Package 'ofGEM'

June 25, 2017

Title A Meta-Analysis Approach with Filtering for Identifying Gene-Level Gene-Environment Interactions with Genetic Association Data

Version 1.0

Date 2017-07-20

Author Jiebiao Wang, Qianying Liu and Lin S. Chen

Maintainer Jiebiao Wang <randel.wang@gmail.com>

Description Offers a gene-based meta-analysis test with filtering to detect gene-environment interactions (GxE) with association data. It first conducts a meta-filtering test to filter out unpromising SNPs by combining all samples in the consortia data. It then runs a test of omnibus-filtering-based GxE meta-analysis (ofGEM) that combines the strengths of the fixed- and random-effects meta-analysis with meta-filtering. It can also analyze data from multiple ethnic groups.

License GPL

Depends CompQuadForm, MASS, forestplot

URL https://github.com/randel/ofGEM

BugReports https://github.com/randel/ofGEM/issues

RoxygenNote 6.0.1

R topics documented:

---

forest_plot   *Forest plot*

Description

It makes a forest plot for gene-environment interactions (GxE) for each study and each SNP in a gene

Usage

```
forest_plot(coef, se, sort = TRUE, exp = FALSE)
```

Arguments

coef	the matrix for the GxE coefficients. Each row represents a SNP, and each column denotes a study. If the matrix has colnames and/or rownames for SNPs and studies respectively. They will be shown in the forest plot. This is the coefficients from linear regression or generalized liear models.
se	the matrix for the stand errors for GxE estimates. Each row represents a SNP, and each column denotes a study.
sort	logical. If TRUE, the SNPs are ordered by the mean effect sizes across different studies. The default is TRUE.
exp	logical. If TRUE, coef will be exponential transformed. This works for coefs obtained from logistic regressions. The default is FALSE.

Value

A forest plot for each study ordered by SNPs.

Examples

```
coef = matrix(rnorm(6 * 6), 6, 6)
se = matrix(abs(runif(6 * 6, 0.1, 0.15)), 6, 6)

forest_plot(coef, se)
```

---

ofGEM	*A meta-analysis approach with filtering for identifying gene-level gene-environment interactions with genetic association data*

Description

This function first conducts a meta-filtering test to filter out unpromising SNPs. It then runs a test of omnibus-filtering-based GxE meta-analysis (ofGEM) that combines the strengths of the fixed- and random-effects meta-analysis with meta-filtering. It can also analyze data from multiple ethnic groups. The p-values are calculated using a sequential sampling approach.

Usage

```
ofGEM(Z, X, R, weight, threshold = 0.1, maxSim = 1e+06, tol = 10)
```

Arguments

Z	the test statistics for gene-environment interactions (GxE). Each row is a SNP, and each column is a study. For multi-ethnic groups, Z is a list with each element as a matrix for each ethnic group.
X	the filtering statistics for GxE. Each row is a SNP, and each column is a study. For multi-ethnic groups, x is a list with each element as a matrix for each ethnic group.
R	the correlation matrix to simulate test and filtering statistics under the null distribution. The simulated test and filtering statistics are used for testing. For multi-ethnic groups, R is a list with each element as a correlation matrix for each ethnic group.

weight	the weight vector for each study, or the weight matrix for each SNP and each study. If the weight is common across SNPs, it is a vector with a length equal to the number of studies. If the weight is different across SNPs, it is a matrix with each row for a SNP and each column as a study.
threshold	a fixed p-value threshold for filtering. The default is 0.1.
maxSim	the maximum number of samples to be simulated for the test and filtering statistics under the null. The default is 1e6.
tol	the tolerance number to stop the sequential sampling procedure. We count the number of simulated test statistics with an absolute value larger than that of the calculated one based on the data for every 100 simulations. The sampling will stop if the count reaches tol. The default is 10. If tol = 0, the number of simulations equals to maxSim.

Value

A list containing

pval_random_mf	the p-value based on random-effects meta-analysis with meta-filtering.
pval_fixed_mf	the p-value based on fixed-effects meta-analysis with meta-filtering.
pval_ofGEM	the p-value based on aggregating the p-values of fixed- and random-effects meta-analyses with meta-filtering using Fisher's method.
nsim	the number of simulations that are performed.

References

Wang, Liu, Pierce, Huo, Nicolae, Olopade, Ahsan, & Chen (2017+). A meta-analysis approach with filtering for identifying gene-level gene-environment interactions with genetic association data. In preparation.

Examples

```
data(sim_dat)

pval = ofGEM(Z = sim_dat$Z, X = sim_dat$X, R = sim_dat$R, weight = rep(1/6, 6))
```

---

sim_dat	*A Simulated Example data*

Description

This simulated data list is for demonstration.

Value

A list containing

Z	the simulated test statistics for GxE. Each row is a SNP, and each column is a study.
X	the simulated filtering statistics for GxE. Each row is a SNP, and each column is a study.
R	the simulated correlation matrix to simulate test and filtering statistics under the null distribution. The simulated test and filtering statistics are used for testing.

Examples

```
data(sim_dat)
```

Index