# Package ‘GEWIST’

March 22, 2017

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

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### Description

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

### Details

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Author(s)

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

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**

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

distribution of interaction effect size. Possible distributions are:

- 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

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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>
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<th>Description</th>
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<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,</td>
</tr>
<tr>
<td></td>
<td>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,</td>
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<td>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</td>
</tr>
<tr>
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<td>VP power at each p-value, from 0.001 to 1 with 0.001 incremental increase.</td>
</tr>
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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

Author(s)

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

References


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)
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