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

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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

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.

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

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 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
```

`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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