Package 'GCIM'

July 25, 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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R topics documented:

`gcim_b` *Perform regression analysis for genetic causality inference model(GCIM) with binary outcome*

Description

This function performs logistic regression analysis for GCIM with binary outcomes using Polygenic Risk Scores (PRS). It reads PRS files that were previously saved by PRS_binary function.

Usage

```
gcim_b(
  bp_tar_phen,
  bp_tar_cov,
  Add_PRS,
  Int_PRS,
  Cov_PRS,
  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
Int_PRS	data frame for interaction PRS values
Cov_PRS	data frame for covariate PRS values
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:
# After running PRS_binary functions to generate PRS files:
# add_prs <- PRS_binary(plink_path, "DummyData", summary_input = add)
# int_prs <- PRS_binary(plink_path, "DummyData", summary_input = gxe)
# cov_prs <- PRS_binary(plink_path, "DummyData", summary_input = trd)

result <- gcim_b("Bphe_target.txt", "Bexp_target.txt",
                 Add_PRS = add_prs, Int_PRS = int_prs, Cov_PRS = cov_prs)

## End(Not run)
```

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gcim_q *Perform regression analysis for genetic causality inference model(GCIM) with quantitative outcome*

Description

This function performs linear regression analysis for GCIM with quantitative outcomes using Polygenic Risk Scores (PRS). It reads PRS files that were previously saved by PRS_quantitative function.

Usage

```
gcim_q(
  qp_tar_phen,
  qp_tar_cov,
  Add_PRS,
  Int_PRS,
  Cov_PRS,
  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	Either file path or data frame for additive PRS values (fallback if files not found)
Int_PRS	Either file path or data frame for interaction PRS values (fallback if files not found)
Cov_PRS	Either file path or data frame for covariate PRS values (fallback if files not found)
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:
# After running PRS_quantitative functions to generate PRS files:
# add_prs <- PRS_quantitative(plink_path, "DummyData", summary_input = add)
# int_prs <- PRS_quantitative(plink_path, "DummyData", summary_input = gxe)
# cov_prs <- PRS_quantitative(plink_path, "DummyData", summary_input = trd)

result <- gcim_q("Qphe_target.txt", "Qexp_target.txt",
                 Add_PRS = add_prs, Int_PRS = int_prs, Cov_PRS = cov_prs)

## End(Not run)
```

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