Package ‘imputeMDR’

February 20, 2015

Type Package

Title The Multifactor Dimensionality Reduction (MDR) Analysis for Incomplete Data

Version 1.1.2

Date 2011-06-28

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Description This package provides various approaches to handling missing values for the MDR analysis to identify gene-gene interactions using biallelic marker data in genetic association studies

License GPL (>= 2)

LazyLoad yes

Repository CRAN

Date/Publication 2012-12-21 09:01:16

NeedsCompilation yes

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The Multifactor Dimensionality Reduction (MDR) Analysis for Incomplete Data

Description

This provides various approaches to handling missing values for the MDR analysis of incomplete data to identify gene-gene interactions using biallelic marker data in genetic association studies

Details

Package: imputeMDR
Type: Package
Version: 1.1.1
Date: 2011-06-28
License: GPL (>2)
LazyLoad: yes

Author(s)

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References


See Also

impute.mdr
**Usage**

```r
impute.mdr(dataset, colresp, cs, combi, cv.fold = 10, na.method = 0, max_iter = 30, randomize = FALSE)
```

**Arguments**

- `dataset` A matrix of SNP data with class variable (response; phenotype; disease status). Genotypes must be coded as allele counts (0, 1, 2). Missing genotypes should be coded as 3.
- `colresp` Column number of class variables in the dataset. No missing value is allowed for the class variable.
- `cs` The value used to indicate "case (affected)" for class variable.
- `combi` The number of SNPs considered simultaneously as predictor variables (An order of interactions to analyze).
- `cv.fold` The number of folds k for k-fold cross-validation.
- `na.method` Options for missing handling approaches. `na.method = 0` for complete data, `na.method = 1` for treating missing genotypes as another genotype category, `na.method=2` for using available data for given number of SNPs under consideration as a model, `na.method=3` for using method of imputing missing information by using EM (expectation-maximization) algorithm.
- `max_iter` The number of maximum iteration in EM impute approach (na.method=3). In order to apply one-step EM approach, set this argument as 1.
- `randomize` Logical. If 'TRUE' the cross validation sets are randomized.

**Value**

- `min.comb` Marker combinations with the minimum error rate in each cross validation.
- `train.erate` Training errors for selected marker combination.
- `test.erate` Test error of the selected marker combination.
- `best.combi` The best combination that was selected most frequently across k-fold cross validation.

**Author(s)**

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**References**

Examples

```r
## sample data with missing values
data(incomplete)
## analysis example of 2nd order gene-gene interaction test
impute.mdr(incomplete, colresp=1, cs=1, combi=2, cv.fold = 10, na.method=2)
```

---

### incomplete

A simulated example data containing missing values

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**Description**

This data is an example of a simulated case-control study data with 10 10 biallelic marker genotypes (ex : single nucleotide polymorphisms; SNPs) for 200 cases and 200 controls are included. Class variable (response; phenotype; disease status) is in the first column.

**Usage**

data(incomplete)

**Format**

A data frame with 400 observations on the following 11 variables.

- `class` a numeric vector
- `snp1` a numeric vector
- `snp2` a numeric vector
- `snp3` a numeric vector
- `snp4` a numeric vector
- `snp5` a numeric vector
- `snp6` a numeric vector
- `snp7` a numeric vector
- `snp8` a numeric vector
- `snp9` a numeric vector
- `snp10` a numeric vector

**References**


**Examples**

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