## Package 'alabaster.vcf'

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Title Save and Load Variant Data to/from File

Version 1.6.0

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**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.

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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

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readVCF

#### 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)</pre>
```

tmp <- tempfile()
saveObject(vcf, tmp)
readObject(tmp)</pre>

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

Х	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)</pre>
```

tmp <- tempfile()
saveObject(vcf, tmp)</pre>

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