Package 'GEWIST'

July 9, 2025

Type Package

Title Gene Environment Wide Interaction Search Threshold

Version 1.52.0

Depends R (>= 2.10), car

Author Wei Q. Deng, Guillaume Pare

Maintainer Wei Q. Deng <`dengwq@mcmaster.ca`>

Description This 'GEWIST' package provides statistical tools to efficiently optimize SNP prioritization for gene-gene and gene-environment interactions.

License GPL-2

LazyLoad yes

biocViews MultipleComparison, Genetics

git_url https://git.bioconductor.org/packages/GEWIST

git_branch RELEASE_3_21

git_last_commit a3937a7

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-07-09

Contents

`GEWIST-package` *Gene Environment Wide Interaction Search Threshold*

Description

This 'GEWIST' package provides statistical tools to efficiently optimize SNP prioritization for gene-gene and gene-environment interactions.

Details

Package:	PathWei
Type:	Package
Version:	0.99.z
License:	GPL-2
LazyLoad:	yes

Author(s)

Wei Q. Deng <dengwq@mcmaster.ca> Guillaume Pare <pareg@mcmaster.ca>

References

Deng W.Q, Pare G. (2011) A fast algorithm to optimize SNP prioritization for gene-gene and gene-environment interactions. *Genetic Epidemiology*. 35: 729-738. doi: 10.1002/gepi.20624

Pare G, Cook NR, Ridker PM, Chasman DI (2010) On the Use of Variance per Genotype as a Tool to Identify Quantitative Trait Interaction Effects: A Report from the Women's Genome Health Study. *PLoS Genet* 6(6): e1000981. doi:10.1371/journal.pgen.1000981

Levene H. (1960) Robust tests for equality of variances. In *Contributions to Probability and Statistics: Essays in Honor of Harold Hotelling* eds:I. Olkin, S.G. Ghurye, W. Hoeffding, W.G. Madow & H.B.Mann, pp.278-292. Stanford: Stanford University Press.

`effectPDF` *Genetic interaction testing given effect size distribution*

Description

Compute the optimal Variance Prioritization power and corresponding Levene's test p-value threshold for prioritization given the interaction effect size distribution using GEWIST.

Usage

```
effectPDF(distribution = c("beta", "normal", "uniform", "weibull"),
parameter1, parameter2 = NULL, parameter3 = NULL, p, N, theta_c, M,
K = 20000, nb_incr = 50,  range = NULL, verbose = FALSE)
```

Arguments

`distribution`	distribution of interaction effect size. Possible distributions are: "beta" for beta distribution "normal" for normal distribution "uniform" for uniform distribution "weibull" for weibull distribution
`parameter1`	the first parameter used in the corresponding distribution
`parameter2`	the second parameter used in the corresponding distribution, could set to be null
`parameter3`	the third parameter used in the corresponding distribution, could set to be null
`p`	minor allele frequency of the SNP, a number between 0 and 0.5
`N`	sample size
`theta_c`	proportion of quantitative trait variance explained by the covariate, should be a number between 0 and 1
`M`	total number of SNPs to be tested
`K`	number of GEWIST procedures, by default, set to be 20,000
`nb_incr`	number of effect size points in the range to be prioritized using GEWIST; by default set to be 50.
`range`	range of variance explained by interaction effect sizes, a vector of length 2
`verbose`	logical; if TRUE, for each interaction effect size, function returns a data.frame class object listing the VP power at each p-value, from 0.001 to 1 with 0.001 incremental increase.

Value

A list with three components:

`Optimal_VP_power`	VP power to detect interactions at the optimal VP p-value threshold
`Conventional_power`	power to detect interactions without prioritization, i.e, VP power at Levene' test p-value of 1
`Optimal_pval_threshold`	levene'e test p-value at which optimal VP power is achieved

Warning

Computational time is directly proportional to *nb_incr*.

Author(s)

Wei Q. Deng <dengwq@mcmaster.ca> Guillaume Pare <pareg@mcmaster.ca>

References

Deng W.Q, Pare G. (2011) A fast algorithm to optimize SNP prioritization for gene-gene and gene-environment interactions. *Genetic Epidemiology*. 35: 729-738. doi: 10.1002/gepi.20624

Pare G, Cook NR, Ridker PM, Chasman DI (2010) On the Use of Variance per Genotype as a Tool to Identify Quantitative Trait Interaction Effects: A Report from the Women's Genome Health Study. *PLoS Genet* 6(6): e1000981. doi:10.1371/journal.pgen.1000981

Levene H. (1960) Robust tests for equality of variances. In *Contributions to Probability and Statistics: Essays in Honor of Harold Hotelling* eds:I. Olkin, S.G. Ghurye, W. Hoeffding, W.G. Madow & H.B.Mann, pp.278-292. Stanford: Stanford University Press.

Examples

```
# Given a SNP with minor allele frequency of 10% and a sample
# of 10,000 individuals, we are interested in testing interactions
# between this SNP and a covariate of effect size 10%. The
# total number of SNP is 500,000. Assume the unknown interaction
# effect size has a Weibull distribution in the range of 0.05%
# and 0.3% variance explained with 50 increments.Repeat GEWIST
# for each of the 50 interaction effect sizes.


library(GEWIST)
effectPDF(distribution = "weibull", parameter1 = 0.8, parameter2 = 0.3,
parameter3 = NULL, p = 0.1 ,N = 10000, theta_c = 0.1, M = 350000,
K = 20000, nb_incr = 50, range = c(0.05/100,0.3/100), verbose = FALSE)

## End of script
```

`gewistLevene` *Genome Environment Wide Interaction Search Threshold with Levene's test*

Description

Compute the optimal Variance Prioritization power and the corresponding Levene's test prioritization p-value threshold for a given interaction effect size

Usage

```
gewistLevene(p, N, theta_gc, theta_c, M, K = 20000, verbose = FALSE)
```

Arguments

`p`	minor allele frequency of the SNP, a number between 0 and 0.5
`N`	sample size
`theta_gc`	proportion of quantitative trait variance explained by the interaction, should be a number between 0 and 1
`theta_c`	proportion of quantitative trait variance explained by the covariate, should be a number between 0 and 1
`M`	total number of SNPs to be tested
`K`	number of procedures, by default, set to be 20,000
`verbose`	logical; if TRUE, function returns a data.frame class object listing the VP power at each p-value, from 0.001 to 1 with 0.001 incremental increase.

Value

A list with three components:

`Optimal_VP_power`	VP power to detect interactions at the optimal Levene's test p-value threshold
`Conventional_power`	power to detect interactions without prioritization, i.e, VP power at Levene's test p-value of 1
`Optimal_pval_threshold`	levene'e test p-value at which optimal VP power is achieved

Author(s)

Wei Q. Deng <dengwq@mcmaster.ca> Guillaume Pare <pareg@mcmaster.ca>

References

Deng W.Q, Pare G. (2011) A fast algorithm to optimize SNP prioritization for gene-gene and gene-environment interactions. *Genetic Epidemiology* 35: 729-738. doi: 10.1002/gepi.20624

Pare G, Cook NR, Ridker PM, Chasman DI (2010) On the Use of Variance per Genotype as a Tool to Identify Quantitative Trait Interaction Effects: A Report from the Women's Genome Health Study. *PLoS Genet* 6(6): e1000981. doi:10.1371/journal.pgen.1000981

Levene H. (1960) Robust tests for equality of variances. In *Contributions to Probability and Statistics: Essays in Honor of Harold Hotelling* eds:I. Olkin, S.G. Ghurye, W. Hoeffding, W.G. Madow & H.B.Mann, pp.278-292. Stanford: Stanford University Press.

Examples

```
# Given a SNP with minor allele frequency of 10% and a sample
# of 15,000 individuals, we are interested in testing interactions
# between this SNP and a covariate of effect size #10%. The
# total number of SNP is 500,000. Assume the interaction
# explains 0.1% of the quantitative trait variance.
```

```
library(GEWIST)
gewistLevene(p = 0.1, N = 15000, theta_gc =0.1/100, theta_c = 0.1 , M = 500000,
K = 20000, verbose=FALSE)
```

Index