

MafDb.gnomAD.r3.0.GRCh38

February 11, 2020

MafDb.gnomAD.r3.0.GRCh38-package

Annotation package for minor allele frequency data from the Genome Aggregation Database

Description

This annotation package stores minor allele frequency (MAF) data derived from the whole genome variant set release 3.0 of the Genome Aggregation Database (gnomAD). The data are exposed to the user in the form of a `GScores` object, named after the package and loaded into main memory only as different chromosomes and populations are being queried. The class definition and methods to access `GScores` objects are found in the `GenomicScores` software package. To minimize disk space and memory requirements, MAF values larger or equal than 0.1 are stored using two significant digits, while MAF values smaller than 0.1 are stored using one significant digit.

Please consult the gnomAD FAQ page at <http://gnomad.broadinstitute.org/faq> before you use these data for your own research.

Format

`MafDb.gnomAD.r3.0.GRCh38` `GScores` object containing MAF values from gnomAD genomes downloaded on April 20

Author(s)

R. Castelo

Source

Karczewski et al. Variation across 141,456 human exomes and genomes reveals the spectrum of loss-of-function intolerance across human protein-coding genes. bioRxiv, 531210, 2019.

The Genome Aggregation Database (gnomAD), Cambridge, MA (URL: <http://gnomad.broadinstitute.org>) [October 2019, accessed]

See Also

[GScores-class gscores](#) [GenomicScores](#)

Examples

```
library(SNPlocs.Hsapiens.dbSNP149.GRCh38)
library(MafDb.gnomAD.r3.0.GRCh38)

ls("package:MafDb.gnomAD.r3.0.GRCh38")

mafdb <- MafDb.gnomAD.r3.0.GRCh38
mafdb
citation(mafdb)

populations(mafdb)

## lookup allele frequency for rs1129038, a SNP associated with blue and brown eye colors
## (Eiberg et al., Human Genetics, 2008). Blue eye color in humans may be caused by a
## perfectly associated founder mutation in a regulatory element located within the HERC2
## gene inhibiting OCA2 expression.

snpdb <- SNPlocs.Hsapiens.dbSNP149.GRCh38
rng <- snpsById(snpdb, ids="rs1129038")
rng
gscores(mafdb, rng)
gscores(mafdb, GRanges("15:28111713"))

## lookup allele frequency for rs333, a deletion of 32 nucleotides (delta 32) within the CCR5 gene
## associated with resistance to an infection by HIV, the virus that causes AIDS. The homozygous
## state of this delta 32 allele has been reported to be highly protective against HIV-1
## infection (Huang et al., Nature Medicine, 1996) but with no effects on lifespan (Maier et al.,
## bioRxiv, 2019, Gudbjartsson et al., bioRxiv, 2019; Karczewski et al., bioRxiv 2019).

gscores(mafdb, GRanges("3:46373452-46373484"), type="nonsnrs")
```

Index

*Topic **data**

MafDb.gnomAD.r3.0.GRCh38-package,

[1](#)

*Topic **package**

MafDb.gnomAD.r3.0.GRCh38-package,

[1](#)

GenomicScores, [1](#), [2](#)

GScores, [1](#)

gscores, [2](#)

GScores-class, [2](#)

MafDb.gnomAD.r3.0.GRCh38, [1](#)

MafDb.gnomAD.r3.0.GRCh38

(MafDb.gnomAD.r3.0.GRCh38-package),

[1](#)

MafDb.gnomAD.r3.0.GRCh38-package, [1](#)