Package 'alabaster.vcf'

May 15, 2024

Title Save and Load Variant Data to/from File
Version 1.4.0
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.
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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
git_url https://git.bioconductor.org/packages/alabaster.vcf
git_branch RELEASE_3_19
git_last_commit 87779af
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readVCF

Read a VCF object from disk

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)

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

 ${\tt save Object, VCF-method} \quad \textit{Save a VCF object to disk}$

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 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)

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

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