samples. Row names, if present, become the column names of the RangedSummarizedExperiment.</td>
</tr>
<tr>
<td>metadata</td>
<td>An optional list of arbitrary content describing the overall experiment.</td>
</tr>
<tr>
<td>x</td>
<td>A RangedSummarizedExperiment object. The rowRanges setter will also accept a SummarizedExperiment object and will first coerce it to RangedSummarizedExperiment before it sets value on it.</td>
</tr>
<tr>
<td>...</td>
<td>Further arguments to be passed to or from other methods.</td>
</tr>
<tr>
<td>value</td>
<td>A GRanges or GRangesList object.</td>
</tr>
<tr>
<td>subset</td>
<td>An expression which, when evaluated in the context of rowRanges(x), is a logical vector indicating elements or rows to keep: missing values are taken as false.</td>
</tr>
<tr>
<td>select</td>
<td>An expression which, when evaluated in the context of colData(x), is a logical vector indicating elements or rows to keep: missing values are taken as false.</td>
</tr>
</tbody>
</table>
Details

The rows of a RangedSummarizedExperiment object represent ranges (in genomic coordinates) of interest. The ranges of interest are described by a GRanges or a GRangesList object, accessible using the rowRanges function, described below. The GRanges and GRangesList classes contain sequence (e.g., chromosome) name, genomic coordinates, and strand information. Each range can be annotated with additional data; this data might be used to describe the range or to summarize results (e.g., statistics of differential abundance) relevant to the range. Rows may or may not have row names; they often will not.

Constructor

RangedSummarizedExperiment instances are constructed using the SummarizedExperiment function with arguments outlined above.

Accessors

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

rowRanges(x), rowRanges(x) <- value: Get or set the row data. value is a GenomicRanges object. Row names of value must be NULL or consistent with the existing row names of x.

GRanges compatibility (rowRanges access)

Many GRanges and GRangesList operations are supported on RangedSummarizedExperiment objects, using rowRanges. Supported operations include: pcompare, duplicated, end, end<-, granges, is.unsorted, match, mcols, mcols<-, order, ranges, ranges<-, rank, seqinfo, seqinfo<-, seqnames, sort, start, start<-, strand, strand<-, width, width<-. See also ?shift, ?isDisjoint, ?coverage, ?findOverlaps, and ?nearest for more GRanges compatibility methods.

Not all GRanges operations are supported, because they do not make sense for RangedSummarizedExperiment objects (e.g., length, name, as.data.frame, c, splitAsList), involve non-trivial combination or splitting of rows (e.g., disjoin, gaps, reduce, unique), or have not yet been implemented (Ops, map, window, window<->).

Subsetting

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

subset(x, subset, select): Create a subset of x using an expression subset referring to columns of rowRanges(x) (including ‘seqnames’, ‘start’, ‘end’, ‘width’, ‘strand’, and names(rowData(x))) and / or select referring to column names of colData(x).

Extension

RangedSummarizedExperiment is implemented as an S4 class, and can be extended in the usual way, using contains="RangedSummarizedExperiment" in the new class definition.

Author(s)

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See Also

- `SummarizedExperiment-class`
- `shift, isDisjoint, coverage, findOverlaps, and nearest` for more `GRanges` compatibility methods.
- `GRanges` objects in the `GenomicRanges` package.

Examples

```r
nrows <- 200; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(50, 150)),
  IRanges(floor(runif(200, 1e5, 1e6)), width=100),
  strand=sample(c("+", "-"), 200, TRUE),
  feature_id=sprintf("ID%03d", 1:200))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
  row.names=LETTERS[1:6])
rse <- SummarizedExperiment(assays=SimpleList(counts=counts),
  rowRanges=rowRanges, colData=colData)
```

```r
rse
dim(rse)
dimnames(rse)
assayNames(rse)
head(assay(rse))
assays(rse) <- endoapply(assay(rse), asinh)
head(assay(rse))

rowRanges(rse)
rowData(rse) # same as 'mcols(rowRanges(rse))'
colData(rse)

rse[, rse$Treatment == "ChIP"]
```

```r
## cbind() combines objects with the same ranges but different samples:
rsel1 <- rse
rsel2 <- rsel1[, 1:3]
columns(rsel2) <- letters[1:ncol(rsel2)]
cmb1 <- cbind(rsel1, rsel2)
dim(cmb1)
dimnames(cmb1)

## rbind() combines objects with the same samples but different ranges:
rsel1 <- rse
rsel2 <- rsel1[1:50, ]
rownames(rsel2) <- letters[1:nrow(rsel2)]
cmb2 <- rbind(rsel1, rsel2)
dim(cmb2)
dimnames(cmb2)

## Coercion to/from SummarizedExperiment:
se0 <- as(rse, "SummarizedExperiment")
se0
as(se0, "RangedSummarizedExperiment")

## Setting rowRanges on a SummarizedExperiment object turns it into a
## RangedSummarizedExperiment object:
```
se <- se0
rowRanges(se) <- rowRanges
se # RangedSummarizedExperiment

## Sanity checks:
stopifnot(identical(assays(se0), assays(rse)))
stopifnot(identical(dim(se0), dim(rse)))
stopifnot(identical(dimnames(se0), dimnames(rse)))
stopifnot(identical(rowData(se0), rowData(rse)))
stopifnot(identical(colData(se0), colData(rse)))

---

### readKallisto

Input kallisto or kallisto bootstrap results.

#### Description

readKallisto inputs several kallisto output files into a single SummarizedExperiment instance, with rows corresponding to estimated transcript abundance and columns to samples. readKallistoBootstrap inputs kallisto bootstrap replicates of a single sample into a matrix of transcript x bootstrap abundance estimates.

#### Usage

```r
readKallisto(files,
             json = file.path(dirname(files), "run_info.json"),
             h5 = any(grepl("\.h5\$", files)),
             what = KALLISTO_ASSAYS,
             as = c("SummarizedExperiment", "list", "matrix"))
```

```r
readKallistoBootstrap(file, i, j)
```

#### Arguments

- **files**: character() paths to kallisto `abundance.tsv` output files. The assumption is that files are organized in the way implied by kallisto, with each sample in a distinct directory, and the directory containing files `abundance.tsv`, `run_info.json`, and perhaps `abundance.h5`.

- **json**: character() vector of the same length as `files` specifying the location of JSON files produced by kallisto and containing information on the run. The default assumes that json files are in the same directory as the corresponding abundance file.

- **h5**: character() vector of the same length as `files` specifying the location of HDF5 files produced by kallisto and containing bootstrap estimates. The default assumes that HDF5 files are in the same directory as the corresponding abundance file.

- **what**: character() vector of kallisto per-sample outputs to be input. See KALLISTO_ASSAYS for available values.

- **as**: character(1) specifying the output format. See Value for additional detail.

- **file**: character(1) path to a single HDF5 output file.

- **i, j**: integer() vector of row (i) and column (j) indexes to input.
**Value**

A `SummarizedExperiment`, `list`, or `matrix`, depending on the value of argument `as`; by default a `SummarizedExperiment`. The `as="SummarizedExperiment"` `rowData(se)` the length of each transcript; `colData(se)` includes summary information on each sample, including the number of targets and bootstraps, the kallisto and index version, the start time and operating system call used to create the file. `assays()` contains one or more transcript x sample matrices of parameters estimated by kallisto (see `KALLISTO_ASSAYS`).

`as="list"` return value contains information similar to `SummarizedExperiment` with row, column and assay data as elements of the list without coordination of row and column annotations into an integrated data container. `as="matrix"` returns the specified assay as a simple R matrix.

**Author(s)**

Martin Morgan martin.morgan@roswellpark.org

**References**


**Examples**

```r
outputs <- system.file(package="SummarizedExperiment", "extdata", "kallisto")
files <- dir(outputs, pattern="abundance.tsv", full=TRUE, recursive=TRUE)
stopifnot(all(file.exists(files)))

## default: input 'est_counts'
(se <- readKallisto(files, as="SummarizedExperiment"))
str(readKallisto(files, as="list"))
str(readKallisto(files, as="matrix"))

## available assays
KALLISTO_ASSAYS

## one or more assay
readKallisto(files, what=c("tpm", "eff_length"))

## alternatively: read hdf5 files
files <- sub(".tsv", ".h5", files, fixed=TRUE)
readKallisto(files)

## input all bootstraps
xx <- readKallistoBootstrap(files[1])
ridx <- head(which(rowSums(xx) != 0), 3)
cidx <- c(1:5, 96:100)
xx[ridx, cidx]

## selective input of rows (transcripts) and/or bootstraps
readKallistoBootstrap(files[1], i=c(ridx, rev(ridx)), j=cidx)
```
SummarizedExperiment-class

SummarizedExperiment objects

Description

The SummarizedExperiment class is a matrix-like container where rows represent features of interest (e.g. genes, transcripts, exons, etc...) and columns represent samples (with sample data summarized as a DataFrame). A SummarizedExperiment object contains one or more assays, each represented by a matrix-like object of numeric or other mode.

Note that SummarizedExperiment is the parent of the RangedSummarizedExperiment class which means that all the methods documented below also work on a RangedSummarizedExperiment object.

Usage

## Constructor

# See ?RangedSummarizedExperiment for the constructor function.

## Accessors

assayNames(x, ...)
assayNames(x, ...) <- value
assays(x, ...., withDimnames=TRUE)
assays(x, ...., withDimnames=TRUE) <- value
assay(x, i, ...)
assay(x, i, ...) <- value
rowData(x, use.names=TRUE, ...)
rowData(x, ...) <- value
colData(x, ...)
colData(x, ...) <- value
#dim(x)
#dimnames(x)
#dimnames(x) <- value

## Quick colData access

## S4 method for signature 'SummarizedExperiment'
x$name
## S4 replacement method for signature 'SummarizedExperiment'
x$name <- value
## S4 method for signature 'SummarizedExperiment,ANY,missing'
x[[i, j, ...]]
## S4 replacement method for signature 'SummarizedExperiment,ANY,missing'
x[[i, j, ...]] <- value

## Subsetting
## S4 method for signature 'SummarizedExperiment'
x[i, j, ..., drop=TRUE]
## S4 replacement method for signature 'SummarizedExperiment,ANY,ANY,SummarizedExperiment'
x[i, j] <- value
## S4 method for signature 'SummarizedExperiment'
subset(x, subset, select, ...)

## Combining

## S4 method for signature 'SummarizedExperiment'
cbind(..., deparse.level=1)
## S4 method for signature 'SummarizedExperiment'
rbind(..., deparse.level=1)

## On-disk realization
## S4 method for signature 'SummarizedExperiment'
realize(x, BACKEND=getRealizationBackend())

Arguments

x
A SummarizedExperiment object.

... For assay, ... may contain withDimnames, which is forwarded to assays.
For cbind, rbind, ... contains SummarizedExperiment objects to be combined.
For other accessors, ignored.

value An object of a class specified in the S4 method signature or as outlined in ‘Details’.

i, j For assay, assay<-, i is an integer or numeric scalar; see ‘Details’ for additional constraints.
For [, SummarizedExperiment, [, SummarizedExperiment<-, i, j are sub- scripts that can act to subset the rows and columns of x, that is the matrix elements of assays.
For [[, SummarizedExperiment, [[<-, SummarizedExperiment, i is a scalar index (e.g., character(1) or integer(1)) into a column of colData.

name A symbol representing the name of a column of colData.

withDimnames A logical(1), indicating whether dimnames should be applied to extracted assay elements. Setting withDimnames=FALSE increases the speed and memory efficiency with which assays are extracted. withDimnames=TRUE in the getter assays<- allows efficient complex assignments (e.g., updating names of assays, names(assays(x,withDimnames=FALSE)) = ... is more efficient than names(assays(x)) = ...); it does not influence actual assignment of dimnames to assays.

use.names Like mcols(x), by default rowData(x) propagates the rownames of x to the returned DataFrame object (note that for a SummarizedExperiment object, the rownames are also the names i.e. rownames(x) is always the same as names(x)). Setting use.names=FALSE suppresses this propagation i.e. it returns a DataFrame object with no rownames. Use this when rowData(x) fails, which can happen when the rownames contain NAs (because the rownames of a SummarizedExperiment object can contain NAs, but the rownames of a DataFrame object cannot).
drop        A logical(1), ignored by these methods.
deparse.level See \cite{base::cbind} for a description of this argument.
subset     An expression which, when evaluated in the context of rowData(x), is a logical vector indicating elements or rows to keep: missing values are taken as false.
select     An expression which, when evaluated in the context of colData(x), is a logical vector indicating elements or rows to keep: missing values are taken as false.
BACKEND    NULL (the default), or a single string specifying the name of the backend. When the backend is set to NULL, each element of assays(x) is realized in memory as an ordinary array by just calling as.array on it.

Details

The SummarizedExperiment class is meant for numeric and other data types derived from a sequencing experiment. The structure is rectangular like a matrix, but with additional annotations on the rows and columns, and with the possibility to manage several assays simultaneously.

The rows of a SummarizedExperiment object represent features of interest. Information about these features is stored in a DataFrame object, accessible using the function rowData. The DataFrame must have as many rows as there are rows in the SummarizedExperiment object, with each row of the DataFrame providing information on the feature in the corresponding row of the SummarizedExperiment object. Columns of the DataFrame represent different attributes of the features of interest, e.g., gene or transcript IDs, etc.

Each column of a SummarizedExperiment object represents a sample. Information about the samples are stored in a DataFrame, accessible using the function colData, described below. The DataFrame must have as many rows as there are columns in the SummarizedExperiment object, with each row of the DataFrame providing information on the sample in the corresponding column of the SummarizedExperiment object. Columns of the DataFrame represent different sample attributes, e.g., tissue of origin, etc. Columns of the DataFrame can themselves be annotated (via the mcols function). Column names typically provide a short identifier unique to each sample.

A SummarizedExperiment object can also contain information about the overall experiment, for instance the lab in which it was conducted, the publications with which it is associated, etc. This information is stored as a list object, accessible using the metadata function. The form of the data associated with the experiment is left to the discretion of the user.

The SummarizedExperiment container is appropriate for matrix-like data. The data are accessed using the assays function, described below. This returns a SimpleList object. Each element of the list must itself be a matrix (of any mode) and must have dimensions that are the same as the dimensions of the SummarizedExperiment in which they are stored. Row and column names of each matrix must either be NULL or match those of the SummarizedExperiment during construction. It is convenient for the elements of SimpleList of assays to be named.

Constructor

SummarizedExperiment instances are constructed using the SummarizedExperiment function documented in \cite{RangedSummarizedExperiment}.

Accessors

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

assays(x), assays(x) <- value: Get or set the assays. value is a list or SimpleList, each element of which is a matrix with the same dimensions as x.
SummarizedExperiment-class

assay(x, i), assay(x, i) <- value: A convenient alternative to assays(x)[[i]]. assays(x)[[i]] <- value) to get or set the ith (default first) assay element. value must be a matrix of the same dimension as x, and with dimension names NULL or consistent with those of x.

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

rowData(x, use.names=TRUE), rowData(x) <- value: Get or set the row data. value is a DataFrame object.

colData(x), colData(x) <- value: Get or set the column data. value is a DataFrame object.

Row names of value must be NULL or consistent with the existing column names of x.

metadata(x), metadata(x) <- value: Get or set the experiment data. value is a list with arbitrary content.

dim(x): Get the dimensions (features of interest x samples) of the SummarizedExperiment.

dimnames(x), dimnames(x) <- value: Get or set the dimension names. value is usually a list of length 2, containing elements that are either NULL or vectors of appropriate length for the corresponding dimension. value can be NULL, which removes dimension names. This method implies that rownames, rownames<-, colnames, and colnames<- are all available.

Subsetting

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

x[i,j], x[i,j] <- value: Create or replace a subset of x. i, j can be numeric, logical, character, or missing. value must be a SummarizedExperiment object with dimensions, dimension names, and assay elements consistent with the subset x[i,j] being replaced.

subset(x, subset, select): Create a subset of x using an expression subset referring to columns of rowData(x) and/or select referring to column names of colData(x).

Additional subsetting accessors provide convenient access to colData columns

x$name, x$name <- value: Access or replace column name in x.

x[[i,...]], x[[i,...]] <- value: Access or replace column i in x.

Combining

In the code snippets below, ... are SummarizedExperiment objects to be combined.

cbind(...): cbind combines objects with the same features of interest but different samples (columns in assays). The colnames in colData(SummarizedExperiment) must match or an error is thrown. Duplicate columns of rowData(SummarizedExperiment) must contain the same data.

Data in assays are combined by name matching; if all assay names are NULL matching is by position. A mixture of names and NULL throws an error.

metadata from all objects are combined into a list with no name checking.

rbind(...): rbind combines objects with the same samples but different features of interest (rows in assays). The colnames in rowData(SummarizedExperiment) must match or an error is thrown. Duplicate columns of colData(SummarizedExperiment) must contain the same data.

Data in assays are combined by name matching; if all assay names are NULL matching is by position. A mixture of names and NULL throws an error.

metadata from all objects are combined into a list with no name checking.
Implementation and Extension

This section contains advanced material meant for package developers.

SummarizedExperiment is implemented as an S4 class, and can be extended in the usual way, using `contains="SummarizedExperiment"` in the new class definition.

In addition, the representation of the assays slot of SummarizedExperiment is as a virtual class Assays. This allows derived classes (`contains="Assays"`) to easily implement alternative requirements for the assays, e.g., backed by file-based storage like NetCDF or the `ff` package, while re-using the existing SummarizedExperiment class without modification. See Assays for more information.

The current assays slot is implemented as a reference class that has copy-on-change semantics. This means that modifying non-assay slots does not copy the (large) assay data, and at the same time the user is not surprised by reference-based semantics. Updates to non-assay slots are very fast; updating the assays slot itself can be 5x or more faster than with an S4 instance in the slot. One useful technique when working with assay or assays function is use of the `withDimnames=FALSE` argument, which benefits speed and memory use by not copying dimnames from the row- and colData elements to each assay.

Author(s)

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See Also

- RangedSummarizedExperiment objects.
- DataFrame, SimpleList, and Annotated objects in the S4Vectors package.
- The metadata and mcols accessors in the S4Vectors package.
- saveHDF5SummarizedExperiment and loadHDF5SummarizedExperiment in the HDF5Array package for saving/loading an HDF5-based SummarizedExperiment object to/from disk.
- The realize generic function in the DelayedArray package for more information about on-disk realization of objects carrying delayed operations.

Examples

```r
nrows <- 200; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
  row.names=LETTERS[1:6])
se0 <- SummarizedExperiment(assays=SimpleList(counts=counts),
  colData=colData)
se0
dim(se0)
dimnames(se0)
assayNames(se0)
head(assay(se0))
assays(se0) <- endoapply(assays(se0), asinh)
head(assay(se0))
rowData(se0)
colData(se0)
se0[, se0$Treatment == "ChIP"]
subset(se0, select = Treatment == "ChIP")
```
## cbind() combines objects with the same features of interest but different samples:
se1 <- se0
se2 <- se1[,1:3]
colnames(se2) <- letters[seq_len(ncol(se2))]
cmb1 <- cbind(se1, se2)
dim(cmb1)
dimnames(cmb1)

cmb2 <- cbind(se1, se2)
dim(cmb2)
dimnames(cmb2)

## rbind() combines objects with the same samples but different features of interest:
se1 <- se0
se2 <- se1[1:50,]
rownames(se2) <- letters[seq_len(nrow(se2))]
cmb2 <- rbind(se1, se2)
dim(cmb2)
dimnames(cmb2)

## ON-DISK REALIZATION

setRealizationBackend("HDF5Array")
cmb3 <- realize(cmb2)
assay(cmb3, withDimnames=FALSE) # an HDF5Matrix object
Index

*Topic file
- readKallisto, 20

*Topic manip
- makeSummarizedExperimentFromExpressionSet, 12

*Topic methods
- coverage-methods, 4
- findOverlaps-methods, 5
- inter-range-methods, 7
- intra-range-methods, 8
- nearest-methods, 14

*Topic utilities
- coverage-methods, 4
- findOverlaps-methods, 5
- inter-range-methods, 7
- intra-range-methods, 8
- nearest-methods, 14
- $\langle-, SummarizedExperiment-method (SummarizedExperiment-class), 22$
- acbind, Matrix-method (Assays-class), 2
- Annotated, 26
- arbind, Matrix-method (Assays-class), 2
- assay (SummarizedExperiment-class), 22
- assay, SummarizedExperiment, character-method (SummarizedExperiment-class), 22
- assay, SummarizedExperiment, missing-method (SummarizedExperiment-class), 22
- assay, SummarizedExperiment, numeric-method (SummarizedExperiment-class), 22
- assay$\langle-, SummarizedExperiment-class), 22$
- assay$\langle-, SummarizedExperiment, character-method (SummarizedExperiment-class), 22$
- assay$\langle-, SummarizedExperiment, missing-method (SummarizedExperiment-class), 22$
- assay$\langle-, SummarizedExperiment, numeric-method (SummarizedExperiment-class), 22$
- assayNames (SummarizedExperiment-class), 22
- assayNames, SummarizedExperiment-method (SummarizedExperiment-class), 22
- assayNames$\langle-, SummarizedExperiment-class), 22$
- assayNames$\langle-, SummarizedExperiment, character-method (SummarizedExperiment-class), 22$
- Assays, 26
- Assays (Assays-class), 2
- assays (SummarizedExperiment-class), 22
- assays, SummarizedExperiment-method (SummarizedExperiment-class), 22
dimnames<-,SummarizedExperiment,NULL-method (SummarizedExperiment-class), 22
disjointBins (inter-range-methods), 7
disjointBins,RangedSummarizedExperiment-method (inter-range-methods), 7
distance (nearest-methods), 14
distance,ANY,RangedSummarizedExperiment-method (nearest-methods), 14
distance,RangedSummarizedExperiment,ANY-method (nearest-methods), 14
distance,RangedSummarizedExperiment,RangedSummarizedExperiment-method (nearest-methods), 14
distanceToNearest (nearest-methods), 14
distanceToNearest,ANY,RangedSummarizedExperiment-method (nearest-methods), 14
distanceToNearest,RangedSummarizedExperiment,ANY-method (nearest-methods), 14
distanceToNearest,RangedSummarizedExperiment,RangedSummarizedExperiment-method (nearest-methods), 14
duplicated, 18
duplicated,RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
elementMetadata,RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
elementMetadata<-,RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
end, 18
elementMetadata<-,RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
findOverlaps (findOverlaps-methods), 5
findOverlaps (findOverlaps-methods), 5
findOverlaps,Vector,RangedSummarizedExperiment-method (findOverlaps-methods), 5
findOverlaps-methods, 5
loadHDF5SummarizedExperiment, 26
makeGrangesFromDataFrame, 10, 11
makeSummarizedExperimentFromDataFrame, 10
makeSummarizedExperimentFromExpressionSet, 12
makeSummarizedExperimentFromLoom, 13
makeSummarizedExperimentFromExpressionSet, 12
nearest-methods, 5–7, 9, 15
getListElement,Assays-method
getListElement,AssaysInEnv-method
getListElement,Assays-class, 2
getListElement,AssaysInEnv-method
GRanges, 10–12, 16–19
granges, 18
granges,RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
GRangesList, 5–7, 9, 12, 15–18
is.unsorted,RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
isDisjoint, 7, 18, 19
isDisjoint (inter-range-methods), 7
isDisjoint,RangedSummarizedExperiment-method (inter-range-methods), 7
KALLISTO_ASSAYS (readKallisto), 20
length,Assays-method (Assays-class), 2
length,AssaysInEnv-method (Assays-class), 2
length,SummarizedExperiment-method (SummarizedExperiment-class), 22
loadHDF5SummarizedExperiment, 26
makeGrangesFromDataFrame, 10, 11
makeSummarizedExperimentFromDataFrame, 10
makeSummarizedExperimentFromExpressionSet, 12
makeSummarizedExperimentFromLoom, 13
makeSummarizedExperimentFromExpressionSet, 12
nearest-methods, 7
inter-range-methods, 8
intra-range-methods, 8
is.unsorted,RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
isDisjoint, 7, 18, 19
isDisjoint (inter-range-methods), 7
isDisjoint,RangedSummarizedExperiment-method (inter-range-methods), 7
KALLISTO_ASSAYS (readKallisto), 20
length,Assays-method (Assays-class), 2
length,AssaysInEnv-method (Assays-class), 2
length,SummarizedExperiment-method (SummarizedExperiment-class), 22
loadHDF5SummarizedExperiment, 26
makeGrangesFromDataFrame, 10, 11
makeSummarizedExperimentFromDataFrame, 10
makeSummarizedExperimentFromExpressionSet, 12
makeSummarizedExperimentFromLoom, 13
match, 18
mcols, 18, 23, 24, 26
mcols, RangedSummarizedExperiment-method
(RangedSummarizedExperiment-class), 16
mcols<-, RangedSummarizedExperiment-method
(RangedSummarizedExperiment-class), 16
metadata, 26
naiveRangeMapper
(makeSummarizedExperimentFromExpressionSet), 12
names, Assays-method (Assays-class), 2
names, AssaysInEnv-method
(Assays-class), 2
names, RangedSummarizedExperiment-method
(RangedSummarizedExperiment-class), 16
names, SummarizedExperiment-method
(SummarizedExperiment-class), 22
names<-, Assays-method (Assays-class), 2
names<-, AssaysInEnv-method
(Assays-class), 2
names<-, RangedSummarizedExperiment-method
(RangedSummarizedExperiment-class), 16
names<-, SummarizedExperiment-method
(SummarizedExperiment-class), 22
narrow (intra-range-methods), 8
narrow, RangedSummarizedExperiment-method
(intra-range-methods), 8
nearest, 15, 18, 19
nearest (nearby-methods), 14
nearest, ANY, RangedSummarizedExperiment-method
(nearby-methods), 14
nearest, RangedSummarizedExperiment, ANY-method
(nearby-methods), 14
nearest, RangedSummarizedExperiment, RangedSummarizedExperiment-method
(readKallisto), 20
nearest-methods, 14
order, 18
order, RangedSummarizedExperiment-method
(RangedSummarizedExperiment-class), 16
pcompare, 18
pcompare, ANY, RangedSummarizedExperiment-method
size (intra-range-methods), 8
pcompare, RangedSummarizedExperiment, ANY-method
(RangedSummarizedExperiment-class), 16
pcompare, RangedSummarizedExperiment, RangedSummarizedExperiment-method
(RangedSummarizedExperiment-class), 16
precede (nearest-methods), 14
precede, ANY, RangedSummarizedExperiment-method
(nearby-methods), 14
precede, RangedSummarizedExperiment, ANY-method
(nearby-methods), 14
preceed, RangedSummarizedExperiment, RangedSummarizedExperiment-method
(nearby-methods), 14
probeRangeMapper
(makeSummarizedExperimentFromExpressionSet), 12
promoters (intra-range-methods), 8
promoters, RangedSummarizedExperiment-method
(intra-range-methods), 8
RangedSummarizedExperiment, 4–9, 11–15, 22, 24, 26
RangedSummarizedExperiment
(RangedSummarizedExperiment-class), 16
ranges, 18
ranges, RangedSummarizedExperiment-method
(RangedSummarizedExperiment-class), 16
ranges<-, RangedSummarizedExperiment-method
(RangedSummarizedExperiment-class), 16
rank, 18
rank, RangedSummarizedExperiment-method
(RangedSummarizedExperiment-class), 16
rbind, Assays-method (Assays-class), 2
rbind, RangedSummarizedExperiment-method
(SummarizedExperiment-class), 22
readKallisto, 20
readKallistoBootstrap (readKallisto), 20
realize, 26
realize, SummarizedExperiment-method
(SummarizedExperiment-class), 22
replaceROWS, SummarizedExperiment-method
(SummarizedExperiment-class), 22
resize, RangedSummarizedExperiment-method
(intra-range-methods), 8
restrict (intra-range-methods), 8
restrict, RangedSummarizedExperiment-method (intra-range-methods), 8
rowData (SummarizedExperiment-class), 22
rowData, SummarizedExperiment-method (SummarizedExperiment-class), 22
rowData <- (SummarizedExperiment-class), 22
rownames, 12
rowRanges (RangedSummarizedExperiment-class), 16
rowRanges, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
rowRanges <- (RangedSummarizedExperiment-class), 16
rowRanges <-, RangedSummarizedExperiment, NULL-method (RangedSummarizedExperiment-class), 16
rowRanges <-, SummarizedExperiment, GenomicRanges-method (RangedSummarizedExperiment-class), 16
rowRanges <-, SummarizedExperiment, GRangesList-method (RangedSummarizedExperiment-class), 16
rowRanges <-, SummarizedExperiment, NULL-method (RangedSummarizedExperiment-class), 16
saveHDF5SummarizedExperiment, 26
Seqinfo, 11
seqinfo, 18
seqinfo, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
seqinfo <-, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
seqnames, 18
seqnames, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
setListElement, Assays-method (Assays-class), 2
setListElement, AssaysInEnv-method (Assays-class), 2
setListElement, AssaysInEnv-method (Assays-class), 2
setListElement, AssaysInEnv-method (Assays-class), 2
SetListElement, AssaysInEnv-method (Assays-class), 2
SimpleAssays (Assays-class), 2
SimpleAssays-class (Assays-class), 2
SimpleList, 2, 3, 24, 26
sort, 18
sort, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
sparseMatrix, 17
split, RangedSummarizedExperiment, ANY-method (RangedSummarizedExperiment-class), 16
split, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
start, 18
start, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
start <-, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
strand, 18
strand, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
strand, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
subset, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
subset, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
subset, SummarizedExperiment-method (SummarizedExperiment-class), 22
 Subset, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
Subset, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
Subset, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
SummarizedExperiment, 2, 3, 10, 14, 16, 17
SummarizedExperiment (RangedSummarizedExperiment-class),
SummarizedExperiment-class, 19, 22
trim, RangedSummarizedExperiment-method (intra-range-methods), 8
TxDb, 13
updateObject, Assays-method (Assays-class), 2
updateObject, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
updateObject, SummarizedExperiment-method (SummarizedExperiment-class), 22
width, 18
width, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16
width<-, RangedSummarizedExperiment-method (RangedSummarizedExperiment-class), 16