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

March 26, 2015

MafDb.ALL.wgs.phase1.release.v3.20101123-package
Annotation package for minimum allele frequency data from the 1000 Genomes project

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 downloaded in October 2013 from ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/RP11PUR1/all.wgs.phase1.release.vSNRP1P11RS.snps_indels_svs.vcf.gz. See makemafdbpackagekg for more information on how to update these data.

Author(s)

R. Castelo

Source


See Also

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

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

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=MafDbKGdefaultPkgName, genome="hg19", version=NULL, author=NULL, maintainer=NULL, license=NULL, yieldSize=10

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.
makeMafDbPackageKG

Value
Path to the folder containing the created data package.

Author(s)
R. Castelo

See Also
fetchKnownVariantsByID MafDb.ALL.wgs.phased.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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