Package: gsmr (via r-universe)

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Maintainer Zhihong Zhu <z.zhu1@uq.edu.au>

Author Zhihong Zhu, Zhili Zheng, Futao Zhang, Jian Yang

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Type Package

Title gsmr - a tool for SMR and HEIDI analysis

Description A tool perform Generalized Summary-data-based Mendelian Randomization analysis (GSMR) and HEterogeneity In Dependent Instruments analysis to remove pleiotropic outliers (HEIDI-outlier)

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Depends R (>= 2.15), methods, utils, stats

Suggests knitr, rmarkdown

Imports survey

LazyData no

NeedsCompilation no

VignetteBuilder knitr

RoxygenNote 6.0.1

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

RemoteUrl https://github.com/jianyanglab/gsmr

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gsmr-package *gsmr: A tool for GSMR and HEIDI analysis*

Description

Perform Generalized Summary-data-based Mendelian Randomization analysis (GSMR) and HEterogeneity In Dependent Instruments analysis to remove pleiotropic outliers (HEIDI-outlier).

Author(s)

Zhihong Zhu <z.zhu1@uq.edu.au>

Zhili Zheng <zhili.zheng@uq.edu.au>

Futao Zhang <f.zhang5@uq.edu.au>

Jian Yang <jian.yang@uq.edu.au>

References

Zhu, Z. et al. Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, in press. An early verison of the manuscript is available at bioRxiv, 168674.

bi_gsmr *Bi-directional GSMR analysis*

Description

Bi-directional GSMR analysis is composed of a forward-GSMR analysis and a reverse-GSMR analysis that uses SNPs associated with the disease (e.g. at < 5e-8) as the instruments to test for putative causal effect of the disease on the risk factor.

Usage

```
bi_gsmr(bzx, bzx_se, bzx_pval, bzy, bzy_se, bzy_pval, ldrho, snpid, heidi_outlier_flag=T, gwas_thresh=
```

Arguments

bzx	vector, SNP effects on risk factor
bzx_se	vector, standard errors of bzx
bzx_pval	vector, p values for bzx
bzy	vector, SNP effects on disease
bzy_se	vector, standard errors of bzy
bzy_pval	vector, p values for bzy
ldrho	LD correlation matrix of the SNPs

snpid	genetic instruments
n_ref	sample size of the reference sample
heidi_outlier_flag	flag for HEIDI-outlier analysis
gwas_thresh	threshold p-value to select instruments from GWAS for risk factor
heidi_outlier_thresh	HEIDI-outlier threshold
nsnps_thresh	the minimum number of instruments required for the GSMR analysis (we do not recommend users to set this number smaller than 10)
ld_r2_thresh	LD r2 threshold to remove SNPs in high LD
ld_fdr_thresh	FDR threshold to remove the chance correlations between SNP instruments

Value

Estimate of causative effect of risk factor on disease (forward_bxy), the corresponding standard error (forward_bxy_se), p-value (forward_bxy_pval) and SNP index (forward_index), and estimate of causative effect of disease on risk factor (reverse_bxy), the corresponding standard error (reverse_bxy_se), p-value (reverse_bxy_pval), SNP index (reverse_index), SNPs with missing values, with non-significant p-values and those in LD.

Examples

```
data("gsmr")
gsmr_result = bi_gsmr(gsmr_data$bzx, gsmr_data$bzx_se, gsmr_data$bzx_pval, gsmr_data$bzy, gsmr_data$bzy_se, gsmr_
```

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gsmr *Generalized Summary-data-based Mendelian Randomization analysis*

Description

GSMR (Generalised Summary-data-based Mendelian Randomisation) is a flexible and powerful approach that utilises multiple genetic instruments to test for causal association between a risk factor and disease using summary-level data from independent genome-wide association studies.

Usage

```
gsmr(bzx, bzx_se, bzx_pval, bzy, bzy_se, ldrho, snpid, heidi_outlier_flag=T, gwas_thresh=5e-8, heidi_o
```

Arguments

bzx	vector, SNP effects on risk factor
bzx_se	vector, standard errors of bzx
bzx_pval	vector, p values for bzx
bzy	vector, SNP effects on disease

bzy_se	vector, standard errors of bzy
ldrho	LD correlation matrix of the SNPs
snpid	genetic instruments
n_ref	sample size of the reference sample
heidi_outlier_flag	flag for HEIDI-outlier analysis
gwas_thresh	threshold p-value to select instruments from GWAS for risk factor
heidi_outlier_thresh	HEIDI-outlier threshold
nsnps_thresh	the minimum number of instruments required for the GSMR analysis (we do not recommend users to set this number smaller than 10)
ld_r2_thresh	LD r2 threshold to remove SNPs in high LD
ld_fdr_thresh	FDR threshold to remove the chance correlations between SNP instruments

Value

Estimate of causative effect of risk factor on disease (bxy), the corresponding standard error (bxy_se), p-value (bxy_pval), SNP index (used_index), SNPs with missing values, with non-significant p-values and those in LD.

Examples

```
data("gsmr")
gsmr_result = gsmr(gsmr_data$bzx, gsmr_data$bzx_se, gsmr_data$bzx_pval, gsmr_data$bzy, gsmr_data$bzy_se, ldrho, g
```

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heidi_outlier *HEIDI-outlier analysis*

Description

An analysis to detect and eliminate from the analysis instruments that show significant pleiotropic effects on both risk factor and disease

Usage

```
heidi_outlier(bzx, bzx_se, bzx_pval, bzy, bzy_se, ldrho, snpid, n_ref, gwas_thresh=5e-8, heidi_outlier
```

Arguments

bzx	vector, SNP effects on risk factor
bzx_se	vector, standard errors of bzx
bzx_pval	vector, p values for bzx
bzy	vector, SNP effects on disease

bzy_se	vector, standard errors of bzy
ldrho	LD correlation matrix of the SNPs
snpid	genetic instruments
n_ref	sample size of the reference sample
gwas_thresh	threshold p-value to select instruments from GWAS for risk factor
heidi_outlier_thresh	threshold p-value to remove pleiotropic outliers (the default value is 0.01)
nsnps_thresh	the minimum number of instruments required for the GSMR analysis (we do not recommend users to set this number smaller than 10)
ld_r2_thresh	LD r2 threshold to remove SNPs in high LD
ld_fdr_thresh	FDR threshold to remove the chance correlations between SNP instruments

Value

Retained index of genetic instruments, SNPs with missing values, with non-significant p-values and those in LD.

Examples

```
data("gsmr")
filtered_index = heidi_outlier(gsmr_data$bzx, gsmr_data$bzx_se, gsmr_data$bzx_pval, gsmr_data$bzy, gsmr_data$bzy
```

---

std_effect *Standardization of effect size and its standard error*

Description

Standardization of SNP effect and its standard error using z-statistic, allele frequency and sample size

Usage

```
std_effect(snp_freq, b, se, n)
```

Arguments

snp_freq	vector, allele frequencies
b	vector, SNP effects on risk factor
se	vector, standard errors of b
n	vector, per-SNP sample sizes for GWAS of the risk factor

Value

Standardised effect (b) and standard error (se)

Examples

```
data("gsmr")
std_effects = std_effect(gsmr_data$a1_freq, gsmr_data$bzx, gsmr_data$bzx_se, gsmr_data$bzx_n)
```

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