

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 | <i>Is the rowRanges empty?</i> |
|----------------|--------------------------------|

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 | <i>Read a RangedSummarizedExperiment from disk</i> |
|--------------------------------|--|

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 <code>saveObject</code> method for <code>RangedSummarizedExperiment</code> objects. |
| metadata | Named list of metadata for this object, see <code>readObjectFile</code> for details. |
| ... | Further arguments passed to <code>readSummarizedExperiment</code> and internal <code>altReadObject</code> 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 <code>saveObject</code> method for <code>SummarizedExperiment</code> objects. |
| metadata | Named list of metadata for this object, see <code>readObjectFile</code> for details. |
| ... | Further arguments passed to internal <code>altReadObject</code> 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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