dbSNP_info

Description

dbSNP_info() performs an annotation of a given list of SNPs searching information in dbSNP database belonging to NCBI

Usage

```r
dbSNP_info(
  dat=NULL,
  type=c("pos","rs")
  p=FALSE,
  build=37,
  r2=0.99,
  pop="EUR"
)
```

Arguments

dat
> character vector containing rsIDs (E.g: rs647161) or chr:positions (E.g.: 5:134499092) of the SNPs to be searched

type
> argument indicating the type of data to be entered into the function. If "pos" the search is performed by chromosome (1, 2, ..., 22, X, Y, MT):position. If is "rs" the search is performed by SNP name.

p
> Parallelization. If is FALSE (default) the search is carried out without parallelisation. If TRUE, the function parallelises the searches

build
> If is 37 (default), the search is performed by build loci 37. If 38, the search is performed by build loci 38

r2   squared Pearson correlation coefficient when searching for variants in LD.
     Default = 0.99

pop
     population to use as reference panel when searching for variants in LD.
     Default = "EUR"

Details

The window size is set by default to 500 kb when searching for variants in LD

Value

a dataframe containing the following values:

term
                Entered term to annotate

rsID
                Alternative names of the SNP

gene
                Gene to which it belongs

alleles
                Alleles. Ref>Alt

GRCh37, GRCh38
                Chromosome position in Build 37 and Build 38

rs_ld
                SNPs in linkage disequilibrium

Examples

[Run examples](#)

```
library(SNPannot)
```