

Package ‘GCIM’

July 23, 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.

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gcim_b	<i>Perform regression analysis for GCIM with binary outcome</i>
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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, verbose = TRUE)
```

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	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
verbose	Logical, whether to print progress messages (default: TRUE)

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	<i>Perform regression analysis for GCIM with continuous outcome</i>
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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, verbose = TRUE)
```

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
verbose	Logical, whether to print progress messages (default: TRUE)

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)
```

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