Package 'alabaster.string'

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Title Save and Load Biostrings to/from File

Version 1.12.0

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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 2
saveObject,XStringSet-method 3

Index **4**

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.

Author(s)

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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)
```

Index

altReadObject, *2*

loadXStringSet *(*readXStringSet*)*, 2

QualityScaledDNAStringSet, *2*
QualityScaledXStringSet, *3*

readObject, *2*
readObjectFile, *2*
readXStringSet, 2, *3*

saveObject, *2*
saveObject,XStringSet-method, 3
stageObject,XStringSet-method
*(*saveObject,XStringSet-method*)*, *3*

XStringSet, *2*, *3*