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

Suggests rmarkdown, knitr, testthat, BiocStyle, jsonlite

VignetteBuilder knitr

RoxygenNote 7.2.3

biocViews DataImport, DataRepresentation

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R topics documented:

`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()))
```

`loadSummarizedExperiment` *Load a SummarizedExperiment*

Description

Default loading of SummarizedExperiments based on the metadata stored by the corresponding `stageObject` method.

Usage

```
loadSummarizedExperiment(exp.info, project)
```

Arguments

exp.info	Named list containing the metadata for this experiment.
project	Any argument accepted by the acquisition functions, see ?acquireFile. By default, this should be a string containing the path to a staging directory.

Value

A SummarizedExperiment or RangedSummarizedExperiment object.

Author(s)

Aaron Lun

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"

# Staging it:
tmp <- tempfile()
dir.create(tmp)
info <- stageObject(se, dir=tmp, "rna-seq")

# And loading it back in:
loadSummarizedExperiment(info, tmp)
```

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stageObject,SummarizedExperiment-method

Stage a SummarizedExperiment

Description

Save a SummarizedExperiment to file inside the staging directory.

Usage

```
## S4 method for signature 'SummarizedExperiment'
stageObject(x, dir, path, child = FALSE, meta.name = "experiment.json", ...)

## S4 method for signature 'RangedSummarizedExperiment'
stageObject(x, dir, path, child = FALSE, ..., skip.ranges = FALSE)
```

Arguments

x	A SummarizedExperiment object or one of its subclasses.
dir	String containing the path to the staging directory.
path	String containing a prefix of the relative path inside dir where x is to be saved. The actual path used to save x may include additional components, see Details.
child	Logical scalar indicating whether x is a child of a larger object.
meta.name	String containing the name of the metadata file.
...	Further arguments to pass to the SummarizedExperiment method. For the SummarizedExperiment itself, all further arguments are just ignored.
skip.ranges	Logical scalar indicating whether to avoid saving the rowRanges.

Details

meta.name is only needed to set up the output path, for consistency with the stageObject contract. Callers should make sure to write the metadata to the same path by using .writeMetadata to create the JSON file.

If skip.ranges=TRUE, the RangedSummarizedExperiment method just calls the SummarizedExperiment method, i.e., rowRanges are not saved. This avoids the hassle of switching classes and the associated problems, e.g., https://github.com/Bioconductor/SummarizedExperiment/issues/29. Note that any subsequent loadObject call on the staged assets will return a non-ranged SummarizedExperiment.

If x is a RangedSummarizedExperiment with "empty" rowRanges (i.e., a GRangesList with zero-length entries), stageObject will save it to file without any genomic range information. This means that any subsequent loadObject on the staged assets will return a non-ranged SummarizedExperiment.

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

A named list of metadata that follows the summarized_experiment schema. The contents of x are saved into a path subdirectory inside dir.

Author(s)

Aaron Lun

Examples

```
tmp <- tempfile()
dir.create(tmp)

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"

dir.create(tmp)
stageObject(se, dir=tmp, "rna-seq")
list.files(file.path(tmp, "rna-seq"))
```

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