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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Assays-class

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:

```
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```
• (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<-`, `getElement`, `setElement`, `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<-`, `setElement`, 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 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

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

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

```r
## 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

```r
## 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

```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, 99*start(rse0))

isDisjoint(rse0) # FALSE
```
intra-range-methods

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'
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:

```r
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

```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[1:61])
rse0 <- SummarizedExperiment(assays=SimpleList(counts=counts),
                             rowRanges=rowRanges, colData=colData)

rse1 <- shift(rse0, 1)
stopifnot(identical(
                     rowRanges(rse1),
                     shift(rowRanges(rse0), 1))
```


```r
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

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

Arguments

- \texttt{df} A \texttt{data.frame} or \texttt{DataFrame} object. If not, the function first tries to turn \texttt{df} into a \texttt{data.frame} with \texttt{as.data.frame(df)}.

- ... Additional arguments passed on to \texttt{makeGRangesFromDataFrame}

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

- \texttt{starts.in.df.are.0based} \texttt{TRUE} or \texttt{FALSE} (the default). If \texttt{TRUE}, then the start positions of the genomic ranges in \texttt{df} are considered to be \textit{0-based} and are converted to \textit{1-based} in the returned \texttt{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 (\url{http://genome.ucsc.edu/cgi-bin/hgTables}).

Value

A \texttt{RangedSummarizedExperiment} object with rowRanges and a single assay

Author(s)

M. Ramos

See Also

- \texttt{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,
                 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**

```r
makeSummarizedExperimentFromExpressionSet(from,
                                          mapFun=naiveRangeMapper,
                                          ...)"```

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

**Arguments**

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

**Value**

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

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

**Author(s)**

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

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

Examples

```r
## ---------------------------------------------------------------------
## GOING FROM ExpressionSet TO SummarizedExperiment
## ---------------------------------------------------------------------
data(sample.ExpressionSet, package="Biobase")

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

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

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

## ---------------------------------------------------------------------
## GOING FROM SummarizedExperiment TO ExpressionSet
## ---------------------------------------------------------------------
example(RangedSummarizedExperiment)  # to create 'rse'
rse
as(rse, "ExpressionSet")
```

makeSummarizedExperimentFromLoom

*Make a SummarizedExperiment from a `.loom` hdf5 file*

Description

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

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

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 \texttt{?nearest} in the \texttt{GenomicRanges} package for the details of how \texttt{nearest} and family operate on \texttt{GenomicRanges} and \texttt{GRangesList} objects.

\textbf{Value}

See \texttt{?nearest} in the \texttt{GenomicRanges} package.

\textbf{See Also}

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

\textbf{Examples}

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

res <- nearest(rse0)  # missing subject
res
stopifnot(identical(res, nearest(rowRanges(rse0))))

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

RangedSummarizedExperiment-class

RangedSummarizedExperiment objects

Description

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

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

Constructor

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

Accessors

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

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

Many GRanges and GRangesList operations are supported on RangedSummarizedExperiment objects, using rowRanges.

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

See also `?shift`, `?isDisjoint`, `?coverage`, `?findOverlaps`, and `?nearest` for more GRanges compatibility methods.

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

### Subsetting

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

```
subset(x, subset, select)
```

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

### Extension

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

### Author(s)

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### See Also

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

### Examples

```r
nrows <- 200; ncols <- 6
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
rowRanges <- GRanges(rep(c("chr1", "chr2"), c(50, 150)),
                     IRanges(floor(runif(200, 1e5, 1e6)), width=100),
                     strand=sample(c("+", "-"), 200, TRUE),
                     feature_id=sprintf("ID%03d", 1:200))
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                      row.names=LETTERS[1:6])
rse <- SummarizedExperiment(assays=SimpleList(counts=counts),
```
```r
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:
rsel <- rse
rsel1 <- rse[, 1:3]
colnames(rsel2) <- letters[1:ncol(rsel2)]
cmb1 <- cbind(rsel1, rsel2)
dim(cmb1)
dimnames(cmb1)

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

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

as(se0, "RangedSummarizedExperiment")

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

## Sanity checks:
stopifnot(identical(assays(se0), assays(rse)))
stopifnot(identical(dim(se0), dim(rse)))
stopifnot(identical(dimnames(se0), dimnames(rse)))
stopifnot(identical(rownames(se0), rownames(rsel2)))
stopifnot(identical(colData(se0), colData(rsel)))
```
SummarizedExperiment-class

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

```r
# See ?RangedSummarizedExperiment for the constructor function.
```

## Accessors

```r
assayNames(x, ...) <- value
assays(x, withDimnames=TRUE, ...) <- value
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

```r
## 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
```r
## 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

\[
\text{assays}(x, \text{withDimnames}=\text{FALSE}) \leftarrow \text{assays}(x, \text{withDimnames}=\text{FALSE})
\]

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.
- `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 DelayedMatrix 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 DelayedArrays to avoid any extra memory allocation during the matrix rbinding. Otherwise, the matrices are combined as-is; note that this may still return DelayedMatrix 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 <code>contains="SummarizedExperiment"</code> 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 (<code>contains="Assays"</code>) 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**

```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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