

Package ‘SumVg’

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Type Package

Title Total heritability explained by all variants in genome-wide association studies (GWAS) based on summary statistics with standard error estimates

Version 1.0

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Description This package estimates SNP-based heritability in GWAS based on summary statistics, and provides standard error (SE) estimates of the heritability. The method is based on an empirical Bayes approach, and does not require any distributional assumptions of the SNP effects.

Imports locfdr, sfsmisc

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Encoding UTF-8

NeedsCompilation no

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SumVg	<i>Sum of variance explained by all SNPs in GWAS (for a continuous trait), with standard error estimate</i>
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Description

This function estimates the sum of variance explained (i.e. heritability) by all SNPs in GWAS of a continuous trait, with standard error estimate

Usage

```
SumVg(zall, totalN, method = "paraboot", d = 1, repl = 50, out = "unconditional")
```

Arguments

<code>zall</code>	A vector of z-statistics from a GWAS (or meta-analyses of GWAS); the z-statistics are assumed to be LD-pruned
<code>totalN</code>	Total sample size
<code>method</code>	Describes the method for standard error estimation. Options include: "jack"(jackknife); "paraboot"(parametric bootstrap using the corrected z value as mean for simulation); "fdrboot1"(parametric bootstrap using the observed z value as mean with consideration of local fdr) ; "fdrboot2"(parametric bootstrap using the corrected z value as mean with consideration of local fdr)
<code>d</code>	The number of observations to be left out in each jackknife replicate
<code>repl</code>	Number of replications for resampling
<code>out</code>	Describes the type of sum of Vg. Options include "conditional" (conditional on H1) and "unconditional".

Details

This function estimates the sum of variance explained (i.e. heritability) by all SNPs in GWAS of a continuous trait. The standard error is estimated using various resampling approaches.

Value

<code>Est.SumVg</code>	The estimated sum of variance explained by all SNPs in GWAS
<code>SE.SumVg</code>	The standard error of the estimated sum of variance

Author(s)

Hon-Cheong So

References

So, H.C., Li, M. and Sham, P.C. (2011) Uncovering the total heritability explained by all true susceptibility variants in a genome-wide association study. *Genet Epidemiol*, 35, 447-456.
 So, H.C., Xue, X. and Sham, P.C. (2023) SumVg: Total heritability explained by all variants in genome-wide association studies based on summary statistics with standard error estimates.

Examples

```
zall = rnorm(10000)
SumVg(zall=zall, totalN=5000, method="jack", d=2000, repl=5, out="unconditional" )
```

SumVg.binary	<i>Sum of variance explained by all SNPs in GWAS (for a binary trait), with standard error estimate</i>
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Description

This function estimates the sum of variance explained (i.e. heritability) by all SNPs in GWAS of a binary trait, with standard error estimate

Usage

```
SumVg.binary(zall, method = "paraboot", d = 1, repl = 200, out = "unconditional", SE, K, MAF )
```

Arguments

zall	A vector of z-statistics from a GWAS (or meta-analyses of GWAS) for a binary outcome; z-statistics are assumed to be LD-pruned
method	Describes the method for standard error estimation. Options include: "jack"(jackknife) "paraboot"(parametric bootstrap using the corrected z value as mean for simulation) "fdrboot1"(parametric bootstrap using the observed z value as mean with consideration of local fdr) "fdrboot2"(parametric bootstrap using the corrected z value as mean with consideration of local fdr)
d	The number of observations to be left out in each jackknife replicate
repl	Number of replications for resampling
out	Describes the type of sum of Vg. Options include "conditional" (conditional on H1) and "unconditional".
SE	Standard error of the logistic regression coefficients (a vector)
K	Prevalence of disease
MAF	Vector of minor allele frequencies for the corresponding SNPs (does not need to match to the effect allele)

Details

This function estimates the sum of variance explained (i.e. heritability) by all SNPs in GWAS of a binary trait. The standard error is estimated using various resampling approaches.

Value

Est.SumVg	The estimated sum of variance explained by all SNPs in GWAS
SE.SumVg	The standard error of the estimated sum of variance

Author(s)

Hon-Cheong So

References

So, H.C., Li, M. and Sham, P.C. (2011) Uncovering the total heritability explained by all true susceptibility variants in a genome-wide association study *Genet Epidemiol*, 35, 447-456.

So, H.C., Xue, X. and Sham, P.C. (2023) SumVg: Total heritability explained by all variants in genome-wide association studies based on summary statistics with standard error estimates.

Examples

```
##simulate z-statistics under the complete null
## SE and MAF are made up for reference only
zall = rnorm(n=1000)
SumVg.binary(zall=zall, method="paraboot", d=1, repl=5, out="unconditional",
             SE= rep(0.1,1000), K=0.01, MAF=rep(0.2, 1000) )
```

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