

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 | levене'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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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'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
- 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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