

Package ‘alabaster.string’

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Title Save and Load Biostrings to/from File

Version 1.5.0

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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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|----------------|--------------------------------------|
| readXStringSet | <i>Read an XStringSet from disk.</i> |
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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 [QualityScaledDNAStrngSet](#) with quality scores.

See Also

"[saveObject,XStringSet-method](#)", to save an [XStringSet](#) to disk.

Examples

```
library(Biostrings)
stuff <- DNAStrngSet(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)
```

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