Package 'alabaster.se'

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Title Load and Save SummarizedExperiments from File

Version 1.7.0

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Description Save SummarizedExperiments into file artifacts, and load them back into memory.
This is a more portable alternative to serialization of such objects into RDS files.
Each artifact is associated with metadata for further interpretation;
downstream applications can enrich this metadata with context-specific properties.

Depends SummarizedExperiment, alabaster.base

Imports methods, alabaster.ranges, alabaster.matrix, BiocGenerics,
S4Vectors, IRanges, GenomicRanges, jsonlite

Suggests rmarkdown, knitr, testthat, BiocStyle

VignetteBuilder knitr

RoxygenNote 7.3.1

biocViews DataImport, DataRepresentation

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emptyRowRanges   *Is the* rowRanges *empty?*

Description

Check the [rowRanges](#) of a [RangedSummarizedExperiment](#) is empty, i.e., a [GRangesList](#) with no ranges.

Usage

```
emptyRowRanges(x)
```

Arguments

x   A [RangedSummarizedExperiment](#) object or the contents of its [rowRanges](#).

Details

Metadata in [mcols](#) is ignored for the purpose of this discussion, as this can be moved to the [rowData](#)(x) of the base [SummarizedExperiment](#) class without loss. In other words, non-empty [mcols](#) will not be used to determine that the rowRanges is not empty. However, non-empty fields in the [metadata](#) or in the inner [mcols](#) of the [GRanges](#) will trigger a non-emptiness decision.

Value

A logical scalar indicating whether x has empty rowRanges.

Examples

```
emptyRowRanges(SummarizedExperiment())
emptyRowRanges(SummarizedExperiment(rowRanges=GRanges()))
emptyRowRanges(SummarizedExperiment(rowRanges=GRangesList()))
```

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readRangedSummarizedExperiment
                        Read a RangedSummarizedExperiment from disk

---

Description

Read a [RangedSummarizedExperiment](#) from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in [readObject](#).

Usage

```
readRangedSummarizedExperiment(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, itself created using the [saveObject](#) method for [RangedSummarizedExperiment](#) objects.
metadata	Named list of metadata for this object, see [readObjectFile](#) for details.
...	Further arguments passed to [readSummarizedExperiment](#) and internal [altReadObject](#) calls.

Value

A [RangedSummarizedExperiment](#) object.

Author(s)

Aaron Lun

See Also

["saveObject,RangedSummarizedExperiment-method"](#), to save the RangedSummarizedExperiment to disk.

Examples

```
# Mocking up an experiment:
mat <- matrix(rpois(10000, 10), ncol=10)
colnames(mat) <- letters[1:10]
rownames(mat) <- sprintf("GENE_%i", seq_len(nrow(mat)))

gr <- GRanges("chrA", IRanges(1:1000, width=10))
se <- SummarizedExperiment(list(counts=mat), rowRanges=gr)
se$stuff <- LETTERS[1:10]
rowData(se)$blah <- runif(1000)
metadata(se)$whee <- "YAY"

tmp <- tempfile()
saveObject(se, tmp)
readObject(tmp)
```

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readSummarizedExperiment

Read a SummarizedExperiment from disk

Description

Read a [SummarizedExperiment](#) from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in [readObject](#).

Usage

```
readSummarizedExperiment(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, itself created using the saveObject method for SummarizedExperiment objects.
metadata	Named list of metadata for this object, see readObjectFile for details.
...	Further arguments passed to internal altReadObject calls.

Value

A SummarizedExperiment object.

Author(s)

Aaron Lun

See Also

"saveObject,SummarizedExperiment-method", to save the SummarizedExperiment to disk.

Examples

```
# Mocking up an experiment:
mat <- matrix(rpois(10000, 10), ncol=10)
colnames(mat) <- letters[1:10]
rownames(mat) <- sprintf("GENE_%i", seq_len(nrow(mat)))

se <- SummarizedExperiment(list(counts=mat))
se$stuff <- LETTERS[1:10]
rowData(se)$blah <- runif(1000)
metadata(se)$whee <- "YAY"

tmp <- tempfile()
saveObject(se, tmp)
readObject(tmp)
```

---

saveRangedSummarizedExperiment

Save a RangedSummarizedExperiment to disk

Description

Save a RangedSummarizedExperiment to its on-disk representation.

Usage

```
## S4 method for signature 'RangedSummarizedExperiment'
saveObject(x, path, ...)
```

Arguments

x	A [RangedSummarizedExperiment](#) object or one of its subclasses.
path	String containing the path to a directory in which to save x.
...	Further arguments to pass to ["saveObject,SummarizedExperiment-method"](#) and internal [altSaveObject](#) calls.

Value

x is saved into path and NULL is invisibly returned.

Author(s)

Aaron Lun

See Also

[readRangedSummarizedExperiment](#), to read the RangedSummarizedExperiment back into the R session.

Examples

```
mat <- matrix(rpois(10000, 10), ncol=10)
colnames(mat) <- letters[1:10]
rownames(mat) <- sprintf("GENE_%i", seq_len(nrow(mat)))

gr <- GRanges("chrA", IRanges(1:1000, width=10))
se <- SummarizedExperiment(list(counts=mat), rowRanges=gr)
se$stuff <- LETTERS[1:10]
rowData(se)$blah <- runif(1000)
metadata(se)$whee <- "YAY"

tmp <- tempfile()
saveObject(se, tmp)
list.files(tmp, recursive=TRUE)
```

---

saveSummarizedExperiment

Save a SummarizedExperiment to disk

Description

Save a [SummarizedExperiment](#) to its on-disk representation.

Usage

```
## S4 method for signature 'SummarizedExperiment'
saveObject(x, path, SummarizedExperiment.allow.dataframe.assay = FALSE, ...)
```

Arguments

x	A [SummarizedExperiment](#) object or one of its subclasses.
path	String containing the path to a directory in which to save x.
SummarizedExperiment.allow.dataframe.assay	
	Logical scalar indicating whether to allow data frames as assays of x.
...	Further arguments to pass to internal [altSaveObject](#) calls.

Details

By default, we consider the presence of data frames in the assays to be an error. Users should coerce these into an appropriate matrix type, e.g., a dense matrix or a sparse dgCMatrix. If a DataFrame as an assay is truly desired, users may set [options](#)(alabaster.se.reject_data.frames=FALSE) to skip the error. Note that this only works for [DataFrame](#) objects - data.frame objects will not be saved correctly.

Value

x is saved into path and NULL is invisibly returned.

Author(s)

Aaron Lun

See Also

[readSummarizedExperiment](#), to read the SummarizedExperiment back into the R session.

Examples

```
mat <- matrix(rpois(10000, 10), ncol=10)
colnames(mat) <- letters[1:10]
rownames(mat) <- sprintf("GENE_%i", seq_len(nrow(mat)))

se <- SummarizedExperiment(list(counts=mat))
se$stuff <- LETTERS[1:10]
rowData(se)$blah <- runif(1000)
metadata(se)$whee <- "YAY"

tmp <- tempfile()
saveObject(se, tmp)
list.files(tmp, recursive=TRUE)
```

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