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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R topics documented:

`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)
```

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` *ORMDR : Odds ratio based multifactor-dimensioinality reduction method*

Description

ORMDR usesthe 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` *sample data*

Description

sample data with 20 SNPs and one class variable

Usage

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

Examples

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

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