Package 'alabaster.string'

February 23, 2024

Title Save and Load Biostrings to/from File

Version 1.2.0

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.

License MIT + file LICENSE

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_18

git_last_commit 51fce80

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-02-23

Author Aaron Lun [aut, cre]

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

R topics documented:

---

loadXStringSet   *Load a DNAStringSet*

Description

Load a [DNAStringSet](#) 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 ?[acquireFile](#). By default, this should be a string containing the path to a staging directory.

Value

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

Examples

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

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

---

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

x	A XStringSet or any of its subclasses, in particular a QualityScaledXStringSet.
dir	String containing the path to the staging directory.
path	String containing a prefix of the relative path inside dir where x is to be saved. The actual path used to save x may include additional components, see Details.
child	Logical scalar indicating whether x is a child of a larger object.
...	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)

Aaron Lun

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)
```

Index