

Package: MiSTr (via r-universe)

August 23, 2024

Type Package

Title Mixed effects Score Test for continuous outcomes

Version 1.0.4

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Description Test for association between a set of SNPS/genes and continuous or binary outcomes by including variant characteristic information and using (weighted) score statistics.

License LGPL (>= 2.1)

URL <https://github.com/mcanouil/MiSTr>, <https://m.canouil.dev/MiSTr>

BugReports <https://github.com/mcanouil/MiSTr/issues>

Depends R (>= 3.4.0)

Imports stats, CompQuadForm (>= 1.4.3), broom

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

Encoding UTF-8

LazyData true

LazyLoad yes

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

Repository <https://mcanouil.r-universe.dev>

RemoteUrl <https://github.com/mcanouil/MiSTr>

RemoteRef HEAD

RemoteSha 8244ada23875903c6741e313b16e687ef52fc22c

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mist

*mist***Description**

Test for association between a set of SNPs/genes and continuous outcomes by including variant characteristic information and using score statistics.

Usage

```
mist(
  y,
  X,
  G,
  Z,
  method = "liu",
  model = c("guess", "continuous", "binary"),
  weight.beta = NULL,
  maf = NULL
)
```

Arguments

- | | |
|-------------|---|
| y | [numeric] A numeric vector of the continuous outcome variables. Missing values are not allowed. |
| X | [numeric] A numeric matrix of covariates with rows for individuals and columns for covariates. If there is no covariate, it does not need to be specified |
| G | [numeric] A numeric genotype matrix with rows for individuals and columns for SNPs. Each SNP should be coded as 0, 1, and 2 for AA, Aa, aa, where A is a major allele and a is a minor allele. Missing genotypes are not allowed. |
| Z | [numeric] a numeric matrix of second level covariates for variant characteristics. Each row corresponds to a variant and each column corresponds to a variant characteristic. If there is no second level covariates, a vector of 1 should be used. |
| method | [character] A method to compute the p-value and the default value is "liu". Method "davies" represents an exact method that computes the p-value by inverting the characteristic function of the mixture chisq. Method "liu" represents an approximation method that matches the first 3 moments. |
| model | [character] A character vector specifying the model. Default is to "guess". Possible choices are "guess", "continuous" (linear regression) or "binary" (logistic regression). |
| weight.beta | [numeric] A numeric vector of parameters of beta function which is the weight for score statistics. The default value is NULL, <i>i.e.</i> no weight. Default weight value could be c(1, 25). |
| maf | [numeric] A numeric vector of MAF (minor allele frequency) for each SNP. |

Value

- S.tau score Statistic for the variant heterogeneous effect.
- S.pi score Statistic for the variant mean effect.
- p.value.S.tau P-value for testing the variant heterogeneous effect.
- p.value.S.pi P-value for testing the variant mean effect.
- p.value.overall Overall p-value for testing the association between the set of SNPS/genes and outcomes. It combines p.value.S.pi and p.value.S.tau by using Fisher's procedure.

Examples

```
library(MiSTr)
data(mist_data)
attach(mist_data)

mist(
  y = phenotypes[, "y_taupi"],
  X = phenotypes[, paste0("x_cov", 0:2)],
  G = genotypes,
  Z = variants_info[, 1, drop = FALSE]
)

mist(
  y = phenotypes[, "y_binary"],
  X = phenotypes[, paste0("x_cov", 0:2)],
  G = genotypes,
  Z = variants_info[, 1, drop = FALSE]
)
```

mist_data

mist_data

Description

mist_data

Usage

mist_data

Format

A [\[list\]](#) object.

Details

mist_data contains:

- phenotypes a data.frame with outcomes (continuous and binary) and covariates.
- G a numeric matrix of genotypes
- Z a numeric matrix with information on variants, *i.e.*, group, maf and effect.

print.mist

Print method for mist objec

Description

Print method for mist objec

Usage

```
## S3 method for class 'mist'  
print(x, ...)
```

Arguments

x [\[mist\]](#)
... Other arguments (Not used).

Value

list

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