Package 'alabaster.se'

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Title Load and Save SummarizedExperiments from File

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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()))
```

`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)
```

---

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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