

Package: BWMR (via r-universe)

October 1, 2026

Title Bayesian Weighted Mendelian Randomization (BWMR)

Version 0.1.1

Description Inference the causality based on BWMR method.

License GPL (>= 3)

URL <https://github.com/jiazhao97/BWMR>

BugReports <https://github.com/jiazhao97/BWMR/issues/>

Depends R (>= 3.5.0)

Imports ggplot2

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Repository <https://mrcieu.r-universe.dev>

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RemoteUrl <https://github.com/remlapmot/BWMR>

RemoteRef suggestions

RemoteSha 481637f636270c486160e0347c3e5110d175a6ed

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BWMR

*Bayesian Weighted Mendelian Randomization***Description**

Performs variational EM inference for the BWMR model, estimating the causal effect of an exposure on an outcome using summary-level GWAS data.

Usage

```
BWMR(gammahat, Gammahat, sigmaX, sigmaY, alpha = 100, sqsigma0 = (1e+06)^2)
```

Arguments

<code>gammahat</code>	Numeric vector of SNP-exposure effect estimates.
<code>Gammahat</code>	Numeric vector of SNP-outcome effect estimates.
<code>sigmaX</code>	Numeric vector of standard errors for the SNP-exposure effects.
<code>sigmaY</code>	Numeric vector of standard errors for the SNP-outcome effects.
<code>alpha</code>	Numeric scalar; concentration parameter for the Beta prior on the proportion of valid instruments. Default is 100.
<code>sqsigma0</code>	Numeric scalar; prior variance for beta. Default is $(1e6)^2$, representing a diffuse prior.

Value

A list containing:

<code>beta</code>	Causal effect estimate.
<code>se_beta</code>	Standard error of the causal effect estimate.
<code>P_value</code>	P-value from a chi-squared test (1 df).
<code>weights</code>	Posterior mean weights for each SNP.
<code>tau</code>	Estimate of the pleiotropy noise parameter.
<code>sigma</code>	Estimate of the instrument strength parameter.
<code>mu_pi</code>	Posterior mean of the proportion of valid instruments.
<code>plot1</code>	Scatter plot of SNP effects with error bars (ggplot2).
<code>plot2</code>	ELBO convergence plot (ggplot2).
<code>plot3</code>	Bar chart of posterior mean weights per SNP (ggplot2).
<code>plot4</code>	Weighted scatter plot with regression line (ggplot2).

Examples

```
data(ExampleData)
result <- BWMR(
  gammahat = ExampleData$beta.exposure,
  Gammahat = ExampleData$beta.outcome,
  sigmaX    = ExampleData$se.exposure,
  sigmaY    = ExampleData$se.outcome
)
result$beta
result$P_value
```

BWMR_quick

*Bayesian Weighted Mendelian Randomization (no plots)***Description**

A faster version of [BWMR\(\)](#) that omits diagnostic plots. Suitable for simulation studies or large-scale analyses where plotting is unnecessary.

Usage

```
BWMR_quick(
  gammahat,
  Gammahat,
  sigmaX,
  sigmaY,
  alpha = 100,
  sqsigma0 = (1e+06)^2
)
```

Arguments

<code>gammahat</code>	Numeric vector of SNP-exposure effect estimates.
<code>Gammahat</code>	Numeric vector of SNP-outcome effect estimates.
<code>sigmaX</code>	Numeric vector of standard errors for the SNP-exposure effects.
<code>sigmaY</code>	Numeric vector of standard errors for the SNP-outcome effects.
<code>alpha</code>	Numeric scalar; concentration parameter for the Beta prior on the proportion of valid instruments. Default is 100.
<code>sqsigma0</code>	Numeric scalar; prior variance for beta. Default is $(1e6)^2$, representing a diffuse prior.

Value

A list containing:

beta	Causal effect estimate.
se_beta	Standard error of the causal effect estimate.
P_value	P-value from a chi-squared test (1 df).
tau	Estimate of the pleiotropy noise parameter.
sigma	Estimate of the instrument strength parameter.
mu_pi	Posterior mean of the proportion of valid instruments.

Examples

```
data(ExampleData)
result <- BWMR_quick(
  gammahat = ExampleData$beta.exposure,
  Gammahat = ExampleData$beta.outcome,
  sigmaX   = ExampleData$se.exposure,
  sigmaY   = ExampleData$se.outcome
)
result$beta
result$P_value
```

ExampleData

Example Mendelian randomization genotype summary level dataset

Description

An example Mendelian randomization dataset.

Usage

```
ExampleData
```

Format

ExampleData:

A data frame with 76 rows and 5 columns:

SNP SNP genotype

beta.exposure SNP-exposure estimates

beta.outcome SNP-outcome estimates

se.exposure Standard errors of the SNP-exposure estimates

se.outcome Standard errors of the SNP-outcome estimates

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* **datasets**

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