Package ‘SummarizedExperiment’

May 30, 2024

**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.

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

**URL**  https://bioconductor.org/packages/SummarizedExperiment

**BugReports**  https://github.com/Bioconductor/SummarizedExperiment/issues

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**Encoding**  UTF-8

**Depends**  R (>= 4.0.0), methods, MatrixGenerics (>= 1.1.3), GenomicRanges (>= 1.55.2), Biobase

**Imports**  utils, stats, tools, Matrix, BiocGenerics (>= 0.37.0), S4Vectors (>= 0.33.7), IRanges (>= 2.23.9), GenomeInfoDb (>= 1.13.1), S4Arrays (>= 1.1.1), DelayedArray (>= 0.27.1)

**Suggests**  HDF5Array (>= 1.7.5), annotate, AnnotationDbi, hgu95av2.db, GenomicFeatures, TxDb.Hsapiens.UCSC.hg19.knownGene, jsonlite, rhdf5, airway (>= 1.15.1), BiocStyle, knitr, rmarkdown, RUnit, testthat, digest

**VignetteBuilder**  knitr


**git_url**  https://git.bioconductor.org/packages/SummarizedExperiment

**git_branch**  RELEASE_3_19
## Assays-class

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

```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)

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 of a RangedSummarizedExperiment object

Description

This man page documents the coverage method for RangedSummarizedExperiment objects.

Usage

```r
## 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),
```
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 count0overlaps, 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

```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)

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)))
```

---

**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 \( \ldots \) 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

```r
## 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'
terminators(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, start, end, width, fix, ignore.strand, both, upstream,
downstream, keep.all.ranges

See ?GenomicRanges::shift 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:

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

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

See ?GenomicRanges::shift in the GenomicRanges 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 GenomicRanges package where intra range transformations of a GenomicRanges or GRangesList object 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)))
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)
))
```
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**

- **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 seqlevels, 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](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
## 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,
strad = c("+", ",", "+", "x", "."), expr0 = 3:7,
expr1 = 8:12, expr2 = 12:16,
row.names = paste0("GENE", letters[5:1]))

df

exRSE <- makeSummarizedExperimentFromDataFrame(df)
exRSE
```
Description

Coercion between \texttt{RangedSummarizedExperiment} and \texttt{ExpressionSet} is supported in both directions.

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

Usage

\begin{verbatim}
makeSummarizedExperimentFromExpressionSet(from, mapFun=naiveRangeMapper, ...)
\end{verbatim}

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

Arguments

- \texttt{from} \hspace{1cm} An \texttt{ExpressionSet} object.
- \texttt{mapFun} \hspace{1cm} A function which takes an \texttt{ExpressionSet} object and returns a \texttt{GRanges}, or \texttt{GRangesList} object which corresponds to the genomic ranges used in the \texttt{ExpressionSet}. The \texttt{rownames} of the returned \texttt{GRanges} are used to match the \texttt{featureNames} of the \texttt{ExpressionSet}.
  - The \texttt{naiveRangeMapper} function is used by default.
- ... \hspace{1cm} Additional arguments passed to \texttt{mapFun}.
- \texttt{txDbPackage} \hspace{1cm} A character string with the Transcript Database to use for the mapping.
- \texttt{key} \hspace{1cm} A character string with the Gene key to use for the mapping.

Value

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

The range mapping functions return a \texttt{GRanges} object, with the \texttt{rownames} corresponding to the \texttt{featureNames} of the \texttt{ExpressionSet} object.
makeSummarizedExperimentFromLoom

Make a SummarizedExperiment from a `.loom` hdf5 file

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")
```
**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 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](http://loompy.org/loompy-docs/format/index.html) for a specification of the `.loom` format.

**Examples**

```r
## BASIC EXAMPLE

file <- system.file(
    package="SummarizedExperiment", 
    extdata", "example.loom"
)

se <- makeSummarizedExperimentFromLoom(file)

se

assay(se)

metadata(se)
```
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"),
    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.
- `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
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),
                            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")
))
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

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

## Accessors

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

## Subsetting

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

## rowRanges access

```r
## 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 `rowData`.

- **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.

- **checkDimnames**: By default the rownames and colnames of the supplied assay(s) are checked for consistency with those of the `SummarizedExperiment` object (or derivative) to construct. More precisely, the rownames and colnames of each assay must be `NULL` or identical to those of the object. Use `checkDimnames=FALSE` to skip this check.

- **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 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.

\[
\text{rowRanges}(x), \text{rowRanges}(x) \leftarrow \text{value}: \text{Get or set the row data. value is a GenomicRanges object. Row names of value must be NULL or consistent with the existing row names of x.}
\]

GRanges compatibility (rowRanges access)

Many \texttt{GRanges} and \texttt{GRangesList} operations are supported on RangedSummarizedExperiment objects, using \texttt{rowRanges}.

Supported operations include: \texttt{pcompare}, \texttt{duplicated}, \texttt{end}, \texttt{end<-}, \texttt{granges}, \texttt{is.unsorted}, \texttt{match}, \texttt{mcols}, \texttt{mcols<-}, \texttt{order}, \texttt{ranges}, \texttt{ranges<-}, \texttt{rank}, \texttt{seqinfo}, \texttt{seqinfo<-}, \texttt{seqnames}, \texttt{sort}, \texttt{start}, \texttt{start<-}, \texttt{strand}, \texttt{strand<-}, \texttt{width}, \texttt{width<-}.

See also \texttt{shift}, \texttt{isDisjoint}, \texttt{coverage}, \texttt{findOverlaps}, and \texttt{nearest} for more \texttt{GRanges} compatibility methods.

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

Subsetting

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

\[
\text{subset}(x, \text{subset}, \text{select}): \text{Create a subset of x using an expression subset referring to columns of rowRanges(x) (including 'seqnames', 'start', 'end', 'width', 'strand', and names(rowData(x)) and/or select referring to column names of colData(x).}
\]

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)

Martin Morgan, mtmorgan@fhcrc.org

See Also

- \texttt{SummarizedExperiment-class}
- \texttt{shift}, \texttt{isDisjoint}, \texttt{coverage}, \texttt{findOverlaps}, and \texttt{nearest} for more \texttt{GRanges} compatibility methods.
- \texttt{GRanges} objects in the \texttt{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)
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)))

---

### 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'
rbind(..., deparse.level=1)
## S4 method for signature 'SummarizedExperiment'
cbind(..., deparse.level=1)
## S4 method for signature 'SummarizedExperiment'
combineRows(x, ..., delayed=TRUE, fill=NA, use.names=TRUE)
## S4 method for signature 'SummarizedExperiment'
combineCols(x, ..., delayed=TRUE, fill=NA, use.names=TRUE)

## 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 rbind, cbind, ... 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 getter returns the assays as-is whereas setting withDimnames=TRUE return them with possibly modified dimnames.

See "Top-level dimnames vs assay-level dimnames" section in the SummarizedExperiment vignette for more information about this and some examples.

Setting withDimnames=FALSE in the setter (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

assays(x, withDimnames=FALSE) <- assays(x, withDimnames=FALSE)

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.

use.names

For rowData: 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).

For combineRows and combineCols: See Combining section below.

drop

A logical(1), ignored by these methods.

deparse.level

See ?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.

delayed, fill

See combineRows and combineCols in Combining section below.

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 so long as they be of the same dimensions.

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.

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.

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.

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 NAs, 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 `rbind`. Otherwise, the matrices are combined as-is; note that this may still return `DelayedMatrixs` 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.

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 `rbind`. Otherwise, the matrices are combined as-is; note that this may still return `DelayedMatrixs` 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 NAs 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 `ncols` accessor 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")

## 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)

## 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)

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