

# Package ‘alabaster.string’

December 30, 2024

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

**Version** 1.7.0

**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** 383a583

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-12-30

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

**Maintainer** Aaron Lun <[infinite.monkeys.with.keyboards@gmail.com](mailto:infinite.monkeys.with.keyboards@gmail.com)>

## Contents

readXStringSet . . . . .	2
saveObject,XStringSet-method . . . . .	3
<b>Index</b>	<b>4</b>

---

readXStringSet	<i>Read an XStringSet from disk.</i>
----------------	--------------------------------------

---

## 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 <a href="#">saveObject</a> method for <a href="#">XStringSet</a> objects.
metadata	Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.
...	Further arguments passed to internal <a href="#">altReadObject</a> 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 <a href="#">XStringSet</a> or any of its subclasses such as a <a href="#">QualityScaledXStringSet</a> .
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

altReadObject, [2](#)

loadXStringSet (readXStringSet), [2](#)

QualityScaledDNASet, [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](#)