Package 'GCIM'

July 24, 2025

Title The genetic causality inference model(GCIM) is a statistical method for detecting the causal direction in GxE interaction studies.

Version 0.0.0.9000

Description GCIM is a statistical method, which deciphers the causal direction of GxE interaction in complex traits and disease.

License `use_mit_license()`, `use_gpl3_license()` or friends to pick a license

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2.9000

R topics documented:

Index

---

gcim_b   *Perform regression analysis for GCIM with binary outcome*

Description

This function performs logistic regression analysis for Genetic causality inference model (GCIM) with binary outcomes using Polygenic Risk Scores (PRS).

Usage

```
gcim_b(bp_tar_phen, bp_tar_cov, Add_PRS, Int_PRS, Cov_PRS)
```

Arguments

bp_tar_phen	File path for the target phenotype data (FID, IID, Outcome format)
bp_tar_cov	File path for the target covariate data (FID, IID, Covariate, Confounders format)
Add_PRS	data frame for additive PRS values
Int_PRS	data frame for interaction PRS values
Cov_PRS	data frame for covariate PRS values

Value

List containing model summary and diagnostic information

Examples

```
## Not run:
# Using data frames (from GxEprs output)
result <- gcim_b("phenotype.txt", "covariates.txt",
                   Add_PRS, Int_PRS, Cov_PRS)

## End(Not run)
```

---

gcim_q   *Perform regression analysis for GCIM with continuous outcome*

Description

This function performs linear regression analysis for Gene-Covariate Interaction Modeling (GCIM) with continuous outcomes using Polygenic Risk Scores (PRS).

Usage

```
gcim_q(qp_tar_phen, qp_tar_cov, Add_PRS, Int_PRS, Cov_PRS)
```

Arguments

`qp_tar_phen`	File path for the target phenotype data (FID, IID, Outcome format)
`qp_tar_cov`	File path for the target covariate data (FID, IID, Covariate, Confounders format)
`Add_PRS`	Either file path or data frame for additive PRS values
`Int_PRS`	Either file path or data frame for interaction PRS values
`Cov_PRS`	Either file path or data frame for covariate PRS values

Value

List containing model summary and diagnostic information

Examples

```
## Not run:
result <- gcim_q("phenotype.txt", "covariates.txt",
                      Add_PRS, Int_PRS, Cov_PRS)

## End(Not run)
```

Index