

# Package ‘alabaster.vcf’

December 27, 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** 2024-12-27  
**Author** Aaron Lun [aut, cre]  
**Maintainer** Aaron Lun <[infinite.monkeys.with.keyboards@gmail.com](mailto:infinite.monkeys.with.keyboards@gmail.com)>

## Contents

readVCF . . . . .	2
saveObject,VCF-method . . . . .	3
<b>Index</b>	<b>4</b>

---

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 <a href="#">saveObject</a> method for <a href="#">VCF</a> objects.
metadata	Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.
...	Further arguments passed to internal <a href="#">altReadObject</a> 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 <a href="#">VCF</a> 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](#)