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.

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

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

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

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R topics documented:

Assays–class   *Assays objects*

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 performaing 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 preferrable 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(rowRanges(x), ...)
```

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

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).

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

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

Value

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

The range mapping functions return a [GRanges](#) object, with the rownames corresponding to the [featureNames](#) of the [ExpressionSet](#) object.

Author(s)

Jim Hester, james.f.hester@gmail.com

See Also

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

Examples

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

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

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

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

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

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

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

---

makeSummarizedExperimentFromLoom

Make a SummarizedExperiment from a '.loom' hdf5 file

Description

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

Usage

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

Arguments

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

Value

A [SummarizedExperiment](#) object with row and column data and one or more assays.

Author(s)

Martin Morgan

See Also

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

Examples

```
## ---------------------------------------------------------------------
## BASIC EXAMPLE
## ---------------------------------------------------------------------

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 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(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(),
                     checkDimnames=TRUE)

## 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.

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 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)))
```

```
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=FALSE return them with possibly modified dimnames.

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 rbinding. 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 NAs 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 NAs, 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 [DelayedArray](#)s to avoid any extra memory allocation during the matrix rbinding. 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 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")

## 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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