package ‘ORMDR’

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mdr.c MDR : Multifactor Dimensionality Reduction

Description

MDR method classifies the combination of multilocus tgenotypes into high-risk and low-risk groups based on a simple comparison of the ratios of the number of cases and controls.

Usage

mdr.c(dataset,colresp/cs,combi,cv.fold=10,randomize=TRUE)
ORMDR : Odds ratio based multifactor-dimensionality reduction method

Description
ORMDR uses the odds ratio as a new quantitative measure of disease risk.

Usage
ormdr(dataset, bestcombi, cs, colresp, CI.Asy, CI.Boot, B)

Arguments

dataset  SNP data set with class variable
bestcombi best combination from mdr.c function
cs  how to code "case" class
colresp  location of class variable in dataset
CI.Asy  indicator whether asymptotic CI is calculated or not
CI.Boot  indicator whether bootstrap CI is calculated or not
B  number of bootstrap samples
sample.dat

Value

...  

Examples

data(sample.dat)
z<-mdr.c(sample.dat, colresp=21, cs=1, combi=2, cv.fold = 10)
ormdr(sample.dat,bestcombi=as.numeric(z$best.combi),cs=1,colresp=21,CI.Asy=TRUE,CI.Boot=TRUE,B=1000)

 sample.dat            sample data

Description

sample data with 20 SNPs and one class variable

Usage

data(sample.dat)

Examples

data(sample.dat)
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