Package 'GxEprsDummy'

May 30, 2023

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

Version 0.0.0.9000

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Description what the package does (one paragraph).
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2 Bcov_discovery

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

```
Column 1 Family ID
```

Column 2 Individual ID

Column 3 standardized covariate

Column 4 square of the standardized covariate

Column 5 confounder 1

Column 6 confounder 2

Column 7 confounder 3

Column 8 confounder 4

Column 9 confounder 5

Column 10 confounder 6

Column 11 confounder 7

Column 12 confounder 8

Column 13 confounder 9

Column 14 confounder 10

Column 15 confounder 11

Column 16 confounder 12

Column 17 confounder 13

Bcov_target 3

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

Column 1 Family ID

Column 2 Individual ID

Column 3 standardized covariate

Column 4 square of the standardized covariate

Column 5 confounder 1

Column 6 confounder 2

Column 7 confounder 3

Column 8 confounder 4

Column 9 confounder 5

Column 10 confounder 6

Column 11 confounder 7

Column 12 confounder 8

Column 13 confounder 9

Column 14 confounder 10

Column 15 confounder 11

Column 16 confounder 12

Column 17 confounder 13

Bphe_target

Bphe_discovery	Phenotype data file of the discovery dataset when the outcome is bi-
	nary This contains phenotype information of the individuals in the dis-
	covery 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

Column 1 Family ID

Column 2 Individual ID

Column 3 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

Column 1 Family ID

Column 2 Individual ID

Column 3 phenotype (0=controls, 1=cases)

DummyData 5

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

6 GWEIS_binary

```
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 $B_{add.sum}$

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_confounder	S
	Number of confounding variables in the discovery dataset

thread Number of threads used

PRS_binary 7

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, .be

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

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

```
Column 1 Family ID
```

Column 2 Individual ID

Column 3 standardized covariate

Column 4 square of the standardized covariate

Column 5 confounder 1

Column 6 confounder 2

Column 7 confounder 3

Column 8 confounder 4

Column 9 confounder 5

Column 10 confounder 6

Column 11 confounder 7

Column 12 confounder 8

Column 13 confounder 9

Column 14 confounder 10

Column 15 confounder 11

Column 16 confounder 12

Column 17 confounder 13

Qcov_target 9

Qcov_target	Covariate data file of the target dataset when the outcome is quantita- tive 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

Column 1 Family ID

Column 2 Individual ID

Column 3 standardized covariate

Column 4 square of the standardized covariate

Column 5 confounder 1

Column 6 confounder 2

Column 7 confounder 3

Column 8 confounder 4

Column 9 confounder 5

Column 10 confounder 6

Column 11 confounder 7

Column 12 confounder 8

Column 13 confounder 9

Column 14 confounder 10

Column 15 confounder 11

Column 16 confounder 12

Column 17 confounder 13

10 Qphe_target

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

Column 1 Family IDColumn 2 Individual IDColumn 3 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

Column 1 Family IDColumn 2 Individual IDColumn 3 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

 ${\tt Bcov_target} \quad Covariate \ file \ containing \ family \ ID, individual \ ID, standardized \ covariate, square$

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
```

```
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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