

Package ‘GCIM’

July 26, 2025

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

Version 0.0.1.000

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

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extract_prs_data	<i>Extract PRS data from GCIM results for further analysis</i>
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Description

This helper function extracts the individual PRS datasets from GCIM results for further analysis or inspection.

Usage

```
extract_prs_data(gcim_result)
```

Arguments

`gcim_result` Result object from `gcim_b` function

Value

List containing the three PRS datasets (add_prs, int_prs, cov_prs)

Examples

```
## Not run:
result <- gcim_b("Bphe_target.txt", "Bexp_target.txt",
                Add_PRS = q, Int_PRS = r, Cov_PRS = p)
prs_data <- extract_prs_data(result)
add_prs <- prs_data$add_prs
int_prs <- prs_data$int_prs
cov_prs <- prs_data$cov_prs

## End(Not run)
```

extract_prs_data_q *Extract PRS data from GCIM quantitative results for further analysis*

Description

This helper function extracts the individual PRS datasets from GCIM quantitative results for further analysis or inspection.

Usage

```
extract_prs_data_q(gcim_result)
```

Arguments

gcim_result Result object from gcim_q function

Value

List containing the three PRS datasets (add_prs, int_prs, cov_prs)

Examples

```
## Not run:
result <- gcim_q("Qphe_target.txt", "Qexp_target.txt",
                Add_PRS = q, Int_PRS = r, Cov_PRS = p)
prs_data <- extract_prs_data_q(result)
add_prs <- prs_data$add_prs
int_prs <- prs_data$int_prs
cov_prs <- prs_data$cov_prs

## End(Not run)
```

gcim_b	<i>Perform regression analysis for genetic causality inference model(GCIM) with binary outcome</i>
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Description

This function performs logistic regression analysis for GCIM with binary outcomes using Polygenic Risk Scores (PRS). It can read PRS files from temporary directories or use provided PRS data objects.

Usage

```
gcim_b(
  bp_tar_phen,
  bp_tar_cov,
  Add_PRS = NULL,
  Int_PRS = NULL,
  Cov_PRS = NULL,
  temp_dir = tempdir(),
  verbose = TRUE,
  scale_prs = TRUE,
  save_temp_files = 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	data frame for additive PRS values or NULL to read from temp files
Int_PRS	data frame for interaction PRS values or NULL to read from temp files
Cov_PRS	data frame for covariate PRS values or NULL to read from temp files
temp_dir	Directory path containing PRS files (default: tempdir())
verbose	Logical, whether to print progress messages (default: TRUE)
scale_prs	Logical, whether to scale PRS values (default: TRUE)
save_temp_files	Logical, whether to save temporary PRS files (default: TRUE)

Value

List containing model summary and diagnostic information

Examples

```
## Not run:
# Method 1: Using PRS_binary outputs directly
q <- PRS_binary(plink_path, "DummyData", summary_input = add) # Additive PRS
r <- PRS_binary(plink_path, "DummyData", summary_input = gxe) # Interaction PRS
p <- PRS_binary(plink_path, "DummyData", summary_input = trd) # Covariate PRS

result <- gcim_b("Bphe_target.txt", "Bexp_target.txt",
```

```

Add_PRS = q, Int_PRS = r, Cov_PRS = p)

# Method 2: Reading from .prs.sscore files in temp directory
result <- gcim_b("Bphe_target.txt", "Bexp_target.txt",
  Add_PRS = NULL, Int_PRS = NULL, Cov_PRS = NULL,
  temp_dir = "/path/to/prs/files")

## End(Not run)

```

gcim_q	<i>Perform regression analysis for genetic causality inference model(GCIM) with quantitative outcome</i>
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Description

This function performs linear regression analysis for GCIM with quantitative outcomes using Polygenic Risk Scores (PRS). It can read PRS files from temporary directories or use provided PRS data objects.

Usage

```

gcim_q(
  qp_tar_phen,
  qp_tar_cov,
  Add_PRS = NULL,
  Int_PRS = NULL,
  Cov_PRS = NULL,
  temp_dir = tempdir(),
  verbose = TRUE,
  scale_prs = TRUE,
  save_temp_files = 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	data frame for additive PRS values or NULL to read from temp files
Int_PRS	data frame for interaction PRS values or NULL to read from temp files
Cov_PRS	data frame for covariate PRS values or NULL to read from temp files
temp_dir	Directory path containing PRS files (default: tempdir())
verbose	Logical, whether to print progress messages (default: TRUE)
scale_prs	Logical, whether to scale PRS values (default: TRUE)
save_temp_files	Logical, whether to save temporary PRS files (default: TRUE)

Value

List containing model summary and diagnostic information

Examples

```
## Not run:
# Method 1: Using PRS_quantitative outputs directly
q <- PRS_quantitative(plink_path, "DummyData", summary_input = add) # Additive PRS
r <- PRS_quantitative(plink_path, "DummyData", summary_input = gxe) # Interaction PRS
p <- PRS_quantitative(plink_path, "DummyData", summary_input = trd) # Covariate PRS

result <- gcim_q("Qphe_target.txt", "Qexp_target.txt",
  Add_PRS = q, Int_PRS = r, Cov_PRS = p)

# Method 2: Reading from .prs.sscore files in temp directory
result <- gcim_q("Qphe_target.txt", "Qexp_target.txt",
  Add_PRS = NULL, Int_PRS = NULL, Cov_PRS = NULL,
  temp_dir = "/path/to/prs/files")

## End(Not run)
```

plot_gcim_diagnostics

Plot diagnostic plots for GCIM quantitative model

Description

This function creates diagnostic plots for the linear regression model from GCIM quantitative analysis.

Usage

```
plot_gcim_diagnostics(gcim_result, which = 1:4)
```

Arguments

gcim_result	Result object from gcim_q function
which	Integer vector specifying which plots to create (1-4) 1: Residuals vs Fitted, 2: Normal Q-Q plot, 3: Scale-Location, 4: Cook's distance

Value

Creates diagnostic plots

Examples

```
## Not run:
result <- gcim_q("Qphe_target.txt", "Qexp_target.txt",
  Add_PRS = q, Int_PRS = r, Cov_PRS = p)
plot_gcim_diagnostics(result)

## End(Not run)
```

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