

# Package ‘MantelCorr’

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**Title** Compute Mantel Cluster Correlations

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**Description** Computes Mantel cluster correlations from a (p x n)  
numeric data matrix (e.g. microarray gene-expression data).

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**Depends** R (>= 2.10)

**Imports** stats

**License** GPL (>= 2)

**biocViews** Clustering

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| ClusterGeneList | <i>Generate Genes from a Cluster List</i> |
|-----------------|-------------------------------------------|

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## Description

'ClusterGeneList' produces a list of both significant and nonsignificant genes from each respective cluster type

## Usage

```
ClusterGeneList(clus, clustlist.sig, x.data)
```

## Arguments

|               |                                                                   |
|---------------|-------------------------------------------------------------------|
| clus          | 'clusters' object returned by 'GetClusters'                       |
| clustlist.sig | 'SignificantClusters' object returned by 'ClusterList'            |
| x.data        | original (p x n) numeric data matrix (e.g., gene-expression data) |

## Value

A list with components:

SignificantClusterGenes

significant cluster genes returned from 'ClusterList'

NonSignificantClusterGenes

nonsignificant cluster genes returned from 'ClusterList'

## Note

argument 'x.data' should have an ID gene variable, 'probes', attached as a 'dimnames' attribute

## Author(s)

Brian Steinmeyer

## See Also

'GetClusters' 'ClusterList'

## Examples

```
# simulate a p x n microarray expression dataset, where p = genes and n = samples
data.sep <- rbind(matrix(rnorm(1000), ncol=50), matrix(rnorm(1000, mean=5), ncol=50))
noise <- matrix(runif(40000), ncol=1000)
data <- t(cbind(data.sep, noise))
data <- data[1:200, ]
# data has p = 1,050 genes and n = 40 samples
```

```
clusters.result <- GetClusters(data, 100, 100)
dist.matrices <- DistMatrices(data, clusters.result$clusters)
mantel.corr <- MantelCorrs(dist.matrices$Dfull, dist.matrices$Dsubsets)
permutation.result <- PermutationTest(dist.matrices$Dfull, dist.matrices$Dsubsets, 100, 40, 0.05)

# generate both significant and non-significant gene clusters
cluster.list <- ClusterList(permutation.result, clusters.result$cluster.sizes, mantel.corr)

# significant and non-significant cluster genes (expression values)
cluster.genes <- ClusterGeneList(clusters.result$clusters, cluster.list$SignificantClusters, data)
```

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**ClusterList***Generate a Cluster List*

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### Description

'ClusterList' generates a list of both significant and nonsignificant clusters, with cluster number, Mantel cluster correlation and size

### Usage

```
ClusterList(p.val, clus.size, mantel.corr)
```

### Arguments

|             |                                                                        |
|-------------|------------------------------------------------------------------------|
| p.val       | permutation p-value returned from 'PermutationTest'                    |
| clus.size   | vector of k cluster sizes returned from 'GetCluster'                   |
| mantel.corr | original, unpermuted k Mantel correlations returned from 'MantelCorrs' |

### Value

A list with components:

SignificantClusters

clusters with significant Mantel correlation, equal to or larger than the permutation p-value returned by 'PermutationTest'

NonSignificantClusters

clusters with nonsignificant Mantel correlation, smaller than the permutation p-value returned by 'PermutationTest'

### Author(s)

Brian Steinmeyer

### See Also

'PermutationTest'

**Examples**

```
# simulate a p x n microarray expression dataset, where p = genes and n = samples
data.sep <- rbind(matrix(rnorm(1000), ncol=50), matrix(rnorm(1000, mean=5), ncol=50))
noise <- matrix(runif(40000), ncol=1000)
data <- t(cbind(data.sep, noise))
data <- data[1:200, ]
# data has p = 1,050 genes and n = 40 samples

clusters.result <- GetClusters(data, 100, 100)
dist.matrices <- DistMatrices(data, clusters.result$clusters)
mantel.corrs <- MantelCorrs(dist.matrices$Dfull, dist.matrices$Dsubsets)
permutation.result <- PermutationTest(dist.matrices$Dfull, dist.matrices$Dsubsets, 100, 40, 0.05)

# generate both significant and non-significant gene clusters
cluster.list <- ClusterList(permutation.result, clusters.result$cluster.sizes, mantel.corrs)
```

---

|              |                                       |
|--------------|---------------------------------------|
| DistMatrices | <i>Compute Dissimilarity Matrices</i> |
|--------------|---------------------------------------|

---

**Description**

'DistMatrices' uses 'dist' to compute dissimilarity matrices for 'data' and each cluster k from 'GetClusters'

**Usage**

```
DistMatrices(x.data, cluster.assignment)
```

**Arguments**

|                    |                                                                  |
|--------------------|------------------------------------------------------------------|
| x.data             | original 'data' matrix                                           |
| cluster.assignment | cluster assignment vector, "clusters", returned by 'GetClusters' |

**Value**

returns a list with two components:

|          |                                              |
|----------|----------------------------------------------|
| Dsubsets | dissimilarity matrices for each cluster k    |
| Dfull    | dissimilarity matrix for the original 'data' |

**Note**

'GetClusters' should be executed prior to 'DistMatrices'

**Author(s)**

Brian Steinmeyer

See Also

'GetClusters'

Examples

```
# simulate a p x n microarray expression dataset, where p = genes and n = samples
data.sep <- rbind(matrix(rnorm(1000), ncol=50), matrix(rnorm(1000, mean=5), ncol=50))
noise <- matrix(runif(40000), ncol=1000)
data <- t(cbind(data.sep, noise))
data <- data[1:200, ]
# data has p = 1,050 genes and n = 40 samples

clusters.result <- GetClusters(data, 100, 100)
dissimilarity.matrices <- DistMatrices(data, clusters.result$clusters)
```

---

|             |                                                            |
|-------------|------------------------------------------------------------|
| GetClusters | <i>Over-Partition a (p x n) Data Matrix using 'kmeans'</i> |
|-------------|------------------------------------------------------------|

---

Description

'GetClusters' uses an overly large k with the 'kmeans' function to over-partition p variables (rows = genes) from n objects (cols = samples) from a given data matrix 'x.data'

Usage

```
GetClusters(x.data, num.k, num.iters)
```

Arguments

|           |                                         |
|-----------|-----------------------------------------|
| x.data    | p x n data matrix of numeric values     |
| num.k     | number of k partitions desired          |
| num.iters | number of iterations - recommend >= 100 |

Value

'GetClusters' returns a list with the following components:

|               |                                      |
|---------------|--------------------------------------|
| clusters      | cluster assignment from 'kmeans'     |
| cluster.sizes | size of each cluster k from 'kmeans' |

Note

The input data matrix, x.data, must be numeric (e.g., gene-expression values). We recommend using 'num.k' = one-half the number of genes and 'num.iters' greater than 50

**Author(s)**

Brian Steinmeyer

**See Also**

'kmeans'

**Examples**

```
# simulate a p x n microarray expression dataset, where p = genes and n = samples
data.sep <- rbind(matrix(rnorm(1000), ncol=50), matrix(rnorm(1000, mean=5), ncol=50))
noise <- matrix(runif(40000), ncol=1000)
data <- t(cbind(data.sep, noise))
data <- data[1:200, ]
# data has p = 1,050 genes and n = 40 samples

clusters.result <- GetClusters(data, 100, 100)
```

---

GolubTrain

*Golub Training Set*

---

**Description**

Samples were taken with Affymetrix Hgu6800 chips and expression levels measured on 7,129 genes (probes). The samples consist of 27 acute lymphoblastic leukemia (ALL) and 11 acute myeloid leukemia (AML) patients. The data values are raw (e.g. no standardization or gene filtering applied).

**Usage**

```
data(GolubTrain)
```

**Format**

A data frame of 7129 observations (genes) with the following 38 variables (samples):

**X1** ALL  
**X2** ALL  
**X3** ALL  
**X4** ALL  
**X5** ALL  
**X6** ALL  
**X7** ALL  
**X8** ALL  
**X9** ALL

**X10** ALL  
**X11** ALL  
**X12** ALL  
**X13** ALL  
**X14** ALL  
**X15** ALL  
**X16** ALL  
**X17** ALL  
**X18** ALL  
**X19** ALL  
**X20** ALL  
**X21** ALL  
**X22** ALL  
**X23** ALL  
**X24** ALL  
**X25** ALL  
**X26** ALL  
**X27** ALL  
**X28** AML  
**X29** AML  
**X30** AML  
**X31** AML  
**X32** AML  
**X33** AML  
**X34** AML  
**X35** AML  
**X36** AML  
**X37** AML  
**X38** AML

**Source**

<http://www.broad.mit.edu/cgi-bin/cancer/datasets.cgi>

**References**

Golub, T.R. Molecular Classification of Cancer: Class Discovery and Class Prediction by Gene Expression Monitoring. Science, vol 286, 531-537, 1999.

**Examples**

```
data(GolubTrain)
```

---

MantelCorrs

---

*Compute Mantel Correlation(s)*


---

### Description

'MantelCorrs' computes the Mantel correlation between two dissimilarity matrices

### Usage

```
MantelCorrs(Dfull, Dsubsets)
```

### Arguments

|          |                                                                                       |
|----------|---------------------------------------------------------------------------------------|
| Dfull    | distance matrix returned by 'DistMatrices' using original 'data'                      |
| Dsubsets | list of distance matrices from each k cluster or partition returned by 'DistMatrices' |

### Value

A list with k components

where component i

Mantel correlation for cluster i,  $i = 1, \dots, k$

### Warning

The function is meant to be executed AFTER 'GetClusters' and 'DistMatrices' (see example)

### Note

the value 'k' corresponds to the parameter 'num.k' in 'GetClusters'

### Author(s)

Brian Steinmeyer

### References

Mantel N: The detection of disease clustering and a generalized regression approach. Cancer Research. 27(2), 209-220 (1967).

### See Also

'GetClusters' 'DistMatrices' 'kmeans'

**Examples**

```
# simulate a p x n microarray expression dataset, where p = genes and n = samples
data.sep <- rbind(matrix(rnorm(1000), ncol=50), matrix(rnorm(1000, mean=5), ncol=50))
noise <- matrix(runif(40000), ncol=1000)
data <- t(cbind(data.sep, noise))
data <- data[1:200, ]
# data has p = 1,050 genes and n = 40 samples

clusters.result <- GetClusters(data, 100, 100)
dist.matrices <- DistMatrices(data, clusters.result$clusters)
mantel.corrs <- MantelCorrs(dist.matrices$Dfull, dist.matrices$Dsubsets)
```

PermutatonTest

*Permutation Test for Dissimilarity Matrices***Description**

'PermutationTest' computes and returns an empirical p-value from a null distribution generated by permuting 'Dfull' a total of 'num.per' times.

**Usage**

```
PermutationTest(Dfull, Dsubsets, num.per, num.chips, alpha)
```

**Arguments**

|           |                                                                                |
|-----------|--------------------------------------------------------------------------------|
| Dfull     | dissimilarity matrix from the original (p x n) microarray expression data      |
| Dsubsets  | dissimilarity matrices from each k disjoint clusters returned by 'GetClusters' |
| num.per   | number of permutations                                                         |
| num.chips | number of samples, 'n' from the original (p x n) data matrix                   |
| alpha     | desired level of significance                                                  |

**Details**

For each permutation, k Mantel correlations are computed by correlating the permuted 'Dfull' with each dissimilarity matrix 'Dsubsets' from the 'k' clusters returned by 'GetClusters'. The absolute value of the maximum Mantel cluster correlation is retained at each permutation. These 'num.per' maximum correlations are then used to generate a null distribution for distance metric independence, with the p-value taken from the (1 - 'alpha') percentile of this permutation distribution.

**Value**

returns the permuted p-value for the 'alpha' selected level of significance

**Warning**

(p x n) data matrix should be numeric (e.g. gene-expression levels)

**Note**

The function is meant to be executed AFTER 'GetClusters', 'DistMatrices' and 'MantelCorr' (see example)

**Author(s)**

Brian Steinmeyer

**See Also**

'GetClusters' 'DistMatrices' 'MantelCorrs'

**Examples**

```
# simulate a p x n microarray expression dataset, where p = genes and n = samples
data.sep <- rbind(matrix(rnorm(1000), ncol=50), matrix(rnorm(1000, mean=5), ncol=50))
noise <- matrix(runif(40000), ncol=1000)
data <- t(cbind(data.sep, noise))
data <- data[1:200, ]
# data has p = 1,050 genes and n = 40 samples

clusters.result <- GetClusters(data, 100, 100)
dist.matrices <- DistMatrices(data, clusters.result$clusters)
mantel.corrs <- MantelCorrs(dist.matrices$Dfull, dist.matrices$Dsubsets)
permutation.result <- PermutationTest(dist.matrices$Dfull, dist.matrices$Dsubsets, 100, 40, 0.05)
```

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