# Package ‘alabaster.string’

June 19, 2025

**Title** Save and Load Biostrings to/from File

**Version** 1.9.0

**Date** 2023-12-29

**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.

**License** MIT + file LICENSE

**Depends** Biostrings, alabaster.base

**Imports** utils, methods, S4Vectors

**Suggests** BiocStyle, rmarkdown, knitr, testthat

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

**biocViews** DataImport, DataRepresentation

**git_url** https://git.bioconductor.org/packages/alabaster.string

**git_branch** devel

**git_last_commit** 9bcfeb5

**git_last_commit_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-06-19

**Author** Aaron Lun [aut, cre]

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

## 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.

### 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)
```

# Index