MafDb.ESP6500SI.V2.SSA137.dbSNP138
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MafDb.ESP6500SI.V2.SSA137.dbSNP138-package

Annotation package for minimum allele frequency data from the
NHLBI ESP project

Description

This annotation package stores minimum allele frequency (MAF) data values frozen from the
NHLBI Exome Sequencing (ESP) 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.ESP6500SI.V2.SSA137.dbSNP138 MafDb object containing MAF values from 6500 ESP exomes downloaded in October 2014.

See Also

makeMafDbPackageESP MafDb.ALL.wgs.phase1.release.v3.20101123 MafDb-class fetchKnown-VariantsByID VariantFiltering

Author(s)

R. Castelo

Source

Exome Variant Server, NHLBI GO Exome Sequencing Project (ESP), Seattle, WA (URL: http://evs.gs.washington.edu/EVS) [October, 2014, accessed]
**makeMafDbPackageESP**

**Examples**

```r
library(MafDb ESP6500SI.V2.SSA137.dbSNP138)
ls("package:MafDb ESP6500SI.V2.SSA137.dbSNP138")
MafDb ESP6500SI.V2.SSA137.dbSNP138
```

**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**

```r
makeMafDbPackageESP(destDir=path.expand("~"), MafDbURL=MafDbESPdefaultURL, MafDbPkgName=MafDbESPdefaultPkgName, genome="hg19", version=NULL, author=NULL, maintainer=NULL, license=NULL, yieldSize=1000000)
```

**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.
makeMafDbPackageESP

Value
Path to the folder containing the created data package.

Author(s)
R. Castelo

See Also
fetchKnownVariantsByID
MafDb.ESP6500SI.V2.SSA137.dbSNP138

Examples

MafDbESPdefaultURL ## default URL from where makeMafDbPackageESP() fetches the MAF data
MafDbESPdefaultPkgName ## default name for the package that makeMafDbPackageESP() creates

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

## End(Not run)
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