MafDb.ALL.wgs.phase1.release.v3.20101123

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MafDb.ALL.wgs.phase1.release.v3.20101123-package

Annotation package for minimum allele frequency data from the 1000 Genomes project

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Description

This annotation package stores minimum allele frequency (MAF) data values frozen from the 1000 Genomes project. The data is stored in the form of a SQLite database and is loaded automatically in the form of a MafDb object. The name of the exposed object matches the name of the package and part of the filename that contained the data imported into the package. The class definition and methods to access MafDb objects are found in the `VariantFiltering` software package.

Format

`MafDb.ALL.wgs.phase1.release.v3.20101123`   MafDb object containing MAF values from the 1000 Genomes project do

Author(s)

R. Castelo

Source

The 1000 Genomes Project Consortium. An integrated map of genetic variation from 1,092 human genomes. Nature, 491:56-65, 2012. (URL: `ftp://ftp.1000genomes.ebi.ac.uk`) [October, 2013, accessed]

See Also

makeMafDbPackageKG MafDb.ESP6500SI.V2.SSA137.dbSNP138 MafDb-class fetchKnownVariantsByID VariantFiltering

Examples

```
library(MafDb.ALL.wgs.phase1.release.v3.20101123)

ls("package:MafDb.ALL.wgs.phase1.release.v3.20101123")

MafDb.ALL.wgs.phase1.release.v3.20101123
```

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makeMafDbPackageKG   *Make a MafDb annotation data package from the 1000 Genomes Project*

Description

This function creates an annotation data package for a MafDb object. Its primary purpose is to ease the task of fetching and packaging newer minimum allele frequency data.

Usage

```
makeMafDbPackageKG(destDir=path.expand("~"), MafDbURL=MafDbKGdefaultURL, MafDbPkgName=MafDbKGdefault
                genome="hg19", version=NULL, author=NULL, maintainer=NULL, license=NULL, yieldSize=10000
```

Arguments

destDir	Destination directory for the newly created package.
MafDbURL	URL to the source VCF file(s). By default, it points to the URL holding the data currently stored in the package that defines this function.
MafDbPkgName	Name of the newly created package. This will define as well the name of the exported MafDb object.
genome	Version of the human genome, following UCSC nomenclature. Necessary for the internal call to the readVcf() function from the VariantAnnotation package.
version	Version to put on the new package. By default, the version corresponds to the version of the package that defines this function, bumping the second version number.
author	Author to put on the new package. By default, the author corresponds to the author of the package that defines this function.
maintainer	Maintainer to put on the new package. By default, the maintainer corresponds to the maintainer of the package that defines this function.
license	License to put on the new package. By default, the license corresponds to the license of the package that defines this function.
yieldSize	In the case source tabix VCF files, they are not read at once, but scanned in batches whose size is determined by this argument. By default is set to one million variants but it may be reduced to lower main memory requirements.

Value

Path to the folder containing the created data package.

Author(s)

R. Castelo

See Also

fetchKnownVariantsByID MafDb.ALL.wgs.phase1.release.v3.20101123

Examples

```
MafDbKGdefaultURL ## default URL from where makeMafDbPackageKG() fetches the MAF data

MafDbKGdefaultPkgName ## default name for the package that makeMafDbPackageKG() creates

## Not run:
## the previous two default values can be overridden when calling makeMafDbPackageKG()
makeMafDbPackageKG()

## End(Not run)
```

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