

# Package ‘alabaster.string’

September 29, 2023

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

**Version** 1.0.1

**Date** 2023-05-01

**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** methods

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

**VignetteBuilder** knitr

**RoxygenNote** 7.2.1

**biocViews** DataImport, DataRepresentation

**git\_url** <https://git.bioconductor.org/packages/alabaster.string>

**git\_branch** RELEASE\_3\_17

**git\_last\_commit** 7341cde

**git\_last\_commit\_date** 2023-05-01

**Date/Publication** 2023-09-29

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loadXStringSet      *Load a DNStringSet*

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### Description

Load a [DNStringSet](#) object, typically from a FASTA or FASTQ file generated by the corresponding [stageObject](#) method.

### Usage

```
loadXStringSet(seq.info, project)
```

### Arguments

|          |  |
|----------|--|
| seq.info | A named list of metadata for this object.  |
| project  | Any argument accepted by the acquisition functions, see <a href="#">?acquireFile</a> . By default, this should be a string containing the path to a staging directory. |

### Value

A [DNStringSet](#) containing DNA sequences. This may also be a [QualityScaledDNStringSet](#) with quality scores.

### Examples

```
library(Biostrings)
stuff <- DNStringSet(c("AAA", "CC", "G", "TTTT"))

tmp <- tempfile()
dir.create(tmp)
info <- stageObject(stuff, tmp, path="dna_thing")
loadXStringSet(info, project=tmp)
```

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stageObject,XStringSet-method  
*Stage a XStringSet*

---

### Description

Stage a XStringSet by saving it to the appropriate file format.

### Usage

```
## S4 method for signature 'XStringSet'
stageObject(x, dir, path, child = FALSE, ...)
```

**Arguments**

|                    |   |
|--------------------|---|
| <code>x</code>     | A <a href="#">XStringSet</a> or any of its subclasses, in particular a <a href="#">QualityScaledXStringSet</a> .  |
| <code>dir</code>   | String containing the path to the staging directory.  |
| <code>path</code>  | String containing a prefix of the relative path inside <code>dir</code> where <code>x</code> is to be saved. The actual path used to save <code>x</code> may include additional components, see <a href="#">Details</a> . |
| <code>child</code> | Logical scalar indicating whether <code>x</code> is a child of a larger object.   |
| <code>...</code>   | Further arguments to pass to specific methods.  |

**Value**

A list containing metadata for `x`. A subdirectory is created at `path` inside `dir` and the contents of `x` are saved to various files within that subdirectory. If `x` is a [QualityScaledXStringSet](#), a FASTQ file is created instead of a FASTA file.

**Author(s)**

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**Examples**

```
library(Biostrings)
stuff <- DNASTringSet(c("AAA", "CC", "G", "TTTT"))

tmp <- tempfile()
dir.create(tmp)
stageObject(stuff, tmp, path="dna_thing")
list.files(tmp, recursive=TRUE)
```

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