

# Package ‘GxEprsDummy’

June 1, 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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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>
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### 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

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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>
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**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

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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>
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### 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)

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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>
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### 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)

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

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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_trd.sum</i>
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**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,
  Bphe_discovery,
  Bcov_discovery,
  thread = 20,
  summary_output = "B_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\_trd.sum

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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_add.sum and interaction SNP effects named B_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\_add.sum and interaction SNP effects named B\_gxe.sum

### Usage

```
GWEIS_binary(
  plink_path,
  b_file,
  Bphe_discovery,
  Bcov_discovery,
  thread = 20,
  summary_output1 = "B_add.sum",
  summary_output2 = "B_gxe.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	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_output1	Name of the additive SNP effects of the GWEIS summary statistics file specified by the user
summary_output2	Name of the interaction SNP effects of the GWEIS summary statistics file specified by the user

**Value**

This function will perform GWEIS and output

`B_add.sum`

`B_gxe.sum`

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<code>PRs_binary</code>	<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 <code>B_trd.sum</code>, <code>B_add.sum</code> and <code>B_gxe.sum</code></i>
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**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_input = "B_trd.sum",
  summary_output = "B_trd"
)
```

**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>summary_input</code>	Name of the summary statistics file specified by the user
<code>summary_output</code>	Name of the PRS file generated using provided summary statistics file specified by the user

**Value**

This function will output

`B_trd.sscore`

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Qcov_discovery	<i>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</i>
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## 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



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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>
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### 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

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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>
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---

**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>
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**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

---

```
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**

<code>Bphe_target</code>	Phenotype file containing family ID, individual ID and phenotype of the target dataset as columns, without heading
<code>Bcov_target</code>	Covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the target dataset as columns, without heading
<code>n_confounders</code>	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,
  iterations = 1000,
  input_score1 = "B_add.sscore",
  input_score2 = "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
input_score2	The .sscore file generated using additive SNP effects of GWEIS summary statistics
input_score3	The .sscore file generated using interaction SNP effects of GWEIS summary statistics

**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,
  input_score1 = "B_trd.sscore",
  input_score2 = "B_add.sscore",
  input_score3 = "B_gxe.sscore",
  Model
)
```

**Arguments**

<code>Bphe_target</code>	Phenotype file containing family ID, individual ID and phenotype of the target dataset as columns, without heading
<code>Bcov_target</code>	Covariate file containing family ID, individual ID, standardized covariate, square of standardized covariate, and/or confounders of the target dataset as columns, without heading
<code>input_score1</code>	The .sscore file generated using additive SNP effects of GWAS summary statistics
<code>input_score2</code>	The .sscore file generated using additive SNP effects of GWEIS summary statistics
<code>input_score3</code>	The .sscore file generated using interaction SNP effects of GWEIS summary statistics
<code>Model</code>	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, $\text{PRS\_trd}$ and $\text{PRS\_add}$ are the polygenic risk scores computed using additive SNP effects of GWAS and GWEIS summary statistics respectively, and $\text{PRS\_gxe}$ is the polygenic risk scores computed using GxE interaction SNP effects of GWEIS summary statistics.)

**Value**

This function will output

`Bsummary.txt`

`Individual_risk_values.txt`

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