

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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Assays-class	<i>Assays objects</i>
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Description

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`, ``names<-``, `getListElement`, `setListElement`, `dim`, `[]`, ``[<-``, `rbind`, `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, `[]` as well as replacement methods `names<-`, `setListElement`, and `[<-`, 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

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

names(a)
names(a) <- c("a1", "a2")
names(a)
getListElement(a, "a2")

rbind(a, a)
cbind(a, a)

## -----
## COPY-ON-CHANGE CONTRACT
## -----

## ShallowSimpleListAssays objects have copy-on-change semantics but not
## AssaysInEnv objects. For example:
ssla <- as(SimpleList(m1, m2), "ShallowSimpleListAssays")
aie <- as(SimpleList(m1, m2), "AssaysInEnv")

## No names on 'ssla' and 'aie':
names(ssla)
names(aie)

ssla2 <- ssla
aie2 <- aie
names(ssla2) <- names(aie2) <- c("A1", "A2")

names(ssla) # still NULL (as expected)

names(aie) # changed! (because the names<-,AssaysInEnv method is not
# implemented in a way that respects the copy-on-change
# contract)

```

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

```
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))))
```

findOverlaps-methods *Finding overlapping ranges in RangedSummarizedExperiment objects*

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

```
## 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.

`select`, `ignore.strand`

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

```
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)

hits <- findOverlaps(rse0, rse1)
hits
stopifnot(identical(hits, findOverlaps(rowRanges(rse0), rowRanges(rse1))))
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`:

$$f(\text{rowRanges}(x), \dots)$$

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]))
```

intra-range-methods *Intra range transformations of a RangedSummarizedExperiment object*

Description

This man page documents the *intra range transformations* that are supported on [RangedSummarizedExperiment](#) objects.

Usage

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

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

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

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

```
## S4 method for signature 'RangedSummarizedExperiment'
promoters(x, upstream=2000, downstream=200)
```

```
## S4 method for signature 'RangedSummarizedExperiment'
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)

```

Arguments

<code>df</code>	A <code>data.frame</code> or DataFrame object. If not, then the function first tries to turn <code>df</code> into a data frame with <code>as.data.frame(df)</code> .
<code>...</code>	Additional arguments passed on to makeGRangesFromDataFrame
<code>seqinfo</code>	Either <code>NULL</code> , or a Seqinfo object, or a character vector of seqlevels, or a named numeric vector of sequence lengths. When not <code>NULL</code> , it must be compatible with the genomic ranges in <code>df</code> i.e. it must include at least the sequence levels represented in <code>df</code> .

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

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

# 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

<code>from</code>	An ExpressionSet object.
<code>mapFun</code>	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 <code>rownames</code> of the returned GRanges are used to match the <code>featureNames</code> of the ExpressionSet . The <code>naiveRangeMapper</code> function is used by default.
<code>...</code>	Additional arguments passed to <code>mapFun</code> .
<code>txDbPackage</code>	A character string with the Transcript Database to use for the mapping.
<code>key</code>	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.hester@gmail.com

See Also

- [RangedSummarizedExperiment](#) objects.
- [ExpressionSet](#) objects in the **Biobase** package.
- [TxDb](#) objects in the **GenomicFeatures** package.

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
## -----

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

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

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

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

## S4 method for signature 'RangedSummarizedExperiment,ANY'
distanceToNearest(x, subject, ignore.strand=FALSE, ...)
## S4 method for signature 'ANY,RangedSummarizedExperiment'
distanceToNearest(x, subject, ignore.strand=FALSE, ...)
```

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 through 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

```
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 `class?SummarizedExperiment` also work on a RangedSummarizedExperiment object. The methods documented below are additional methods that are specific to RangedSummarizedExperiment objects.

Usage

Constructor

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

Accessors

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

Subsetting

```
## S4 method for signature 'RangedSummarizedExperiment'
subset(x, subset, select, ...)
```

rowRanges access

see 'GRanges compatibility', below

Arguments

assays	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.
--------	--

rowData	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.
rowRanges	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.
colData	An optional DataFrame describing the samples. Row names, if present, become the column names of the RangedSummarizedExperiment.
metadata	An optional list of arbitrary content describing the overall experiment.
x	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.
...	Further arguments to be passed to or from other methods.
value	A GRanges or GRangesList object.
subset	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.
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.

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 contains 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

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

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

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

## cbind() combines objects with the same ranges but different samples:
rse1 <- rse
rse2 <- rse1[ , 1:3]
colnames(rse2) <- letters[1:ncol(rse2)]
cmb1 <- cbind(rse1, rse2)
dim(cmb1)
dimnames(cmb1)

## rbind() combines objects with the same samples but different ranges:
rse1 <- rse
rse2 <- rse1[1:50, ]
rownames(rse2) <- letters[1:nrow(rse2)]
cmb2 <- rbind(rse1, rse2)
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)))

```

Description

WARNING: readKallisto() is deprecated. Please use tximeta() from the **tximeta** package instead.

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

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

```
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)

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References

<http://pachterlab.github.io/kallisto> software for quantifying transcript abundance.

Examples

```
## Not run:
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)

## End(Not run)
```

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, withDimnames=TRUE, ...)
assay(x, i, withDimnames=TRUE, ...) <- 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=getAutoRealizationBackend())
```

Arguments

x	A SummarizedExperiment object.
...	For assay, arguments in ... are 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 subscripts 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 the dimnames of the SummarizedExperiment object should be applied (i.e. copied) to the extracted assays. More precisely, setting withDimnames=FALSE in the <i>getter</i> returns the assays <i>as-is</i> whereas setting withDimnames=FALSE return them with possibly modified dimnames. Setting withDimnames=FALSE in the <i>setter</i> (assays<-) is required when the dimnames on the supplied assays are not identical to the dimnames on the SummarizedExperiment object; it does not influence actual assignment of dimnames to assays (they’re always stored as-is). Note that <pre>assays(x, withDimnames=FALSE) <- assays(x, withDimnames=FALSE)</pre> is guaranteed to always work and be a no-op. This is not the case if withDimnames=TRUE is used or if withDimnames is not specified.

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

`assay(x, i)`, `assay(x, i) <- value`: A convenient alternative (to `assays(x)[[i]]`, `assays(x)[[i]] <- value`) to get or set the *i*th (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, `x`, `y` and `...` 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.

`combineRows(x, ..., use.names=TRUE, delayed=TRUE, fill=NA)`: `combineRows` acts like more flexible `rbind`, returning a `SummarizedExperiment` with features equal to the concatenation of features across all input objects. Unlike `rbind`, it permits differences in the number and identity of the columns, differences in the available `rowData` fields, and even differences in the available `assays` among the objects being combined.

If `use.names=TRUE`, each input object must have non-`NULL`, non-duplicated column names. These names do not have to be the same, or even shared, across the input objects. The column names of the returned `SummarizedExperiment` will be a union of the column names across all input objects. If a column is not present in an input, the corresponding assay and `colData` entries will be filled with `fill` and `NA`s, respectively, in the combined `SummarizedExperiment`.

If `use.names=FALSE`, all objects must have the same number of columns. The column names of the returned object is set to `colnames(x)`. Any differences in the column names between input objects are ignored.

Data in assays are combined by matching the names of the assays. If one input object does not contain a named assay present in other input objects, the corresponding assay entries in the returned object will be set to `fill`. If all assay names are `NULL`, matching is done by position. A mixture of named and unnamed assays will throw an error.

If `delayed=TRUE`, assay matrices are wrapped in `DelayedArrays` to avoid any extra memory allocation during the matrix `rbinding`. Otherwise, the matrices are combined as-is; note that this may still return `DelayedMatrix`s if the inputs were also `DelayedMatrix` objects.

If any input is a `RangedSummarizedExperiment`, the returned object will also be a `RangedSummarizedExperiment`. The `rowRanges` of the returned object is set to the concatenation of the `rowRanges` of all inputs. If any input is a `SummarizedExperiment`, the returned `rowRanges` is converted into a `GRangesList` and the entries corresponding to the rows of the `SummarizedExperiment` are set to zero-length `GRanges`. If all inputs are `SummarizedExperiment` objects, a `SummarizedExperiment` is also returned.

`rowData` are combined using `combineRows` for `DataFrame` objects. It is not necessary for all input objects to have the same fields in their `rowData`; missing fields are filled with `NA`s for the corresponding rows in the returned object.

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

`combineCols(x, ..., use.names=TRUE, delayed=TRUE, fill=NA)`: `combineCols` acts like more flexible `cbind`, returning a `SummarizedExperiment` with columns equal to the concatenation

of columns across all input objects. Unlike `cbind`, it permits differences in the number and identity of the rows, differences in the available `colData` fields, and even differences in the available `assays` among the objects being combined.

If `use.names=TRUE`, each input object must have non-NULL, non-duplicated row names. These names do not have to be the same, or even shared, across the input objects. The row names of the returned `SummarizedExperiment` will be a union of the row names across all input objects. If a row is not present in an input, the corresponding assay and `rowData` entries will be filled with `fill` and `NA`s, respectively, in the combined `SummarizedExperiment`.

If `use.names=FALSE`, all objects must have the same number of rows. The row names of the returned object is set to `rownames(x)`. Any differences in the row names between input objects are ignored.

Data in assays are combined by matching the names of the assays. If one input object does not contain a named assay present in other input objects, the corresponding assay entries in the returned object will be set to `fill`. If all assay names are `NULL`, matching is done by position. A mixture of named and unnamed assays will throw an error.

If `delayed=TRUE`, assay matrices are wrapped in `DelayedArrays` to avoid any extra memory allocation during the matrix `rbinding`. Otherwise, the matrices are combined as-is; note that this may still return `DelayedMatrix`s if the inputs were also `DelayedMatrix` objects.

If any input is a `RangedSummarizedExperiment`, the returned object will also be a `RangedSummarizedExperiment`. The `rowRanges` of the returned object is set to a merge of the `rowRanges` of all inputs, where the coordinates for each row are taken from the input object that contains that row. Any conflicting ranges for shared rows will raise a warning and all `rowRanges` information from the offending `RangedSummarizedExperiment` will be ignored. If any input is a `SummarizedExperiment`, the returned `rowRanges` is converted into a `GRangesList` and the entries corresponding to the unique rows of the `SummarizedExperiment` are set to zero-length `GRanges`. If all inputs are `SummarizedExperiment` objects, a `SummarizedExperiment` is also returned.

`colData` are combined using `combineRows` for `DataFrame` objects. It is not necessary for all input objects to have the same fields in their `colData`; missing fields are filled with `NA`s for the corresponding columns in the returned object.

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 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.

Author(s)

Martin Morgan; `combineRows` and `combineCols` by Aaron Lun

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

```
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)

## 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
## -----
library(DelayedArray)
setAutoRealizationBackend("HDF5Array")
cmb3 <- realize(cmb2)
assay(cmb3, withDimnames=FALSE) # an HDF5Matrix object
```

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