

MafDb.ESP6500SI.V2.SSA137.dbSNP138

October 7, 2014

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 Oc

Author(s)

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Source

Exome Variant Server, NHLBI GO Exome Sequencing Project (ESP), Seattle, WA (URL: <http://evs.gs.washington.edu/EVS>) [October, 2013, accessed]

See Also

[makeMafDbPackageESP](#) [MafDb.ALL.wgs.phase1.release.v3.20101123](#) [MafDb-class fetchKnown-VariantsByID](#) [VariantFiltering](#)

Examples

```
library(MafDb.ESP6500SI.V2.SSA137.dbSNP138)

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

MafDb.ESP6500SI.V2.SSA137.dbSNP138
```

```
makeMafDbPackageESP  Make a MafDb annotation data package from the NHLBI GO ESP 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

```
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.

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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