Package ‘GEWIST’

November 6, 2018

Type     Package
Title    Gene Environment Wide Interaction Search Threshold
Version  1.26.0
Depends  R (>= 2.10), car
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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
biocViews MultipleComparison, Genetics
git_url https://git.bioconductor.org/packages/GEWIST
git_branch RELEASE_3_8
git_last_commit b3773a7
git_last_commit_date 2018-10-30
Date/Publication 2018-11-05

R topics documented:

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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
effectPDF

Package: PathWei
Type: Package
Version: 0.99.z
License: GPL-2
LazyLoad: yes

Author(s)
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References

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’ 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%
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
gewistLevene

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)
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