

Package: alabaster.tree (via r-universe)

October 31, 2026

Title Load and Save TreeSummarizedExperiment from File

Version 0.99.0

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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.tree>,
<https://microbiome.github.io/alabaster.tree>

BugReports <https://github.com/microbiome/alabaster.tree/issues>

Depends TreeSummarizedExperiment, alabaster.base

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

Suggests ape, knitr, testthat, BiocStyle, rmarkdown

VignetteBuilder knitr

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Config/pak/sysreqs cmake make libicu-dev libuv1-dev libssl-dev libnode-dev zlib1g-dev

Repository <https://bioc.r-universe.dev>

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readTreeSummarizedExperiment	
<i>Read a TreeSummarizedExperiment from disk</i>	

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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