Package 'GxEprsDummy'

May 29, 2023

Title What the Package Does (One Line, Title Case)

Version 0.0.0.9000

Description What the package does (one paragraph).

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Depends R (>= 2.10)

LazyData true

R topics documented:

`Bcov_discovery` *Covariate data file of the discovery dataset when the outcome is binary This contains covariate information of the individuals in the discovery dataset following confounders*

Description

Covariate data file of the discovery dataset when the outcome is binary This contains covariate information of the individuals in the discovery dataset following confounders

Usage

```
Bcov_discovery
```

Format

A dataframe with 7916 rows and 18 columns

Family ID \item Individual ID \item standardized covariate \item square of the standardized covariate \item confounder 1 \item confounder 2 \item confounder 3 \item confounder 4 \item confounder 5 \item confounder 6 \item confounder 7 \item confounder 8 \item confounder 9 \item confounder 10 \item confounder 11 \item confounder 12 \item confounder 13 \item confounder 14

`Bcov_target` *Covariate data file of the target dataset when the outcome is binary This contains covariate information of the individuals in the target dataset following confounders*

Description

Covariate data file of the target dataset when the outcome is binary This contains covariate information of the individuals in the target dataset following confounders

Usage

```
Bcov_target
```

Format

A dataframe with 1939 rows and 18 columns

Family ID \item Individual ID \item standardized covariate \item square of the standardized covariate \item confounder 1 \item confounder 2 \item confounder 3 \item confounder 4 \item confounder 5 \item confounder 6 \item confounder 7 \item confounder 8 \item confounder 9 \item confounder 10 \item confounder 11 \item confounder 12 \item confounder 13 \item confounder 14

`Bphe_discovery`	*Phenotype data file of the discovery dataset when the outcome is binary This contains phenotype information of the individuals in the discovery dataset*

Description

Phenotype data file of the discovery dataset when the outcome is binary This contains phenotype information of the individuals in the discovery dataset

Usage

```
Bphe_discovery
```

Format

A dataframe with 7916 rows and 3 columns

Family ID \item Individual ID \item phenotype (1=controls, 2=cases)

`Bphe_target`	*Phenotype data file of the target dataset when the outcome is binary This contains phenotype information of the individuals in the target dataset*

Description

Phenotype data file of the target dataset when the outcome is binary This contains phenotype information of the individuals in the target dataset

Usage

```
Bphe_target
```

Format

A dataframe with 1939 rows and 3 columns

Family ID \item Individual ID \item phenotype (0=controls, 1=cases)

`DummyData` *PLINK binary data files This contains DummyData.fam, DummyData.bim and DummyData.bed files, all in one*

Description

PLINK binary data files This contains DummyData.fam, DummyData.bim and DummyData.bed files, all in one

Usage

```
DummyData
```

Format

The data files follow the general PLINK format

`GWAS_binary` *GWAS_binary function This function performs GWAS using plink2 and outputs the GWAS summary statistics file with additive SNP effects named B_trd.sum*

Description

GWAS_binary function This function performs GWAS using plink2 and outputs the GWAS summary statistics file with additive SNP effects named B_trd.sum

Usage

```
GWAS_binary(
  plink_path,
  b_file,
  pheno_file,
  covar_file,
  n_confounders,
  thread,
  summary_output = NULL
)
```

Arguments

`plink_path`	Path to the PLINK executable application
`b_file`	Prefix of the binary files, where all .fam, .bed and .bim files have a common prefix
`pheno_file`	Name (with file extension) of the phenotype file containing family ID, individual ID and phenotype of the discovery dataset as columns, without heading
`covar_file`	Name (with file extension) of the covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the discovery dataset as columns, without heading

n_confounders
: Number of confounding variables in the discovery dataset

thread
: Number of threads used

Value

This function will perform GWAS and output

B_trd.sum

GWEIS_binary *GWEIS_binary function This function performs GWEIS using plink2 and outputs the GWEIS summary statistics files with additive SNP effects named B_add.sum and interaction SNP effects named B_gxe.sum*

Description

GWEIS_binary function This function performs GWEIS using plink2 and outputs the GWEIS summary statistics files with additive SNP effects named B_add.sum and interaction SNP effects named B_gxe.sum

Usage

```
GWEIS_binary(
  plink_path,
  b_file,
  pheno_file,
  covar_file,
  n_confounders,
  thread,
  summary_output1 = NULL,
  summary_output2 = NULL
)
```

Arguments

plink_path
: Path to the PLINK executable application

b_file
: Prefix of the binary files, where all .fam, .bed and .bim files have a common prefix

pheno_file
: Phenotype file containing family ID, individual ID and phenotype of the discovery dataset as columns, without heading

covar_file
: Covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the discovery dataset as columns, without heading

n_confounders
: Number of confounding variables in the discovery dataset

thread
: Number of threads used

Value

This function will perform GWEIS and output

`B_add.sum`

`B_gxe.sum`

`PRS_binary` *PRS_binary function This function uses plink2 and outputs PRSs of each individual in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum*

Description

PRS_binary function This function uses plink2 and outputs PRSs of each individual in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum

Usage

```
PRS_binary(
  plink_path,
  b_file,
  summary_input1 = "B_trd.sum",
  summary_input2 = "B_add.sum",
  summary_input3 = "B_gxe.sum",
  summary_output1 = NULL,
  summary_output2 = NULL,
  summary_output3 = NULL
)
```

Arguments

`plink_path`	Path to the PLINK executable application
`b_file`	Prefix of the binary files, where all .fam, .bed and .bim files have a common prefix

Value

This function will output

`B_trd.sscore`

`B_add.sscore`

`B_gxe.sscore`

`Qcov_discovery` *Covariate data file of the discovery dataset when the outcome is quantitative This contains covariate information of the individuals in the discovery dataset following confounders*

Description

Covariate data file of the discovery dataset when the outcome is quantitative This contains covariate information of the individuals in the discovery dataset following confounders

Usage

```
Qcov_discovery
```

Format

A dataframe with 6426 rows and 18 columns

Family ID \item Individual ID \item standardized covariate \item square of the standardized covariate \item confounder 1 \item confounder 2 \item confounder 3 \item confounder 4 \item confounder 5 \item confounder 6 \item confounder 7 \item confounder 8 \item confounder 9 \item confounder 10 \item confounder 11 \item confounder 12 \item confounder 13 \item confounder 14

`Qcov_target` *Covariate data file of the target dataset when the outcome is quantitative This contains covariate information of the individuals in the target dataset following confounders*

Description

Covariate data file of the target dataset when the outcome is quantitative This contains covariate information of the individuals in the target dataset following confounders

Usage

```
Qcov_target
```

Format

A dataframe with 1579 rows and 18 columns

Family ID \item Individual ID \item standardized covariate \item square of the standardized covariate \item confounder 1 \item confounder 2 \item confounder 3 \item confounder 4 \item confounder 5 \item confounder 6 \item confounder 7 \item confounder 8 \item confounder 9 \item confounder 10 \item confounder 11 \item confounder 12 \item confounder 13 \item confounder 14

`Qphe_discovery`	*Phenotype data file of the discovery dataset when the outcome is quantitative This contains phenotype information of the individuals in the discovery dataset*

Description

Phenotype data file of the discovery dataset when the outcome is quantitative This contains phenotype information of the individuals in the discovery dataset

Usage

```
Qphe_discovery
```

Format

A dataframe with 6426 rows and 3 columns

Family ID \item Individual ID \item phenotype

`Qphe_target`	*Phenotype data file of the target dataset when the outcome is quantitative This contains phenotype information of the individuals in the target dataset*

Description

Phenotype data file of the target dataset when the outcome is quantitative This contains phenotype information of the individuals in the target dataset

Usage

```
Qphe_target
```

Format

A dataframe with 1579 rows and 3 columns

Family ID \item Individual ID \item phenotype

`results_permuted_binary` *results_permuted_binary function This function uses plink2 and outputs PRSs of each individual in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum*

Description

results_permuted_binary function This function uses plink2 and outputs PRSs of each individual in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum

Usage

```
results_permuted_binary(
  Bphe_target,
  Bcov_target,
  n_confounders,
  input_score1 = "B_trd.sscore",
  input_score2 = "B_add.sscore",
  input_score3 = "B_gxe.sscore"
)
```

Arguments

`Bphe_target`	Phenotype file containing family ID, individual ID and phenotype of the target dataset as columns, without heading
`Bcov_target`	Covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the target dataset as columns, without heading
`n_confounders`	Number of confounding variables in the target dataset

Value

This function will output

`Individual_risk_values.txt`

`results_regular_binary` *results_regular_binary function This function uses plink2 and outputs PRSs of each individual in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum*

Description

results_regular_binary function This function uses plink2 and outputs PRSs of each individual in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum

Usage

```
results_regular_binary(
  Bphe_target,
  Bcov_target,
  n_confounders,
  input_score1 = "B_trd.sscore",
  input_score2 = "B_add.sscore",
  input_score3 = "B_gxe.sscore"
)
```

Arguments

`Bphe_target`	Phenotype file containing family ID, individual ID and phenotype of the target dataset as columns, without heading
`Bcov_target`	Covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the target dataset as columns, without heading
`n_confounders`	Number of confounding variables in the target dataset

Value

This function will output

`Individual_risk_values.txt`

`summary_permuted_binary`

summary_permuted_binary function This function uses plink2 and outputs the p value of permuted model in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum

---

Description

summary_permuted_binary function This function uses plink2 and outputs the p value of permuted model in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum

Usage

```
summary_permuted_binary(
  Bphe_target,
  Bcov_target,
  n_confounders,
  iterations = 1000,
  input_score1 = "B_trd.sscore",
  input_score2 = "B_add.sscore",
  input_score3 = "B_gxe.sscore"
)
```

Arguments

Bphe_target	Phenotype file containing family ID, individual ID and phenotype of the target dataset as columns, without heading
Bcov_target	Covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the target dataset as columns, without heading
n_confounders	Number of confounding variables in the target dataset

Value

This function will output

`B_permuted_p.txt`

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summary_regular_binary

summary_regular_binary function This function uses plink2 and outputs the summary of regular model in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum

---

Description

summary_regular_binary function This function uses plink2 and outputs the summary of regular model in the target dataset, using pre-generated GWAS and GWEIS summary statistics files named B_trd.sum, B_add.sum and B_gxe.sum

Usage

```
summary_regular_binary(
  Bphe_target,
  Bcov_target,
  n_confounders,
  input_score1 = "B_trd.sscore",
  input_score2 = "B_add.sscore",
  input_score3 = "B_gxe.sscore"
)
```

Arguments

`Bphe_target`	Phenotype file containing family ID, individual ID and phenotype of the target dataset as columns, without heading
`Bcov_target`	Covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the target dataset as columns, without heading
`n_confounders`	Number of confounding variables in the target dataset

Value

This function will output

`Bsummary.txt`

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