

# Package ‘GEWIST’

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**Type** Package

**Title** Gene Environment Wide Interaction Search Threshold

**Version** 1.53.0

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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

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 GEWIST-package

*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.

### Details

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

### Author(s)

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### 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.

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 effectPDF

*Genetic interaction testing given effect size distribution*


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### 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:<br>"beta" for beta distribution<br>"normal" for normal distribution<br>"uniform" for uniform distribution<br>"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

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## 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
```

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|              |                                                                                |
|--------------|--------------------------------------------------------------------------------|
| gewistLevene | <i>Genome Environment Wide Interaction Search Threshold with Levene's test</i> |
|--------------|--------------------------------------------------------------------------------|

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## 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's test p-value at which optimal VP power is achieved

**Author(s)**

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**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

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**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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