

Package ‘digeR’

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Type Package

Title GUI tool for analyzing 2D DIGE data

Version 1.2

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Description An easy to use Graphical User Interfact for spots correlation analysis, score plot, classification, feature selection and power analysis for 2D DIGE experiment data.

Depends R (>= 2.6.0), gWidgets, MASS, pls, e1071, adabag, randomForest, ROCR, caTools, class, ellipse

License GPL (>= 2)

LazyLoad yes

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digeR-package	<i>digeR Graphical User Interface</i>
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Description

digeR is an easy to use GUI tool for 2D gel or 2D DIGE data analysis. It provides functions for spots correlation analysis, score plot, classification, feature selection and power anlaysis

Details

Package: digeR
 Type: Package
 Version: 1.2
 Date: 2009-07-26
 License: GPL (>= 2)
 LazyLoad: yes

The manual and example can be found with `vignette("digeR")`.

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digeR

digeR GUI

Description

Start the Graphical User Interface for digeR.

digeR supports spots correlation analysis, score plot, classification, feature selection and power analysis.

Usage

`digeR()`

Details

digeR GUI options:

File

Open

Upload_gel_image

Quit

Read in data and image, quit

upload the txt file

upload the JPG image as a reference for spots correlation analysis

dispose the GUI

Correlation

Dataset

Spot List

Selected feature

Load features

Pearson, Kendall, Spearman

Show the correlation

Correlation Coefficiency

Show spot ID

Show number

Spots correlation analysis

select the group to look at

select the spot to look at

upload the feature list from feature selection

upload the feature list from an saved R workspace

type of correlation coefficient to be calculated: "pearson" (default), "kendall", or "spearman"

plot the spots with required correlation

change the coefficiency threshold

plot spots with ID

Show ID for those spots with required correlation

Score Plot

Plot Type

PCA and PLSR score plot

select either PCA or PLSR score plot

Top N component
 Pair-wise
 Component 1 and 2
 Group
 With label
 Scaling
 Plot

Classification

Methods
 Scaling
Arguments
 Method
 "moment"
 "mle"
 "mve"
 "t"
 nComp
 N-fold CV
 nboot
 Selected feature
 Load features
 leave-one-out cv
 N-fold cv
 Bootstrap
 Run classification
 Save
 Legened
 ROC curve
 Prediction result

Feature Selection

Method
 Scaling
Arguments
 Method
 Ncomp
 Top
 Ntree
 Mtry
 Mfinal
 Run feature selection
 Select featuers
 Save features

Power

Single Spots
 Gel
 Significant level
 Power
 Sample size per group
 Spot Number

plot score plot with top N components
 plot selected 2 components
 two components in the pairwise plot
 set the color for the two groups
 plot the sample ID
 scale the data before plotting
 plot the score plot

Classification

select the method for the classification
 scale the data before classification

 way for estimate the covariance matrix.
 standard estimators of the mean and variance
 MLEs,
 to use cov.mve
 robust estimates based on a t distribution
 number of component for fitting PCR or PLSR
 number of fold in the cross validation
 number of bootstrap in the classification
 upload the feature list from feature selection
 upload the feature list from an saved R workspace
 classification with leave-one-out cross validation
 classification with n-fold cross validation
 classification with bootstrap
 press button to do the classification
 save the prediction results into an R workspace
 where the legend will be put
 generate ROC plot
 store the classification results in the selected items

Select important features
 select feature selection method
 scale the data before feature selection

same as Method in Classification
 same as ncomp in Classification
 select the top n variables from the feature selection
 number of trees to grow in randomForest
 Number of variables randomly sampled as candidates at each split. Default sqrt(number
 the number of iterations for which boosting is run or the number of trees to use
 press to start feature selection
 store the selected features in the selected items
 save the features into an R workspace

Power analysis

univariate power analysis
 multivariate power analysis for experiment design
 set the significant level
 set the power level to be achieved
 sample size for achieving certain significant level and power in each group
 set the spots to calculated

Calculate calculate the one being left blank (either power, sample size or significant level)

Note

digeR is built upon gWidgets package. Make sure gWidgets package is properly installed.

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prostate

Prostate cancer serum 2D DIGE data

Description

The 2D DIGE experiment was carried out on 32 serum samples from patients (18 prostate cancer (Gleason 5) and 14 benign prostatic hyperplasia (BPH)). 300 spots were selected and logarithms form was taken. The spots coordinates are included as first two columns for the spots correlation study. It followed by spots expression data.

Usage

```
data(prostate)
```

Format

x x coordinate

y y coordinate

BPH_N BPH patient no. N

G5_N Gleason 5 patient no.N

Details

The prostate data is included in prostate.txt which can be uploaded into digeR.

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