

Package ‘GxEprs’

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Title GxE Interaction in Polygenic Risk Score Models for Quantitative and Binary Traits

Version 1.0

Description

The 'GxEprs' is an R package to detect and estimate GxE. It uses a novel PRS model that can enhance the prediction accuracy by utilising GxE effects. It performs Genome Wide Association Studies (GWAS) and Genome Wide Environment Interaction Studies (GWEIS) using a discovery dataset. The package has the ability to obtain polygenic risk scores (PRSs) for a target sample. Finally it predicts the risk values of each individual in the target sample.

URL <https://github.com/DoviniJ/GxEprsDummy/tree/main>

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Bcov_discovery	<i>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</i>
----------------	--

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

Column 18 Confounder 14

Bcov_target	<i>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</i>
-------------	--

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

Column 18 Confounder 14

Bphe_discovery	<i>Phenotype data file of the discovery dataset when the outcome is binary This contains phenotype information of the individuals in the discovery dataset</i>
----------------	--

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	<i>Phenotype data file of the target dataset when the outcome is binary This contains phenotype information of the individuals in the target dataset</i>
-------------	--

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.bim`*PLINK .bim file*

Description

PLINK .bim file

Usage`DummyData.bim`**Format**

This follows PLINK general format

Column 1 Chromosome ID**Column 2** SNP ID**Column 3** Position of centimorgans**Column 4** Base-pair coordinate**Column 5** Minor Allele**Column 6** Reference Allele

`DummyData.fam`*PLINK .fam file*

Description

PLINK .fam file

Usage`DummyData.fam`**Format**

This follows PLINK general format

Column 1 Family ID**Column 2** Individual ID**Column 3** Father's ID**Column 4** Mother's ID**Column 5** Sex**Column 6** Phenotype value

DummyData.map	<i>PLINK .map file</i>
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Description

PLINK .map file

Usage

DummyData.map

Format

This follows PLINK general format

DummyData.ped	<i>PLINK .ped file</i>
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Description

PLINK .ped file

Usage

DummyData.ped

Format

This follows PLINK general format

GWAS_binary	<i>GWAS_binary function This function performs GWAS using plink2 and outputs the GWAS summary statistics file with additive SNP effects named B_out.trd.sum</i>
-------------	---

Description

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

Usage

```
GWAS_binary(
  plink_path,
  b_file,
  Bphe_discovery,
  Bcov_discovery,
  thread = 20,
  summary_output = "B_out.trd.sum"
)
```

Arguments

<code>plink_path</code>	Path to the PLINK executable application
<code>b_file</code>	Prefix of the binary files, where all .fam, .bed and .bim files have a common prefix
<code>Bphe_discovery</code>	Name (with file extension) of the phenotype file containing family ID, individual ID and phenotype of the discovery dataset as columns, without heading
<code>Bcov_discovery</code>	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
<code>thread</code>	Number of threads used
<code>summary_output</code>	Name of the SNP effects of the GWAS summary statistics file specified by the user

Value

This function will perform GWAS and output

<code>B_out.trd.sum</code>	GWAS summary statistics file with additive SNP effects
----------------------------	--

Examples

```
## Not run:
x <- GWAS_binary(plink_path, DummyData, Bphe_discovery, Bcov_discovery,
  thread = 20, summary_output = "B_out.trd.sum")
head(x) #to read the head of all columns in B_out.trd.sum file
x$V1 #to extract the chromosome number (CHROM)
x$V2 #to extract the base pair position (POS)
x$V3 #to extract the SNP ID (ID)
x$V4 #to extract the reference allele (REF)
x$V5 #to extract the alternate allele (ALT)
x$V6 #to extract the minor allele (A1)
x$V7 #to extract whether firth regression is used (FIRTH?)
x$V8 #to extract the type of test performed (TEST)
x$V9 #to extract the nmber of allele observations (OBS_CT)
x$V10 #to extract the odds ration of the SNP effect (OR)
x$V11 #to extract the standard error of log odds (LOG(OR)_SE)
x$V12 #to extract the test statistic (Z_STAT)
x$V13 #to extract the p value (P)
x$V14 #to extract the error code (ERRCODE)

## End(Not run)
```

GWAS_quantitative	<i>GWAS_quantitative function This function performs GWAS using plink2 and outputs the GWAS summary statistics file with additive SNP effects named Q_out.trd.sum</i>
-------------------	---

Description

GWAS_quantitative function This function performs GWAS using plink2 and outputs the GWAS summary statistics file with additive SNP effects named Q_out.trd.sum

Usage

```
GWAS_quantitative(
  plink_path,
  b_file,
  Qphe_discovery,
  Qcov_discovery,
  thread = 20,
  summary_output = "Q_out.trd.sum"
)
```

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
Qphe_discovery	Name (with file extension) of the phenotype file containing family ID, individual ID and phenotype of the discovery dataset as columns, without heading
Qcov_discovery	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
thread	Number of threads used
summary_output	Name of the SNP effects of the GWAS summary statistics file specified by the user

Value

This function will perform GWAS and output

Q_out.trd.sum	GWAS summary statistics file with additive SNP effects
---------------	--

Examples

```
## Not run:
x <- GWAS_quantitative(plink_path, DummyData, Qphe_discovery, Qcov_discovery,
  thread = 20, summary_output = "Q_out.trd.sum")
head(x) #to read the head of all columns in Q_out.trd.sum file
x$V1 #to extract the chromosome number (CHROM)
x$V2 #to extract the base pair position (POS)
x$V3 #to extract the SNP ID (ID)
x$V4 #to extract the reference allele (REF)
x$V5 #to extract the alternate allele (ALT)
x$V6 #to extract the minor allele (A1)
x$V7 #to extract the type of test performed (TEST)
x$V8 #to extract the nmber of allele observations (OBS_CT)
```



```

x$V9 #to extract the SNP effect (BETA)
x$V10 #to extract the standard error of each SNP effect (SE)
x$V11 #to extract the test statistic (T_STAT)
x$V12 #to extract the p value (P)
x$V13 #to extract the error code (ERRCODE)

## End(Not run)

```

GWEIS_binary	<i>GWEIS_binary function This function performs GWEIS using plink2 and outputs the GWEIS summary statistics files with additive SNP effects named B_out.add.sum and interaction SNP effects named B_out.gxe.sum</i>
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Description

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

Usage

```

GWEIS_binary(
  plink_path,
  b_file,
  Bphe_discovery,
  Bcov_discovery,
  thread = 20,
  summary_output = "B_out"
)

```

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
Bphe_discovery	Phenotype file containing family ID, individual ID and phenotype of the discovery dataset as columns, without heading
Bcov_discovery	Covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the discovery dataset as columns, without heading
thread	Number of threads used
summary_output	Name (prefix) of the additive or interaction SNP effects of the GWEIS summary statistics file specified by the user

Value

This function will perform GWEIS and output

`B_out.add.sum`

GWEIS summary statistics file with additive SNP effects

`B_out.gxe.sum`

GWEIS summary statistics file with interaction SNP effects

Examples

```
## Not run:
x <- GWEIS_binary(plink_path, DummyData, Bphe_discovery, Bcov_discovery,
  thread = 20, summary_output = "B_out")
head(x[[1]]) #to extract the head of all columns in B_out.add.sum file
x[[1]]$V1 #to extract the chromosome number (CHROM)
x[[1]]$V2 #to extract the base pair position (POS)
x[[1]]$V3 #to extract the SNP ID (ID)
x[[1]]$V4 #to extract the reference allele (REF)
x[[1]]$V5 #to extract the alternate allele (ALT)
x[[1]]$V6 #to extract the minor allele (A1)
x[[1]]$V7 #to extract whether firth regression is used (FIRTH?)
x[[1]]$V8 #to extract the type of test performed (TEST)
x[[1]]$V9 #to extract the nmber of allele observations (OBS_CT)
x[[1]]$V10 #to extract the odds ration of the SNP effect (OR)
x[[1]]$V11 #to extract the standard error of log odds (LOG(OR)_SE)
x[[1]]$V12 #to extract the test statistic (Z_STAT)
x[[1]]$V13 #to extract the p value (P)
x[[1]]$V14 #to extract the error code (ERRCODE)
head(x[[2]]) #to extract the head of all columns in B_out.gxe.sum file
x[[2]]$V1 #to extract the chromosome number (CHROM)
x[[2]]$V2 #to extract the base pair position (POS)
x[[2]]$V3 #to extract the SNP ID (ID)
x[[2]]$V4 #to extract the reference allele (REF)
x[[2]]$V5 #to extract the alternate allele (ALT)
x[[2]]$V6 #to extract the minor allele (A1)
x[[2]]$V7 #to extract whether firth regression is used (FIRTH?)
x[[2]]$V8 #to extract the type of test performed (TEST)
x[[2]]$V9 #to extract the nmber of allele observations (OBS_CT)
x[[2]]$V10 #to extract the odds ration of the SNP effect (OR)
x[[2]]$V11 #to extract the standard error of log odds (LOG(OR)_SE)
x[[2]]$V12 #to extract the test statistic (Z_STAT)
x[[2]]$V13 #to extract the p value (P)
x[[2]]$V14 #to extract the error code (ERRCODE)

## End(Not run)
```

GWEIS_quantitative *GWEIS_quantitative function This function performs GWEIS using plink2 and outputs the GWEIS summary statistics files with additive SNP effects named `Q_out.add.sum` and interaction SNP effects named `Q_out.gxe.sum`*

Description

GWEIS_quantitative function This function performs GWEIS using plink2 and outputs the GWEIS summary statistics files with additive SNP effects named Q_out.add.sum and interaction SNP effects named Q_out.gxe.sum

Usage

```
GWEIS_quantitative(
  plink_path,
  b_file,
  Qphe_discovery,
  Qcov_discovery,
  thread = 20,
  summary_output = "Q_out"
)
```

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
Qphe_discovery	Phenotype file containing family ID, individual ID and phenotype of the discovery dataset as columns, without heading
Qcov_discovery	Covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the discovery dataset as columns, without heading
thread	Number of threads used
summary_output	Name (prefix) of the additive or interaction SNP effects of the GWEIS summary statistics file specified by the user

Value

This function will perform GWEIS and output

Q_out.add.sum	GWEIS summary statistics file with additive SNP effects
Q_out.gxe.sum	GWEIS summary statistics file with interaction SNP effects

Examples

```
## Not run:
x <- GWEIS_quantitative(plink_path, DummyData, Qphe_discovery, Qcov_discovery,
  thread = 20, summary_output = "Q_out")
head(x[[1]]) #to read the head of all columns in Q_out.add.sum file
x[[1]]$V1 #to extract the chromosome number (CHROM)
x[[1]]$V2 #to extract the base pair position (POS)
x[[1]]$V3 #to extract the SNP ID (ID)
x[[1]]$V4 #to extract the reference allele (REF)
x[[1]]$V5 #to extract the alternate allele (ALT)
```

```

x[[1]]$V6 #to extract the minor allele (A1)
x[[1]]$V7 #to extract the type of test performed (TEST)
x[[1]]$V8 #to extract the nmber of allele observations (OBS_CT)
x[[1]]$V9 #to extract the SNP effect (BETA)
x[[1]]$V10 #to extract the standard error of each SNP effect (SE)
x[[1]]$V11 #to extract the test statistic (T_STAT)
x[[1]]$V12 #to extract the p value (P)
x[[1]]$V13 #to extract the error code (ERRCODE)
head(x[[2]]) #to read the head of all columns in Q_out.gxe.sum file
x[[2]]$V1 #to extract the chromosome number (CHROM)
x[[2]]$V2 #to extract the base pair position (POS)
x[[2]]$V3 #to extract the SNP ID (ID)
x[[2]]$V4 #to extract the reference allele (REF)
x[[2]]$V5 #to extract the alternate allele (ALT)
x[[2]]$V6 #to extract the minor allele (A1)
x[[2]]$V7 #to extract the type of test performed (TEST)
x[[2]]$V8 #to extract the nmber of allele observations (OBS_CT)
x[[2]]$V9 #to extract the SNP effect (BETA)
x[[2]]$V10 #to extract the standard error of each SNP effect (SE)
x[[2]]$V11 #to extract the test statistic (T_STAT)
x[[2]]$V12 #to extract the p value (P)
x[[2]]$V13 #to extract the error code (ERRCODE)

## End(Not run)

```

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_out.trd.sum, B_out.add.sum or B_out.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_out.trd.sum, B_out.add.sum or B_out.gxe.sum

Usage

```

PRS_binary(
  plink_path,
  b_file,
  summary_input = "B_out.trd.sum",
  summary_output = "B_trd"
)

```

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
summary_input	Name of the summary statistics file specified by the user

summary_output

Name of the PRS file generated using provided summary statistics file specified by the user

Value

This function will output

B_trd.sscore PRSs for each target individual using GWAS additive effects

Examples

```
## Not run:
x <- PRS_binary(plink_path, DummyData, summary_input = "B_out.trd.sum",
               summary_output = "B_trd")
head(x) #to read the head of all columns in B_trd.sscore file
x$V1 #to extract the family ID's of target dataset (FID)
x$V2 #to extract the individual ID's of target dataset (IID)
x$V3 #to extract the number of alleles across scored variants (ALLELE_CT)
x$V4 #to extract the sum of named allele dosages (NAMED_ALLELE_DOSAGE_SUM)
x$V5 #to extract the polygenic risk scores (SCORE1_AVG)

## End(Not run)
```

PRS_quantitative	<i>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 Q_out.trd.sum, Q_out.add.sum or Q_out.gxe.sum</i>
------------------	---

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 Q_out.trd.sum, Q_out.add.sum or Q_out.gxe.sum

Usage

```
PRS_quantitative(
  plink_path,
  b_file,
  summary_input = "Q_out.trd.sum",
  summary_output = "Q_trd"
)
```

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
summary_input	Name of the summary statistics file specified by the user
summary_output	Name of the PRS file generated using provided summary statistics file specified by the user

Value

This function will output

`Q_trd.sscore` PRSs for each target individual using GWAS additive effects

Examples

```
## Not run:
x <- PRS_quantitative(plink_path, DummyData, summary_input = "Q_out.trd.sum",
                      summary_output = "Q_trd")
head(x[[1]]) #to read the head of all columns in Q_trd.sscore file
x$V1 #to extract the family ID's of target dataset (FID)
x$V2 #to extract the individual ID's of target dataset (IID)
x$V3 #to extract the number of alleles across scored variants (ALLELE_CT)
x$V4 #to extract the sum of named allele dosages (NAMED_ALLELE_DOSAGE_SUM)
x$V5 #to extract the polygenic risk scores (SCORE1_AVG)

## End(Not run)
```

`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
Column 18 Confounder 14

Qcov_target	<i>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</i>
-------------	--

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
Column 18 Confounder 14

Qphe_discovery	<i>Phenotype data file of the discovery dataset when the outcome is quantitative This contains phenotype information of the individuals in the discovery dataset</i>
----------------	--

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 ID

Column 2 Individual ID

Column 3 Phenotype

Qphe_target	<i>Phenotype data file of the target dataset when the outcome is quantitative This contains phenotype information of the individuals in the target dataset</i>
-------------	--

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 ID

Column 2 Individual ID

Column 3 Phenotype

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,
  iterations = 1000,
  add_score = "B_add.sscore",
  gxe_score = "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
iterations	Number of iterations used in permutation
add_score	The .sscore file generated using additive SNP effects of GWEIS summary statistics
gxe_score	The .sscore file generated using interaction SNP effects of GWEIS summary statistics

Value

This function will output

B_permuted_p.txt
the p value of the permuted model

Examples

```
## Not run:
x <- summary_permuted_binary(Bphe_target, Bcov_target)
x

## End(Not run)
```

```
summary_permuted_quantitative
```

summary_permuted_quantitative 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 Q_trd.sum, Q_add.sum and Q_gxe.sum

Description

summary_permuted_quantitative 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 Q_trd.sum, Q_add.sum and Q_gxe.sum

Usage

```
summary_permuted_quantitative(
  Qphe_target,
  Qcov_target,
  iterations = 1000,
  add_score = "Q_add.sscore",
  gxe_score = "Q_gxe.sscore"
)
```

Arguments

Qphe_target	Phenotype file containing family ID, individual ID and phenotype of the target dataset as columns, without heading
Qcov_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
iterations	Number of iterations used in permutation
add_score	The .sscore file generated using additive SNP effects of GWEIS summary statistics
gxe_score	The .sscore file generated using interaction SNP effects of GWEIS summary statistics

Value

This function will output

```
Q_permuted_p.txt
the p value of the permuted model
```

Examples

```
## Not run:
x <- summary_permuted_quantitative(Qphe_target, Qcov_target)
x

## End(Not run)
```

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,
  trd_score = "B_trd.sscore",
  add_score = "B_add.sscore",
  gxe_score = "B_gxe.sscore",
  Model,
  summary_output = "Bsummary.txt",
  risk_output = "Individual_risk_values.txt"
)
```

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
trd_score	The .sscore file generated using additive SNP effects of GWAS summary statistics
add_score	The .sscore file generated using additive SNP effects of GWEIS summary statistics
gxe_score	The .sscore file generated using interaction SNP effects of GWEIS summary statistics
Model	Specify the model number (1: $y = \text{PRS_trd} + E + \text{PRS_trd} \times E + \text{confounders}$, 2: $y = \text{PRS_add} + E + \text{PRS_add} \times E + \text{confounders}$, 3: $y = \text{PRS_add} + E + \text{PRS_gxe} \times E + \text{confounders}$, 4: $y = \text{PRS_add} + E + \text{PRS_gxe} + \text{PRS_gxe} \times E + \text{confounders}$, 5: $y = \text{PRS_add} + E + E^2 + \text{PRS_gxe} + \text{PRS_gxe} \times E + \text{confounders}$, where y is the outcome variable, E is the covariate of interest, PRS_trd and PRS_add are the polygenic risk scores computed using additive SNP effects of GWAS and GWEIS summary statistics respectively, and PRS_gxe is the polygenic risk scores computed using GxE interaction SNP effects of GWEIS summary statistics.)
summary_output	Name of the model summary file specified by the user

`risk_output` Name of the file containing risk scores of the target individuals specified by the user

Value

This function will output

`Bsummary.txt` the summary of the fitted model

`Individual_risk_values.txt`
the estimated risk values of individuals in the target sample

Examples

```
## Not run:
x <- summary_regular_binary(Bphe_target, Bcov_target,
                           add_score = "B_add.sscore",
                           gxe_score = "B_gxe.sscore",
                           Model = 5,
                           summary_output = "Bsummary.txt",
                           risk_output = "Individual_risk_values.txt")

x[[1]][[1]] #to obtain the content of the Bsummary.txt file
x[[1]][[2]] #to extract "Call" of the model summary
x[[1]][[3]] #to extract terms of the model summary
x[[1]][[4]] #to extract family information of the model summary
x[[1]][[5]] #to extract deviance information of the model summary
x[[1]][[6]] #to extract AIC information of the model summary
x[[1]][[7]] #to extract contrasts of the model summary
x[[1]][[8]] #to extract degrees of freedom (df) of residuals of
             #the model summary
x[[1]][[9]] #to extract "Null deviance" of the model summary
x[[1]][[10]] #to extract degrees of freedom (df) of null deviance
             #of the model summary
x[[1]][[11]] #to extract "iter" of the model summary
x[[1]][[12]] #to extract deviance residuals
x[[1]][[13]] #to extract regrerssion coefficients of the model summary
x[[1]][[14]] #to extract aliesed information of the model summary
x[[1]][[15]] #to extract dispersion information of the model summary
x[[1]][[16]] #to extract degrees of freedom of the model summary
x[[1]][[17]] #to extract unscaled variance covariance matrix of all variables
x[[1]][[18]] #to extract scaled variance covariance matrix of all variables
head(x[[2]]) #to read the head of all columns in Individual_risk_values.txt file
x[[2]][,1] #to extract the column containing family ID's
x[[2]][,2] #to extract the column containing individual ID's
x[[2]][,3] #to extract the column containing predicted risk scores

## End(Not run)
```

summary_regular_quantitative

summary_regular_quantitative 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 *Q_trd.sum*, *Q_add.sum* and *Q_gxe.sum*

Description

summary_regular_quantitative 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 Q_trd.sum, Q_add.sum and Q_gxe.sum

Usage

```
summary_regular_quantitative(
  Qphe_target,
  Qcov_target,
  trd_score = "Q_trd.sscore",
  add_score = "Q_add.sscore",
  gxe_score = "Q_gxe.sscore",
  Model,
  summary_output = "Qsummary.txt",
  risk_output = "Individual_risk_values.txt"
)
```

Arguments

Qphe_target	Phenotype file containing family ID, individual ID and phenotype of the target dataset as columns, without heading
Qcov_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
trd_score	The .sscore file generated using additive SNP effects of GWAS summary statistics
add_score	The .sscore file generated using additive SNP effects of GWEIS summary statistics
gxe_score	The .sscore file generated using interaction SNP effects of GWEIS summary statistics
Model	Specify the model number (1: $y = \text{PRS_trd} + E + \text{PRS_trd} \times E + \text{confounders}$, 2: $y = \text{PRS_add} + E + \text{PRS_add} \times E + \text{confounders}$, 3: $y = \text{PRS_add} + E + \text{PRS_gxe} \times E + \text{confounders}$, 4: $y = \text{PRS_add} + E + \text{PRS_gxe} + \text{PRS_gxe} \times E + \text{confounders}$, where y is the outcome variable, E is the covariate of interest, PRS_trd and PRS_add are the polygenic risk scores computed using additive SNP effects of GWAS and GWEIS summary statistics respectively, and PRS_gxe is the polygenic risk scores computed using GxE interaction SNP effects of GWEIS summary statistics.)
summary_output	Name of the model summary file specified by the user
risk_output	Name of the file containing risk scores of the target individuals specified by the user

Value

This function will output

Qsummary.txt the summary of the fitted model

Individual_risk_values.txt

the estimated risk values of individuals in the target sample

Examples

```
## Not run:
x <- summary_regular_quantitative(Qphe_target, Qcov_target,
                                add_score = "Q_add.sscore",
                                gxe_score = "Q_gxe.sscore",
                                Model = 4,
                                summary_output = "Qsummary.txt",
                                risk_output = "Individual_risk_values.txt")

x[[1]][[1]] #to obtain the content of the Qsummary.txt file
x[[1]][[2]] #to extract "Call" of the model summary
x[[1]][[3]] #to extract terms of the model summary
x[[1]][[4]] #to extract the residuals
x[[1]][[5]] #to extract regrerssion coefficients of the model summary
x[[1]][[6]] #to extract aliesed information of the model summary
x[[1]][[7]] #to extract "sigma" (residual standard error) information
              #of the model summary
x[[1]][[8]] #to extract degrees of freedom of the model summary
x[[1]][[9]] #to extract the R squared value of the model summary
x[[1]][[10]] #to extract the adjusted R squared value of the model summary
x[[1]][[11]] #to extract the test statistic values of the model summary
x[[1]][[12]] #to extract unscaled variance covariance matrix of all variables
head(x[[2]]) #to read the head of all columns in Individual_risk_values.txt file
x[[2]][,1] #to extract the column containing family ID's
x[[2]][,2] #to extract the column containing individual ID's
x[[2]][,3] #to extract the column containing predicted risk scores

## End(Not run)
```

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