Package ‘GEWIST’

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Type  Package
Title  Gene Environment Wide Interaction Search Threshold
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Author  Wei Q. Deng, Guillaume Pare
Maintainer  Wei Q. Deng <dengwq@mcmaster.ca>
Description  This ‘GEWIST’ package provides statistical tools to efficiently optimize SNP prioritization for gene-gene and gene-environment interactions.
License  GPL-2
LazyLoad  yes
biocViews  MultipleComparison, Genetics
NeedsCompilation  no

R topics documented:

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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  Gene Environment Wide Interaction Search Threshold
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


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
effectPDF

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.

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References

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,
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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gewistLevene

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)
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