Package 'alabaster.vcf'

December 30, 2024

Title Save and Load Variant Data to/from File

Version 1.7.0

Date 2024-01-02

Description Save variant calling SummarizedExperiment to file and load them back as VCF objects. 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 alabaster.base, VariantAnnotation

Imports methods, S4Vectors, alabaster.se, alabaster.string, Rsamtools

Suggests knitr, rmarkdown, BiocStyle, testthat

RoxygenNote 7.2.3

VignetteBuilder knitr

biocViews DataImport, DataRepresentation

git_url https://git.bioconductor.org/packages/alabaster.vcf

git_branch devel

git_last_commit 1e871d0

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>

Contents

readVCF   *Read a VCF object from disk*

Description

Read a [VCF](#) object from its on-disk representation.

Usage

```
readVCF(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, usually generated by the [saveObject](#) method for [VCF](#) object.s
metadata	Named list of metadata for this object, see [readObjectFile](#) for details.
...	Further arguments passed to internal [altReadObject](#) calls.

Value

A [VCF](#) object.

Author(s)

Aaron Lun

See Also

[saveObject,VCF-method](#), to save VCF objects to disk.

Examples

```
fl <- system.file("extdata", "structural.vcf", package="VariantAnnotation")
vcf <- readVcf(fl)

tmp <- tempfile()
saveObject(vcf, tmp)
readObject(tmp)
```

`saveObject,VCF-method`   *Save a VCF object to disk*

Description

Save a VCF object to its on-disk representation, namely a VCF file with the same contents.

Usage

```
## S4 method for signature 'VCF'
saveObject(x, path, ...)
```

Arguments

x	Any instance of a VCF class or one of its subclasses.
path	String containing the path to a directory in which to save x.
...	Further arguments to pass to specific methods.

Value

x is saved to file inside `path`, and `NULL` is returned.

Author(s)

Aaron Lun

See Also

[readVCF](#), to read a VCF object back to the R session.

Examples

```
fl <- system.file("extdata", "structural.vcf", package="VariantAnnotation")
vcf <- readVcf(fl)

tmp <- tempfile()
saveObject(vcf, tmp)
```

Index