

Package ‘alabaster.vcf’

June 15, 2025

Title Save and Load Variant Data to/from File
Version 1.8.0
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_21
git_last_commit 7d51566
git_last_commit_date 2025-04-15
Repository Bioconductor 3.21
Date/Publication 2025-06-15
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

<code>x</code>	Any instance of a VCF class or one of its subclasses.
<code>path</code>	String containing the path to a directory in which to save <code>x</code> .
<code>...</code>	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](#)