

Package ‘ORMDR’

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Title ORMDR

Description Odds ratio based multifactor-dimensionality reduction
method for detecting gene-gene interactions

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mdr.c *MDR : Multifactor Dimensionality Reduction*

Description

MDR method classifies the combination of multilocus genotypes 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)
```

Arguments

dataset	SNP data set with class variable
colresp	location of class variable in dataset
cs	how to code "case" class
combi	number of genes for combination
cv.fold	number of fold in cross validation
randomize	logical. If 'TRUE' (the default) the cross validation sets are randomized

Value

min.comb	combination with minimum error rate in each cross validation
train.erate	training error
test.erate	test error
data	dataset
best.combi	best combination

Examples

```
data(sample.dat)
mdr.c(sample.dat, colresp=21, cs=1, combi=2, cv.fold = 10)
```

ormdr	<i>ORMDR : Odds ratio based multifactor-dimensionality reduction method</i>
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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

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	<i>sample data</i>
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Description

sample data with 20 SNPs and one class variable

Usage

```
data(sample.dat)
```

Examples

```
data(sample.dat)
```

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