

# Package ‘GCIM’

July 21, 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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**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2.9000

## R topics documented:

gcim_b	1
gcim_q	2

<b>Index</b>	<b>3</b>
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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 Gene-Covariate Interaction Modeling (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 file paths
result <- gcim_b("phenotype.txt", "covariates.txt",
                 "add_prs.txt", "int_prs.txt", "cov_prs.txt")

# Using data frames (from GxEprs output)
result <- gcim_b("phenotype.txt", "covariates.txt",
                 add_prs_df, int_prs_df, cov_prs_df)

## End(Not run)
```

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gcim\_q

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*Perform regression analysis for GCIM with continuous outcome*


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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_df, int_prs_df, cov_prs_df)

## End(Not run)
```

# Index

gcim\_b, [1](#)  
gcim\_q, [2](#)