Package ‘alabaster.string’

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Title Save and Load Biostrings to/from File

Version 1.13.0

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Description Save Biostrings objects to 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.

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Depends Biostrings, alabaster.base

Imports utils, methods, S4Vectors

Suggests BiocStyle, rmarkdown, knitr, testthat

VignetteBuilder knitr

RoxygenNote 7.2.3

biocViews DataImport, DataRepresentation

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Contents

`readXStringSet` *Read an XStringSet from disk.*

Description

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

Usage

```
readXStringSet(path, metadata, ...)
```

Arguments

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

Value

An XStringSet subclass containing DNA, RNA, protein or custom sequences. This may also be a QualityScaledDNAStringSet with quality scores.

See Also

`"saveObject,XStringSet-method"`, to save an XStringSet to disk.

Examples

```
library(Biostrings)
stuff <- DNAStringSet(c("AAA", "CC", "G", "TTTT"))

tmp <- tempfile()
saveObject(stuff, tmp)
readObject(tmp)
```

`saveObject,XStringSet-method` *Save a XStringSet to disk*

Description

Save a XStringSet to its on-disk representation.

Usage

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

Arguments

`x`	A XStringSet or any of its subclasses such as a QualityScaledXStringSet.
`path`	String containing the path to a directory in which to save `x`.
`...`	Further arguments to pass to specific methods.

Value

The contents of `x` are saved into a `path`, and `NULL` is invisibly returned.

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See Also

`readXStringSet`, to read the XStringSet back into the R session.

Examples

```
library(Biostrings)
stuff <- DNAStringSet(c("AAA", "CC", "G", "TTTT"))

tmp <- tempfile()
saveObject(stuff, tmp)
list.files(tmp, recursive=TRUE)
```

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