

Package ‘SumVg’

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Type Package

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

Version 1.0

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Description This function estimates the total heritability explained by all variants in genome-wide association studies based on summary statistics only. Standard error estimates are provided by various resampling-based approaches.

License GPL(>=2)

LazyLoad yes

References So, H.C. and Sham, P.C. (2014) Standard error estimation of the total heritability explained by all variants in genome-wide association studies based on summary statistics. Submitted.

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SumVg	<i>Total heritability explained by all variants in genome-wide association studies based on summary statistics with standard error estimates</i>
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Description

This function estimates the total heritability explained by all variants in genome-wide association studies based on summary statistics only. Standard error estimates are provided by various resampling-based approaches.

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Author(s)

Hon-Cheong So Maintainer: Hon-Cheong So <hcs085@gmail.com>

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. and Sham, P.C. (2014) Standard error estimation of the total heritability explained by all variants in genome-wide association studies based on summary statistics. Submitted.

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)
<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. This option is only applicable if jackknife is selected for standard error estimation.
<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. and Sham, P.C. (2014) Standard error estimation of the total heritability explained by all variants in genome-wide association studies based on summary statistics. Submitted.

Examples

```
##simulate z-statistics under the complete null
zall = rnorm(n=10000, mean=0, sd = 1)
SumVg.binary(zall=zall, totalN=10000, 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 = 50,
out = "unconditional", caseNo, ctrlNo, K)
```

Arguments

zall	A vector of z-statistics from a GWAS (or meta-analyses of GWAS)
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 This option is only applicable if jackknife is selected for standard error estimation.
repl	Number of replications for resampling
out	Describes the type of sum of Vg. Options include "conditional" (conditional on H1) and "unconditional".
caseNo	Number of cases
ctrlNo	Number of controls
K	Prevalence of disease

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. and Sham, P.C. (2014) Standard error estimation of the total heritability explained by all variants in genome-wide association studies based on summary statistics. Submitted.

Examples

```
##simulate z-statistics under the complete null
zall = rnorm(n=10000, mean=0, sd = 1)
SumVg.binary(zall=zall, method="jack", d=2000, repl=5,
out="unconditional", caseNo=10000, ctrlNo=10000, K=0.01)
```

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*Topic **heritability, variance**
explained, standard error

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