Package ‘GEWIST’

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Description This ‘GEWIST’ package provides statistical tools to efficiently optimize SNP prioritization for gene-gene and gene-environment interactions.
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GEWIST-package ....................................................... 2
effectPDF ............................................................. 2
gewistLevene ......................................................... 4

Index 7
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

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References


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.
**effectPDF**

**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
Levene H. (1960) Robust tests for equality of variances. In Contributions to Probability and Statis-

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

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
- \(\text{verbose}\)  
  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:

- \(\text{Optimal\_VP\_power}\)  
  VP power to detect interactions at the optimal Levene’s test p-value threshold
- \(\text{Conventional\_power}\)  
  power to detect interactions without prioritization, i.e, VP power at Levene’s test p-value of 1
- \(\text{Optimal\_pval\_threshold}\)  
  levene’e test p-value at which optimal VP power is achieved

Author(s)

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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)
Index

* Bonferroni correction
  effectPDF, 2
  GEWIST-package, 2
  gewistLevene, 4
* Levene's Test
  effectPDF, 2
  GEWIST-package, 2
  gewistLevene, 4
* genetic interactions
  effectPDF, 2
  GEWIST-package, 2
  gewistLevene, 4
* quantitative trait
  effectPDF, 2
  GEWIST-package, 2
  gewistLevene, 4
* variance prioritization
  effectPDF, 2
  GEWIST-package, 2
  gewistLevene, 4

effectPDF, 2
GEWIST (GEWIST-package), 2
GEWIST-package, 2
gewistLevene, 4