Package ‘GEWIST’

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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


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**

```r
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’s test p-value of 1
- `Optimal_pval_threshold`: levene’s 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


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)
gewistLevene

Arguments

\[ \begin{align*}
p & \quad \text{minor allele frequency of the SNP, a number between 0 and 0.5} \\
N & \quad \text{sample size} \\
\theta_{gc} & \quad \text{proportion of quantitative trait variance explained by the interaction, should be a number between 0 and 1} \\
\theta_c & \quad \text{proportion of quantitative trait variance explained by the covariate, should be a number between 0 and 1} \\
M & \quad \text{total number of SNPs to be tested} \\
K & \quad \text{number of procedures, by default, set to be 20,000} \\
\text{verbose} & \quad \text{logical; if TRUE, function returns a data.frame class object listing the VP power at each p-value, from 0.001 to 1 with 0.001 incremental increase.}
\end{align*} \]

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


Examples

```r
# 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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