

Package ‘alabaster.se’

April 7, 2025

Title Load and Save SummarizedExperiments from File

Version 1.7.0

Date 2024-10-16

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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

git_url <https://git.bioconductor.org/packages/alabaster.se>

git_branch devel

git_last_commit a745efa

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2025-04-07

Author Aaron Lun [aut, cre]

Maintainer Aaron Lun <infinite.monkeys.with.keyboards@gmail.com>

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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
```

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

| | |
|---|--|
| <code>x</code> | A SummarizedExperiment object or one of its subclasses. |
| <code>path</code> | String containing the path to a directory in which to save <code>x</code> . |
| <code>SummarizedExperiment.allow.dataframe.assay</code> | Logical scalar indicating whether to allow data frames as assays of <code>x</code> . |
| <code>...</code> | 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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