Package ‘alabaster.vcf’

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Title Save and Load Variant Data to/from File

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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 7.2.1

VignetteBuilder knitr

biocViews DataImport, DataRepresentation

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R topics documented:

`loadVCF` *Load a VCF object*

Description

Load a VCF object from its staged file contents.

Usage

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

Arguments

`vcf.info`	Named list of metadata describing a VCF object.
`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

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

See Also

The VcfWrapper class in **alabaster.files**, for saving/loading of another representation of VCF files.

Examples

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

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

`loadVCFHeader` *Load a VCF header*

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.

Users can override this function in `loadVCF` by calling `.altLoadVCFHeader`. This should be set to a function that accepts the same arguments as `loadVCFHeader` and returns a VCFHeader object.

Value

A VCFHeader object.

Author(s)

Aaron Lun

Examples

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

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

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

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

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

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