Package 'GxEprsDummy'

June 15, 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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Encoding UTF-8

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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

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`	*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

Column 18 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

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` *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_out.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_out.trd.sum

Usage

```
GWAS_binary(
  plink_path,
  b_file,
  Bphe_discovery,
  Bcov_discovery,
  thread = 20,
  summary_output = "B_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
`Bphe_discovery`	Name (with file extension) of the phenotype file containing family ID, individual ID and phenotype of the discovery dataset as columns, without heading
`Bcov_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

`B_out.trd.sum`

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 *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*

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`

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` *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*

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

B_out.gxe.sum

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`

`Q_out.gxe.sum`

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`

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` *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*

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`

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`	*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

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`	*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 ID

Column 2 Individual ID

Column 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 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

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

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 = PRS_trd + E + PRS_trd x E + confounders, 2: y = PRS_add + E + PRS_add x E + confounders, 3: y = PRS_add + E + PRS_gxe x E + confounders, 4: y = PRS_add + E + PRS_gxe + PRS_gxe x E + confounders, 5: y = PRS_add + E + E^2 + PRS_gxe + PRS_gxe x E + 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
Individual_risk_values.txt
```

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

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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 = PRS_trd + E + PRS_trd x E + confounders, 2: y = PRS_add + E + PRS_add x E + confounders, 3: y = PRS_add + E + PRS_gxe x E + confounders, 4: y = PRS_add + E + PRS_gxe + PRS_gxe x E + 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
Individual_risk_values.txt
```

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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