

Package ‘phenoDist’

April 5, 2014

Version 1.10.0

Title Phenotypic distance measures

Author Xian Zhang, Gregoire Pau, Wolfgang Huber, Michael Boutros

Maintainer Xian Zhang <x.zhang@dkfz.de>

Depends R (>= 2.9.0), imageHTS, e1071

Suggests GOstats, MASS

Description

PhenoDist is designed for measuring phenotypic distance in image-based high-throughput screening, in order to identify strong phenotypes and to group treatments into functional clusters.

Reference

biocViews CellBasedAssays, Bioinformatics

License LGPL-2.1

URL <http://www.dkfz.de/signaling>,
http://www.embl.de/research/units/genome_biology/huber/

R topics documented:

clusterDist	2
ctlSeparatn	3
distToNeg	4
enrichAnalysis	5
PDMyFactorAnalysis	6
PDMyKS	8
PDMySvmAccuracy	9
PDMySvmWeightVector	10
PDMyWellAvg	11
repCorr	13
repDistRank	14

Index	15
--------------	-----------

`clusterDist`*clusterDist*

Description

Clustering analysis based on a distance matrix.

Usage

```
clusterDist(x, distMatrix, clusterFun=hclust, ...)
```

Arguments

<code>x</code>	An imageHTS object.
<code>distMatrix</code>	A pair-wise distance matrix or a dist object.
<code>clusterFun</code>	A character string defining the cluster function.
<code>...</code>	Additional arguments to be passed to the cluster function.

Details

This function performs a clustering analysis based on a pair-wise distance matrix such as generated by PDMSvmAccuracy.

Value

The return from the cluster function, such as an hclust object returned from the hclust function.

Author(s)

Xian Zhang

See Also

hclust, PDMSvmAccuracy

Examples

```
library(phenoDist)

## load the imageHTS object
load(system.file(kimorph, kimorph.rda, package=phenoDist))
x@localPath <- file.path(tempdir(), kimorph)

## load sample phenotypic distance matrix
load(system.file(kimorph, svmAccPDM_P11.rda, package=phenoDist))

## phenotypic clustering
```

```
phenoCluster <- clusterDist(x, distMatrix=svmAccPDM_P11, clusterFun=hclust, method=ward)

## Not run:
require(GOstats)
GOEnrich <- enrichAnalysis(x, cl=cutree(phenoCluster, k=5), terms=GO, annotation=org.Hs.eg.db, pvalueCutoff=0.0)

## End(Not run)
```

`ctlSeparatn`*Calculate control separation*

Description

This function calculates the Z' -factor between negative and positive controls, based on phenotypic distance measurements.

Usage

```
ctlSeparatn(x, pheno, neg=rLuc, pos=ubc, ...)
```

Arguments

<code>x</code>	An imageHTS object.
<code>pheno</code>	A numeric vector for distances to negative controls, as returned from <code>distToNeg</code> .
<code>neg</code>	A character string to identify negative controls.
<code>pos</code>	A character string to identify positive controls.
<code>...</code>	Additional arguments to be passed to the <code>Zprime</code> function of the <code>imageHTS</code> package.

Details

Phenotypes of negative and positive controls are defined as their phenotypic distance to negative controls. The Z' -factor is a metric measuring the separation between negative controls and positive controls (Zhang et al. 1999). This function calls the `Zprime` function of the `imageHTS` package to calculate the Z' -factor. Please see `Zprime` for detailed description of the definition and calculation of the Z' -factor.

Value

The Z' -factor value.

Author(s)

Xian Zhang

References

J. H. Zhang, T. D. Chung, K. R. Oldenburg. A Simple Statistical Parameter for Use in Evaluation and Validation of High Throughput Screening Assays. *J Biomol Screening*, 1999.

See Also

`distToNeg`, `Zprime`

Examples

```
## see distToNeg.
```

<code>distToNeg</code>	<i>distToNeg</i>
------------------------	------------------

Description

From a pair-wise distance matrix, this function extracts the corresponding distance between a sample and negative controls.

Usage

```
distToNeg(x, distMatrix, neg=r1uc)
```

Arguments

<code>x</code>	An imageHTS object
<code>distMatrix</code>	A pair-wise distance matrix, as generated by <code>PDMSvmAccuracy</code> .
<code>neg</code>	A character string to identify negative controls.

Details

This function averages the distance measurements between the sample and all negative controls on the same plate.

Value

A numeric vector with length equal to the dimension of the distance matrix.

Author(s)

Xian Zhang

See Also

`PDMSvmAccuracy`

Examples

```
library(phenoDist)

## load the imageHTS object
load(system.file(kimorph, kimorph.rda, package=phenoDist))
x@localPath <- file.path(tempdir(), kimorph)

## load sample phenotypic distance matrix
load(system.file(kimorph, svmAccPDM_P11.rda, package=phenoDist))

## replicate ranking
ranking <- repDistRank(x, distMatrix=svmAccPDM_P11)
summary(ranking)

## phenotypic distance to negative control
pheno <- distToNeg(x, distMatrix=svmAccPDM_P11, neg=r1uc)

## separation between negative and positive controls
ctlSeparatn(x, pheno, neg=r1uc, pos=ubc, method=robust)

## replicate correlation coefficient
repCorr(x, pheno)
```

enrichAnalysis

enrichAnalysis

Description

This function performs enrichment analysis on genes within each cluster, with genes from all clusters as the gene universe.

Usage

```
enrichAnalysis(x, cl, terms=c(GO,KEGG), verbose=FALSE, ...)
```

Arguments

x	An imageHTS object.
cl	A named numeric vector, with names being gene Entrez IDs and values indicating grouping.
terms	A character string indicating which annotation should be used. This must be (an abbreviation of) one of the strings 'GO' or 'KEGG'.
verbose	A logical scalar indicating whether progress should be reported.
...	Additional arguments to be passed to the hyperGTest function of the GOstats package.

Details

Gene enrichment analysis tests whether certain gene annotations (e.g., GO terms or KEGG ids) are enriched in genes of interest, compared with the gene universe. This function is designed to analyze gene enrichment in clusters, with genes in the tested cluster being genes of interest and genes in all clusters being the gene universe.

The Hypergeometric test is performed by the `hyperGTest` function of the `GOstats` package. Please refer to `hyperGTest` for additional arguments.

Value

A list of `HyperGResult` instances.

Author(s)

Xian Zhang

See Also

`GOstats`, `clusterDist`

Examples

```
## see clusterDist.
```

PDMyFactorAnalysis *Calculate phenotypic distance matrix by factor analysis*

Description

This function transforms the cell features by factor analysis and computes the phenotypic distance matrix.

Usage

```
PDMyFactorAnalysis(x, unames, selectedCellFtrs, distMethod=c(manhattan,euclidean, correlation,mahalanobis))
```

Arguments

<code>x</code>	An <code>imageHTS</code> object.
<code>unames</code>	A character vector, containing the well names from where to collect the cell features. See <code>getUnames</code> for details.
<code>selectedCellFtrs</code>	A character vector for cell features to be used in the calculation. If missing, all features are used.

<code>distMethod</code>	A character string indicating which distance method should be used. This must be (an abbreviation of) one of the strings 'manhattan', 'euclidean', 'correlation' or 'mahalanobis'.
<code>nFactors</code>	An integer scalar for the number of factors.
<code>scores</code>	A character string indicating the type of scores to be reported by factor analysis. This must be (an abbreviation of) one of the strings 'regression' or 'Bartlett'.
<code>...</code>	Additional arguments to be passed to the <code>factanal</code> function of the <code>stats</code> package.

Details

This function first collects individual cell features in all wells (which could be time and memory consuming), performs factor analysis on cell features and transforms cell features into a certain number of factors, and then the factors are averaged by well and passed to `PDMyWellAvg` to calculate the phenotypic distance matrix.

Value

A symmetric distance matrix with dimensions equaling to the length of `unames`.

Author(s)

Xian Zhang

See Also

`factanal`, `PDMyWellAvg`

Examples

```
library(phenoDist)

## load the imageHTS object
load(system.file(kimorph, kimorph.rda, package=phenoDist))
x@localPath <- file.path(tempdir(), kimorph)

## segmentation and feature extraction
unames <- setdiff(getUnames(x), getUnames(x, content=empty))

## calculate pair-wise svm distance matrix
load(system.file(kimorph, selectedFtrs.rda, package=phenoDist))
pdm <- PDMyFactorAnalysis(x, unames=getUnames(x, plate=1, row=2:3, col=3), selectedCellFtrs, distMethod=euclidean)
pdm
```

PDMyKS

Compute phenotypic distance matrix by Kolmogorov-Smirnov statistics

Description

This function calculates the Kolmogorov-Smirnov statistic between a given sample and the negative control, for each feature, and then computes the phenotypic distance matrix based on the Kolmogorov-Smirnov statistics.

Usage

```
PDMyKS(x, unames, neg=rluc, selectedCellFtrs, distMethod=c(manhattan, euclidean, correlation, mahalanobis))
```

Arguments

x	An imageHTS object.
unames	A character vector, containing the well names from where to collect the cell features. See <code>getUnames</code> for details.
neg	A character string to identify negative controls.
selectedCellFtrs	A character vector for cell features to be used in the calculation. If missing, all features are used.
distMethod	A character string indicating which distance method should be used. This must be (an abbreviation of) one of the strings 'manhattan', 'euclidean', 'correlation' or 'mahalanobis'.

Details

For each well, this function collects features of all cells, and performs a Kolmogorov-Smirnov test for each feature against the corresponding cell features from negative control wells, with the function `ks.test` of the `stats` package. The Kolmogorov-Smirnov statistics are collected for all wells and passed to `PDMyWellAvg` to calculate the phenotypic distance matrix.

Value

A symmetric distance matrix with the number of rows equaling to the length of `unames`.

Author(s)

Xian Zhang

See Also

`ks.test`, `PDMyWellAvg`

Examples

```
library(phenoDist)

## load the imageHTS object
load(system.file(kimorph, kimorph.rda, package=phenoDist))
x@localPath <- file.path(tempdir(), kimorph)

## calculate pair-wise svm distance matrix
load(system.file(kimorph, selectedFtrs.rda, package=phenoDist))
pdm <- PDMSvmAccuracy(x, unames=getUnames(x,plate=1, row=2:3, col=3), neg=rluc, selectedCellFtrs=selectedCellFtrs, dist=dist, verbose=TRUE)
pdm
```

PDMSvmAccuracy

Compute phenotypic distance matrix by SVM classification accuracy

Description

This function performs an SVM classification between two given samples, and calculates the classification accuracy via cross validation as the phenotypic distance between the two samples. For multiple samples, the function returns a pair-wise distance matrix.

Usage

```
PDMSvmAccuracy(x, unames, selectedCellFtrs, cross=5, verbose=FALSE, ...)
```

Arguments

<code>x</code>	An imageHTS object.
<code>unames</code>	A character vector, containing the well names from where to collect the cell features. See <code>getUnames</code> for details.
<code>selectedCellFtrs</code>	A character vector for cell features to be used in the calculation. If missing, all features are used.
<code>cross</code>	An interger scalar indicating how many folds of cross validation should be performed.
<code>verbose</code>	A logical scalar indicating whether progress should be reported.
<code>...</code>	Additional arguments to be passed to the <code>svm</code> function of the <code>e1071</code> package.

Details

For every pair of wells, this function collects features of all cells from both wells, and performs a bi-class classification using Support Vector Machine (SVM). The classification accuracy is defined as the phenotypic distance for the distance matrix.

Value

A symmetric distance matrix with the number of rows equaling to the length of unames.

Author(s)

Xian Zhang

See Also

svm

Examples

```
library(phenoDist)

## load the imageHTS object
load(system.file(kimorph, kimorph.rda, package=phenoDist))
x@localPath <- file.path(tempdir(), kimorph)

## calculate pair-wise svm distance matrix
load(system.file(kimorph, selectedFtrs.rda, package=phenoDist))
pdm <- PDmBySvmAccuracy(x, unames=getUnames(x, plate=1, row=2:3, col=3), selectedCellFtrs=selectedCellFtrs, cross=TRUE)
```

PDmBySvmWeightVector *Compute phenotypic distance matrix by SVM weight vector*

Description

This function performs an SVM classification between a given sample and the negative control, calculates the weight vector, and then computes the phenotypic distance matrix based on the weight vectors.

Usage

```
PDmBySvmWeightVector(x, unames, neg=rluc, selectedCellFtrs, distMethod=c(manhattan,euclidean,correlation))
```

Arguments

x	An imageHTS object.
unames	A character vector, containing the well names from where to collect the cell features. See getUnames for details.
neg	A character string to identify the negative controls.
selectedCellFtrs	A character vector for cell features to be used in the calculation. If missing, all features are used.

distMethod	A character string indicating which distance method should be used. This must be (an abbreviation of) one of the strings 'manhattan', 'euclidean', 'correlation' or 'mahalanobis'.
verbose	A logical scalar indicating whether progress should be reported.
kernel	The kernel argument for the svm function of the e1071 package.
...	Additional arguments to be passed to the svm function of the e1071 package.

Details

For each well, this function collects features of all cells from the well and all cells from the negative control wells, and performs a bi-class classification using Support Vector Machine (SVM). The classification weight vectors are calculated for all wells passed to PDMyWellAvg to compute the phenotypic distance matrix.

Value

A symmetric distance matrix with dimensions equaling to the length of unames.

Author(s)

Xian Zhang

See Also

svm, PDMyWellAvg

Examples

```
library(phenoDist)

## load the imageHTS object
load(system.file(kimorph, kimorph.rda, package=phenoDist))
x@localPath <- file.path(tempdir(), kimorph)

## calculate pair-wise svm distance matrix
load(system.file(kimorph, selectedFtrs.rda, package=phenoDist))
pdm <- PDMySvmWeightVector(x, unames=getUnames(x,plate=1, row=2:3, col=3), neg=rluc, selectedCellFtrs=selected
```

PDMyWellAvg

Compute phenotypic distance matrix with well features

Description

This function computes the phenotypic distance matrix, with cell features averaged by well.

Usage

```
PDMyWellAvg(profiles, selectedWellFtrs, transformMethod=c(none, scale, PCA), distMethod=c(manhattan
```

Arguments

profiles	A data frame, containing the phenotypic profiles, as returned from the summarizeWells function of the imageHTS package.
selectedWellFtrs	A character vector indicating well features to be used in the calculation. If missing, all features are used.
transformMethod	A character string indicating which transformation method should be used. This must be (an abbreviation of) one of the strings 'none', 'scale' or 'PCA'.
distMethod	A character string indicating which distance method should be used. This must be (an abbreviation of) one of the strings 'manhattan', 'euclidean', 'correlation' or 'mahalanobis'.
nPCA	An integer scalar for the number of PCA dimensions to be used in the calculation.

Details

Pair-wise phenotypic distance measurements of the treatments in screen results in a phenotypic distance matrix. The features stored in profiles are transformed with the transformMethod and the distance matrix is calculated with the distMethod.

Value

A symmetric distance matrix with dimensions equaling to the number of rows of profiles.

Author(s)

Xian Zhang

See Also

summarizeWells

Examples

```
library(phenoDist)

## load the imageHTS object
load(system.file(kimorph, kimorph.rda, package=phenoDist))
x@localPath <- file.path(tempdir(), kimorph)

## calculate pair-wise svm distance matrix
load(system.file(kimorph, selectedFtrs.rda, package=phenoDist))
pdm <- PDMyWellAvg(profiles=summarizeWells(x, getUnames(x,plate=1, row=2:3, col=3), conf/featurepar.txt), sele
pdm
```

repCorr	<i>repCorr</i>
---------	----------------

Description

This function calculates the correlation between replicate phenotypes.

Usage

```
repCorr(x, pheno, ...)
```

Arguments

x	An imageHTS object.
pheno	A numeric vector for distance measures to negative control, as returned from <code>distToNeg</code> .
...	Additional arguments to be passed to the <code>cor</code> function of the <code>stats</code> package.

Value

Correlation coefficient returned from the `cor` function of the `stats` package.

Author(s)

Xian Zhang

See Also

`cor`, `distToNeg`

Examples

```
## see distToNeg.
```

`repDistRank`*repDistRank*

Description

For each treatment, this function calculates the ranking of its replicate in terms of phenotypic distance.

Usage

```
repDistRank(x, distMatrix)
```

Arguments

`x` An imageHTS object.
`distMatrix` A pair-wise distance matrix or dist object.

Details

For each treatment, this function ranks the distance measure to its replicate among the distance measurements to all other treatments.

Value

A numeric vector with length equal to the dimension of the distance matrix.

Author(s)

Xian Zhang

See Also

`PDMyWellAvg`

Examples

```
## see distToNeg.
```

Index

clusterDist, [2](#)
ctlSeparatn, [3](#)

distToNeg, [4](#)

enrichAnalysis, [5](#)

PDMyFactorAnalysis, [6](#)
PDMyKS, [8](#)
PDMySvmAccuracy, [9](#)
PDMySvmWeightVector, [10](#)
PDMyWellAvg, [11](#)

repCorr, [13](#)
repDistRank, [14](#)