Package 'GEWIST'

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Type Package

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.

License GPL-2

LazyLoad yes

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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

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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*

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)

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References

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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	*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)

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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.

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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