| coXpress {coXpress} | R Documentation |
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## Find differentially co-expressed groups of genes

### **Description**

coXpress finds groups of genes that are highly correlated in one set of experiments, but no more correlated than can be expected by chance in a second set of experiments.

### **Usage**

****coXpress(d, groups, g1 = NULL, g2 = NULL, whichgroups = NULL, method = "single",

times = 100)

### **Arguments**

| d | a data frame or matrix |
| --- | --- |
| groups | a vector of group memberships as returned by [cutree](http://127.0.0.1:38671/help/library/coXpress/help/cutree) |
| g1 | a vector indicating the columns of the data frame or matrix corresponding to the first condition |
| g2 | a vector indicating the columns of the data frame or matrix corresponding to the second condition |
| whichgroups | a vector of group numbers to examine |
| method | currently only one method is implemented, the default, "single" |
| times | the number of times to randomly sample the data set for each group size |

### **Details**

Groups of genes should be defined by first clustering genes based on a control group of experiments (using [cluster.gene](http://127.0.0.1:38671/help/library/coXpress/help/cluster.gene)) and then cutting the tree using [cutree](http://127.0.0.1:38671/help/library/coXpress/help/cutree).

This function, coXpress, then examines each group, produces a summary statistic of the correlation matrix in the sets of experiments defined by g1 and g2, and then compares those statistic to distributions of n similar summary statistics, generated by selecting groups of random genes of the same size from the same data set.

In the current implemented method, "single", the summary statistic used is the t-statistic taken from a test of the unique, pairwise, pearson correlation coefficents against zero. The proportions of random statistics above the observed statistic are used to create a "probability of randomness" for each group in the two sets of experiments.

A group of genes whose distribution of pairwise correlations is found to be non-random in group 1, and random in group 2, is said to be differentially co-expressed.

### **Value**

A data frame with columns

| group | the number of the group defined in groups |
| --- | --- |
| N | the number of members (genes) in the group |
| t1 | the observed statistic in group 1 |
| t2 | the observed statistic in group 2 |
| pr.g1 | the proportion of random statistics greater than the observed in group 1 |
| pr.g2 | the proportion of random statistics greater than the observed in group 2 |
| mean.corr1 | the mean pearson correlation coefficient between members of the group in the first set of experiments |
| mean.corr2 | the mean pearson correlation coefficient between members of the group in the second set of experiments |
| mean.diff | the mean, pairwise difference between the correlation matrices from the two sets of experiments |

### **Author(s)**

Michael Watson

### **See Also**

[cluster.gene](http://127.0.0.1:38671/help/library/coXpress/help/cluster.gene), [cutree](http://127.0.0.1:38671/help/library/coXpress/help/cutree)

### **Examples**

[Run examples](http://127.0.0.1:38671/help/library/coXpress/Example/coXpress)

 data(golub)

# cluster the data based on the ALL samples

hc.gene <- cluster.gene(golub.df[,1:27],s="pearson",m="average")

# cut the tree at a height of 0.4 (equates to pearson correlation of 0.6)

g <- cutree(hc.gene, h=0.4)

# examine the difference between ALL and AML samples

cox <- coXpress(golub.df, g, 1:27, 28:38)

# examine the top 30

cox[1:30,]

# look at group 21

plot.compare.group(golub.df,g,21,1:27,28:38,

scale.center=TRUE,scale.scale=TRUE,

ylim=c(-5,5))

inspect.group(golub.df,g,21,1:27,28:38)

golub.gnames[g==21,]

# look for groups of genes with >= 10 members

cox[cox$N>=10,]

# look for groups of genes with >= 8 members

# that are non-random in group 1 and random

# in group 2

cox[cox$N>8 & cox$pr.g1<=.05 & cox$pr.g2>=.05, ]

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[Package *coXpress* version 1.5 [Index](http://127.0.0.1:38671/help/library/coXpress/html/00Index.html)]