Package ‘YuGene’

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Type Package

Title A Simple Approach to Scale Gene Expression Data Derived from Different Platforms for Integrated Analyses

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Description Simple method for comparison of gene expression generated across different experiments, and on different platforms; that does not require global renormalization, and is not restricted to comparison of identical probes. YuGene works on a range of microarray dataset distributions, such as between manufacturers. The resulting output allows direct comparisons of gene expression between experiments and experimental platforms.

License GPL (>= 2)

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YuGene-package

Transforms expression datasets to cumulative proportion for comparison using YuGene transform

Description

YuGene is a simple transform that answers the question: where is my gene of interest? across a range of datasets without the need to re-normalise datasets under consideration.

Details

Package: YuGene
Type: Package
Version: 1.1.3
Date: 2015-07-30
License: GPL >= 2

This package provides a single function (YuGene). It takes a log transformed dataset (ie multiple microarray samples in an experiment) and converts the values to a cumulative proportion. Values close to zero have the lowest expression, and values close to 1 have the highest expression. When many datasets have been YuGene transformed, relative expression levels (YuGene values) can be directly compared across experiments without re-normalization without significant loss of sensitivity when compared to quantile normalized data.

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References

Combination of multiple array experiments

Description
Combination of 5 experiments. The data has been YuGene transformed, mapped to Ensembl ID. 2000 genes have been randomly selected.

Usage
data(array)

Format
A list containing the following components:
- data.all: Matrix of 82 samples and 2000 gene expression.
- experiment.all: a factor containing the name of the experiments.
- platform.all: a factor containing the platform of each sample.
- type.all: a factor containing the type of each sample.

Source
The data were downloaded from www.stemformatics.org.

References


Description

log2 transformed samples using Illumina HumanWG-6 chips, 3 of which were controls, and three of which were sampled after the addition of ascorbate to the medium. Details and data available by searching ‘ascorbate’ at www.stemformatics.org. This dataset is a random subset of 5000 genes for smaller package size and faster example times

Usage

data(ascorbate)

Format

A list containing the following components:

gene data frame with 48803 rows and 6 columns. The expression levels of 48803 transcripts for the 6 subjects.

condition a vector of 6 elements indicating the condition of each subject (‘4ng.ml’ or ‘100ng.ml’)

Source

The data were downloaded from www.stemformatics.org datasetID 5006.

References

### Arguments

**X**
- A numeric matrix (or data frame) which provides the data for the principal components analysis. It can contain missing values.

**ncomp**
- Integer, if data is complete `ncomp` decides the number of components and associated eigenvalues to display from the `pcasvd` algorithm and if the data has missing values, `ncomp` gives the number of components to keep to perform the reconstitution of the data using the NIPALS algorithm. If `NULL`, function sets ncomp = min(nrow(X), ncol(X))

**center**
- A logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of X can be supplied. The value is passed to `scale`.

**scale**
- A logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is `FALSE` for consistency with `prcomp` function, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of X can be supplied. The value is passed to `scale`.

**max.iter**
- Integer, the maximum number of iterations in the NIPALS algorithm.

**tol**
- A positive real, the tolerance used in the NIPALS algorithm.

... not used.

### Details

See [pca](#).

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**pca.YuGene**

- Principal component analysis for the 'YuGene' class.

### Description

Performs a principal components analysis thanks to the `pca` function of the `mixOmics` package. The data are centered by study before performing the analysis, if the argument study is given.

### Usage

```r
## S3 method for class 'YuGene'
pca(X, study, ncomp = 2, center = TRUE, scale = FALSE, max.iter = 500, tol = 1e-09, ...)
```

### Arguments

**X**
- A numeric matrix (or data frame) which provides the data for the principal components analysis. It can contain missing values.

**study**
- Factor of the study effect.
pca.YuGene

ncomp integer, if data is complete ncomp decides the number of components and associated eigenvalues to display from the pcasvd algorithm and if the data has missing values, ncomp gives the number of components to keep to perform the reconstitution of the data using the NIPALS algorithm. If NULL, function sets ncomp = \min(nrow(x), ncol(x))

center a logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of x can be supplied. The value is passed to scale.

scale a logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is FALSE for consistency with prcomp function, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of x can be supplied. The value is passed to scale.

max.iter integer, the maximum number of iterations in the NIPALS algorithm.

tol a positive real, the tolerance used in the NIPALS algorithm.

... not used.

Details

If the argument study is given, the data are centered per study prior to performing the PCA with the pca function of the mixOmics package. Otherwise, the PCA is performed on the input data x.

Value

Same outputs as the pca function from the mixOmics package.

pca returns a list with class "pca" and "prcomp" containing the following components:

ncomp the number of principal components used.

sdev the eigenvalues of the covariance/correlation matrix, though the calculation is actually done with the singular values of the data matrix or by using NIPALS.

rotation the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors).

X if retx is true the value of the rotated data (the centred (and scaled if requested) data multiplied by the rotation matrix) is returned.

center, scale the centering and scaling used, or FALSE.

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YuGene

References


Examples

```R
# load data
data(array)

YuGene.data=t(YuGene(t(array$data.all))) # transpose the data to get the samples in columns

# PCA on YuGene data, centered by study
res.pca.yugene.center = pca(YuGene.data, ncomp = 3, scale = TRUE, center = TRUE, study = array$experiment.all)
expl.var = round(res.pca.yugene.center$sdev/sum(res.pca.yugene.center$sdev),4)*100

# plot of the results, one color per cell-type, one shape per study
plot(res.pca.yugene.center$x[,1],res.pca.yugene.center$x[,2], pch = as.numeric(array$experiment.all), col = as.numeric(array$type.all)+1, lwd = 2, cex = 1.5, cex.lab = 1.5,xlab=paste("PC1: ",expl.var[1], ",","%"), ylab=paste("PC2: ",expl.var[2], ",","%"))
title(paste('YuGene multi group data'), cex.main = 1.5)

# PCA on YuGene data, not centered by study
res.pca.yugene = pca(YuGene.data, ncomp = 3, scale = TRUE, center = TRUE)
expl.var = round(res.pca.yugene$sdev/sum(res.pca.yugene$sdev),4)*100

# plot of the results, one color per cell-type, one shape per study
plot(res.pca.yugene$x[,1],res.pca.yugene$x[,2], pch = as.numeric(array$experiment.all), col = as.numeric(array$type.all)+1, lwd = 2, cex = 1.5, cex.lab = 1.5,x.label=paste("PC1: ",expl.var[1], ",","%"), Y.label=paste("PC2: ",expl.var[1], ",","%"))
title(paste('YuGene data'), cex.main = 1.5)
```

YuGene


Description

YuGene is a simple method for comparison of gene expression generated across different experiments, and on different platforms; that does not require global renormalization, and is not restricted to comparison of identical probes. YuGene works on a range of microarray dataset distributions, such as between manufacturers. The resulting output allows direct comparisons of gene expression between experiments and experimental platforms.
Usage

YuGene(data.prop, progressBar = TRUE)

Arguments

data.prop a matrix or data.frame of log intensity values, with samples in columns and expression levels in rows. Can be probe or transcript level. Can be raw or previously (i.e. quantile) normalized data.

progressBar set to FALSE to suppress progress bar

Value

returns an object of class ‘YuGene’: a matrix of the same dimensions with each sample transformed to the cumulative proportion (YuGene) metric.

Note

Support for missing values not yet implemented. Will implement if requested.

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References


See Also

pca

Examples

data(ascorbate) # gene expression data available in YuGene package
# apply the transform to the data
YuGene.transformed <- YuGene(ascorbate$gene)

# show distributions before and after YuGene
# make a copy of current settings
par(mfrow=c(1,2))
plot(density(ascorbategene[,1]),main='Expression values', xlab='log2 expr.');
plot(density(YuGene.transformed[,1]),main='YuGene values',xlab='YuGene value');
par(opar)  # restore original settings

# unadjusted pvals from the quantile normalized data
quant.pvals <- apply(ascorbategene,1,function(row){return(t.test(row[1:3],row[4:6])$p.value))
YuGene.pvals <- apply(YuGene.transformed,1,function(row){return(t.test(row[1:3],row[4:6])$p.value))
plot(quant.pvals,YuGene.pvals,pch='.',main='comparison of pvals before and after YuGene Transform')
text(0.8,0.2,paste("Pearson cor: ",round(cor(quant.pvals,YuGene.pvals,method='pearson'),digits=3))
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