

Package ‘alabaster.vcf’

October 15, 2023

Title Save and Load Variant Data to/from File

Version 1.0.0

Date 2023-02-28

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 7.2.1

VignetteBuilder knitr

biocViews DataImport, DataRepresentation

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

git_branch RELEASE_3_17

git_last_commit d4b06e5

git_last_commit_date 2023-04-25

Date/Publication 2023-10-15

Author Aaron Lun [aut, cre]

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

R topics documented:

loadVCF	2
loadVCFHeader	3
stageObject,VCF-method	4
stageObject,VCFHeader-method	5
Index	6

`loadVCF`*Load a VCF object*

Description

Load a [VCF](#) object from its staged file contents.

Usage

```
loadVCF(vcf.info, project)
```

Arguments

<code>vcf.info</code>	Named list of metadata describing a VCF object.
<code>project</code>	Any argument accepted by the acquisition functions, see ?acquireFile . By default, this should be a string containing the path to a staging directory.

Details

This function assumes that the files were generated by the [stageObject](#) method for [VCF](#) subclasses. It does *not* load a VCF file! Use [scanVcf](#) instead if you want to create a [VCF](#) object from a VCF file.

Value

A [VCF](#) object, expanded or collapsed depending on the specification in `vcf.info`.

Author(s)

Aaron Lun

Examples

```
f1 <- system.file("extdata", "structural.vcf", package="VariantAnnotation")
vcf <- readVcf(f1, genome="hg19")

tmp <- tempfile()
dir.create(tmp)
info <- stageObject(vcf, dir=tmp, path="experiment-1")
loadVCF(info, tmp)
```

loadVCFHeader	<i>Load a VCF header</i>
---------------	--------------------------

Description

Load the headers of a VCF file into a [VCFHeader](#) object.

Usage

```
loadVCFHeader(info, project)
```

Arguments

info	Named list of metadata for a VCF file.
project	Any argument accepted by the acquisition functions, see ?acquireFile . By default, this should be a string containing the path to a staging directory.

Details

As the name suggests, this only loads the headers of the VCF file. To load all contents into memory, use [scanVcf](#) instead.

Value

A [VCFHeader](#) object.

Author(s)

Aaron Lun

Examples

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

tmp <- tempfile()
dir.create(tmp)
info <- stageObject(hdr, dir=tmp, path="header")
loadVCFHeader(info, tmp)
```

stageObject, VCF-method

Stage a VCF object

Description

Save the contents of a [VCF](#) object to file.

Usage

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

Arguments

x	Any instance of a VCF class or one of its subclasses.
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 stageObject, RangedSummarizedExperiment-method .

Details

Note that we do *not* save the contents of x in VCF format. Rather, we re-use the existing machinery for staging SummarizedExperiments from the [alabaster.se](#). This is more amenable for random access by feature/sample and ensures that we are consistent with the expectations of the parent class. Applications requiring actual VCF files can instead use [writeVcf](#) to generate them from x.

Value

The contents of x are saved to file inside path. A named list containing metadata is returned.

Author(s)

Aaron Lun

Examples

```
f1 <- system.file("extdata", "structural.vcf", package="VariantAnnotation")  
vcf <- readVcf(f1, genome="hg19")  
  
tmp <- tempfile()  
dir.create(tmp)  
stageObject(vcf, dir=tmp, path="experiment-1")
```

stageObject, VCFHeader-method
Stage the VCF headers

Description

Save the contents of a [VCFHeader](#) object to file. This is formatted as a valid VCF file that lacks any entries.

Usage

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

Arguments

x	A VCFHeader object.
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.

Value

The contents of x are saved to file inside path. A named list containing metadata is returned.

Author(s)

Aaron Lun

Examples

```
f1 <- system.file("extdata", "structural.vcf", package="VariantAnnotation")  
hdr <- scanVcfHeader(f1)  
  
tmp <- tempfile()  
dir.create(tmp)  
stageObject(hdr, dir=tmp, path="headers")
```

Index

acquireFile, [2](#), [3](#)

loadVCF, [2](#)

loadVCFHeader, [3](#)

scanVcf, [2](#), [3](#)

stageObject, [2](#)

stageObject, VCF-method, [4](#)

stageObject, VCFHeader-method, [5](#)

VCF, [2](#), [4](#)

VCFHeader, [3](#), [5](#)

writeVcf, [4](#)