Package 'alabaster.string'

Title Save and Load Biostrings to/from File

Version 1.6.0

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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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Author Aaron Lun [aut, cre]

Maintainer Aaron Lun <infinite.monkeys.with.keyboards@gmail.com>

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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)
```

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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)

Aaron Lun

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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