Usage

tanova(data, f 1, f2, tp, B=100, FDR=0.05,robustify=FALSE, equal.size=FALSE, longitudinal=TRUE, test.type=0, eb=FALSE, df=0)

Arguments

Data: a num eric gene-by-array matrix. Each row is a gene and each colum n is an array. Longitudinal time course microarrays from the same subject should be consecutive. For example, if there are two subjects A and B. Each has three arrays m easured at tim e 1, 2 and 3. Then the array order should be : A1,A2,A3,B1,B2,B3.

f1: a num eric vector for the firs t factor. The leng th of f1 is e qual to the number of arrays. E ach component of f1 indicates the factor level fo r the corresponding array. The levels should be integers and start from 1.

f2: a numeric vector for the second factor. The length of f2 is equal to the number of arrays. Each component of f2 indicates the factor level fo r the corresponding array. The levels should be integers and start from 1.

tp: a numeric vector for tim e course. The length of tp is equal to th e num ber of arrays. Each component of tp indicates the tim e point for the corresponding arra y. The first tim e point is 1, second time point 2, etc. For non-time course microarrays, set tp=0.

B: number of bootstraps.

FDR: control false discovery rate.

robustify: TRUE or FALSE. If TRUE, the robust statistic will be used.

equal.size: TRUE or FALSE. TRUE for balanced factorial designs.

longitudinal: TRUE or FALSE. TRUE for long itudinal tim e course m icroarrays. FALSE for cross-sectional time course microarrays.

test.type: num eric value 0, 1, 2, 3 or 4. 0: for ge ne classification. The gene s will be classified into five groups according to factor effects (C 1: interactive group; C2: additive group; C3: main effect f1 only; C4: main effect f2 only; C5: no factor effects). 1: test interaction effect; 2: test any factor effect (one-way ANOVA); 3: test main effect f1; 4: test main effect f2.

eb: TRUE or FALSE. TRUE: empirical Bayes estimation for the variance-covariance matrix.

df: integer value. 0: no regular ization of ANOVA direction. Otherwise, the ANOVA direction will be regularized by cubic splines with degrees of freedom equal to the value of df.

Value

If test.type=0. The genes will be classified in to give groups. The function returns a list with the following components:

C1: a vector of the row index of genes classified to C1.

C2: a vector of the row index of genes classified to C2.

C3: a vector of the row index of genes classified to C3.

C4: a vector of the row index of genes classified to C4.

C1.pvalue: a vector of p-values for the interaction effect of C1 genes.

C2.pvalue: a vector of p-values for any factor effect (one-way ANOVA) of C2 genes.

C3.pvalue: a vector of p-values for the main effect f1 of C3 genes.

C4.pvalue: a vector of p-values for the main effect f2 of C4 genes.

C1.delta: a vector of z-scores for th e interaction effect of C1 genes. The z-scores gives the genes a better rank than p-values.

C2.delta: a vector of z-scores for any factor effect (one-way ANOVA) of C2 genes.

C3.delta: a vector of z-scores for the main effect f1 of C3 genes.

C4.delta: a vector of z-scores for the main effect f2 of C4 genes.

a1: a m atrix of the ANOVA direction of C1 ge nes. Each row is the ANOVA direction f or the corresponding C1 genes.

a2: a m atrix of the ANOVA direction of C2 ge nes. Each row is the ANOVA direction f or the corresponding C2 genes.

a3: a m atrix of the ANOVA direction of C3 ge nes. Each row is the ANOVA direction f or the corresponding C3 genes.

a4: a m atrix of the ANOVA direction of C4 ge nes. Each row is the ANOVA direction f or the corresponding C4 genes.

If test.type=1, 2, 3 or 4. The func tion returns the result of testi ng ANOVA structures. The returned list has the following components:

genes: a vector of the row index of significant genes.

pvalue: a vector of the p-values of significant genes.

delta: z-scores of significant genes, which gives the gene rank.

a: a matrix of the ANOVA direction of significant genes. Each row is the ANOVA direction of the gene.

An example:

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data<-matrix(rnorm(1000*36),nrow=1000,ncol=36)

f1<-rep(c(1,2,1,2,1,2),time=6)

f2<-rep(c(1,1,1,2,2,2),time=6)

tp<-rep(c(1,2,3),each=12)

o<-tanova(data=data,f1=f1,f2=f2,tp=tp,test.type=1)

o$genes

o$pvalue

o$delta

o$a
```