Package ‘GEWIST’

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Type Package
Title Gene Environment Wide Interaction Search Threshold
Version 1.18.0
Depends R (>= 2.10), car
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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
NeedsCompilation no

R topics documented:

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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


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
**effectPDF**

- **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)**

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**References**


**Examples**

```r
# 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,
```
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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>p</td>
<td>minor allele frequency of the SNP, a number between 0 and 0.5</td>
</tr>
<tr>
<td>N</td>
<td>sample size</td>
</tr>
<tr>
<td>theta_gc</td>
<td>proportion of quantitative trait variance explained by the interaction, should be a number between 0 and 1</td>
</tr>
<tr>
<td>theta_c</td>
<td>proportion of quantitative trait variance explained by the covariate, should be a number between 0 and 1</td>
</tr>
<tr>
<td>M</td>
<td>total number of SNPs to be tested</td>
</tr>
<tr>
<td>K</td>
<td>number of procedures, by default, set to be 20,000</td>
</tr>
<tr>
<td>verbose</td>
<td>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.</td>
</tr>
</tbody>
</table>

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 &lt;dengwq@mcmaster.ca&gt; Guillaume Pare &lt;pareg@mcmaster.ca&gt;
gewistLevene

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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