

# Package ‘alabaster.vcf’

February 17, 2025

**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** 2025-02-17

**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**

x	Any instance of a <a href="#">VCF</a> 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