Package ‘GEWIST’
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Title Gene Environment Wide Interaction Search Threshold
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Description This ‘GEWIST’ package provides statistical tools to efficiently optimize SNP prioritization for gene-gene and gene-environment interactions.
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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)
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References

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**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**

```r
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.

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References

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%
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 = 20000, 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’s test p-value at which optimal VP power is achieved
gewistLevene

Author(s)

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References


Examples

```r
# 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)
```
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