Package 'alabaster.treese'

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Title Load and Save TreeSummarizedExperiment from File

Version 0.99.1

Date 2026-11-03

Description Save TreeSummarizedExperiment 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.

biocViews DataImport, DataRepresentation, Phylogenetics, Microbiome

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URL https://github.com/microbiome/alabaster.treese, https://microbiome.github.io/alabaster.treese

BugReports https://github.com/microbiome/alabaster.treese/issues

Depends TreeSummarizedExperiment, alabaster.base

Imports methods, alabaster.sce, alabaster.string, Biostrings, jsonlite

Suggests ape, knitr, testthat, BiocStyle, quarto

VignetteBuilder quarto

SystemRequirements Quarto command line tools (https://github.com/quarto-dev/quarto-cli)

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`readTreeSummarizedExperiment` *Read a TreeSummarizedExperiment from disk*

Description

Read a TreeSummarizedExperiment object from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in `readObject`.

Usage

```
readTreeSummarizedExperiment(path, metadata, ...)
```

Arguments

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

Value

A TreeSummarizedExperiment object.

See Also

"`saveObject,TreeSummarizedExperiment-method`", to save the TreeSummarizedExperiment to disk.

Examples

```
# Mocking up a TreeSE:
data(tinyTree, package = "TreeSummarizedExperiment")
mat <- matrix(rpois(100, 10), ncol = 10)
rownames(mat) <- tinyTree[["tip.label"]]
colnames(mat) <- letters[1:10]

tse <- TreeSummarizedExperiment(list(counts = mat), rowTree = tinyTree)
tse[["stuff"]] <- LETTERS[1:10]
referenceSeq(tse) <- Biostrings::DNAStringSet(rep("ACGT", nrow(tse)))

# Staging it:
tmp <- tempfile()
saveObject(tse, tmp)
readObject(tmp)
```

saveTreeSummarizedExperiment *Save a TreeSummarizedExperiment to disk*

Description

Save a TreeSummarizedExperiment to its on-disk representation.

Usage

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

Arguments

x	A TreeSummarizedExperiment 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,SingleCellExperiment-method".

Details

Everything inherited from the SingleCellExperiment parent class is saved by **alabaster.sce**. The TreeSummarizedExperiment-specific slots are saved as follows:

- Each tree in rowTree or colTree is saved as a list containing the fields of the phylo object, where the edge matrix is split into parent and child vectors. This preserves the node numbering and arbitrary tip/node labels, which would not survive a round trip through Newick.
- rowLinks and colLinks are saved as data frames.
- referenceSeq is saved as FASTA via **alabaster.string**. A DNAStringSetList is saved as a list of such sequence sets.

Value

x is saved into path and NULL is invisibly returned.

See Also

readTreeSummarizedExperiment, to read the TreeSummarizedExperiment back into the R session.

Examples

```
# Mocking up a TreeSE:
data(tinyTree, package = "TreeSummarizedExperiment")
mat <- matrix(rpois(100, 10), ncol = 10)
rownames(mat) <- tinyTree[["tip.label"]]
colnames(mat) <- letters[1:10]

tse <- TreeSummarizedExperiment(list(counts = mat), rowTree = tinyTree)
tse[["stuff"]] <- LETTERS[1:10]
referenceSeq(tse) <- Biostrings::DNAStringSet(rep("ACGT", nrow(tse)))
```

```
# Staging it:
tmp <- tempfile()
saveObject(tse, tmp)
list.files(tmp, recursive = TRUE)
```

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