

Package ‘alabaster.vcf’

May 1, 2024

Title Save and Load Variant Data to/from File

Version 1.4.0

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 RELEASE_3_19

git_last_commit 87779af

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-01

Author Aaron Lun [aut, cre]

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

Contents

readVCF	2
saveObject,VCF-method	3
Index	4

readVCF	<i>Read a VCF object from disk</i>
---------	------------------------------------

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 objects.
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

```
f1 <- system.file("extdata", "structural.vcf", package="VariantAnnotation")
vcf <- readVcf(f1)

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

```
f1 <- system.file("extdata", "structural.vcf", package="VariantAnnotation")  
vcf <- readVcf(f1)  
  
tmp <- tempfile()  
saveObject(vcf, tmp)
```

Index

[altReadObject](#), 2

[loadVCF \(readVCF\)](#), 2

[loadVCFHeader \(readVCF\)](#), 2

[readObjectFile](#), 2

[readVCF](#), 2, 3

[saveObject](#), 2

[saveObject, VCF-method](#), 3

[stageObject, VCF-method](#)

[\(saveObject, VCF-method\)](#), 3

[stageObject, VCFHeader-method](#)

[\(saveObject, VCF-method\)](#), 3

[VCF](#), 2, 3