Package 'digeR'

August 5, 2009

Type Package

Title GUI tool for analyzing 2D DIGE data

Version 1.1

Date 2009-07-27

Author Yue Fan, Thomas Brendan Murphy, R. William G. Watson

Maintainer Yue Fan <yue.fan@ucd.ie>

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

R topics documented:

---

digeR-package   *digeR Graphical User Interface*

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

1

Details

Package:	digeR
Type:	Package
Version:	1.1
Date:	2009-07-26
License:	GPL (>= 2)
LazyLoad:	yes

Author(s)

Yue Fan ⟨yue.fan@ucd.ie⟩,Thomas Brendan Murphy, R. William G. Watson

Maintainer: Yue Fan ⟨yue.fan@ucd.ie⟩

---

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	Read in data and image, quit
Open	upload the txt file
Upload_gel_image	upload the JPG image as a reference for spots correlation analysis
Quit	dispose the GUI
────────────	
Correlation	Spots correlation analysis
Dataset	select the group to look at
Spot List	select the spot to look at
Selected feature	upload the feature list from feature selection
Load features	upload the feature list from an saved R workspace
Pearson, Kendall, Spearman	type of correlation coefficient to be calculated: "pearson" (default), "kendall", or "spearn
Show the correlation	plot the spots with required correlation
Correlation Coefficiency	change the coefficiency threshold
Show spot ID	plot spots with ID
Show number	Show ID for those spots with required correlation
────────────	
Score Plot	PCA and PLSR score plot
Plot Type	select either PCA or PLSR score plot

Top N component	plot score plot with top N components
Pair-wise	plot selected 2 components
Component 1 and 2	two components in the pairwise plot
Group	set the color for the two groups
With label	plot the sample ID
Scaling	scale the data before plotting
Plot	plot the score plot

Classification	Classification
Methods	select the method for the classification
Scaling	scale the data before classification
Arguments	
Method	way for estimate the covariance matrix.
"moment"	standard estimators of the mean and variance
"mle"	MLEs,
"mve"	to use cov.mve
"t"	robust estimates based on a t distribution
nComp	number of component for fitting PCR or PLSR
N-fold CV	number of fold in the cross validation
nboot	number of bootstrap in the classification
Selected feature	upload the feature list from feature selection
Load features	upload the feature list from an saved R workspace
leave-one-out cv	classification with leave-one-out cross validation
N-fold cv	classification with n-fold cross validation
Bootstrap	classification with bootstrap
Run classification	press button to do the classification
Save	save the prediction results into an R workspace
Legened	where the legend will be put
ROC curve	generate ROC plot
Prediction result	store the classification results in the selected items

Feature Selection	Select important features
Method	select feature selection method
Scaling	scale the data before feature selection
Arguments	
Method	same as Method in Classification
Ncomp	same as ncomp in Classification
Top	select the top n variables from the feature selection
Ntree	number of trees to grow in randomForest
Mtry	Number of variables randomly sampled as candidates at each split. Default sqrt(number
Mfinal	the number of iterations for which boosting is run or the number of trees to use
Run feature selection	press to start feature selection
Select featuers	store the selected features in the selected items
Save features	save the features into an R workspace

Power	Power analysis
Single Spots	univariate power analysis
Gel	multivariate power analysis for experiment design
Significant level	set the significant level
Power	set the power level to be achieved
Sample size per group	sample size for achieving certain significant level and power in each group
Spot Number	set the spots to calculated

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

The details can be found in digeR manual

Note

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

Author(s)

Yue Fan ⟨yue.fan@ucd.ie⟩,Thomas Brendan Murphy, R. William G. Watson

---

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 logrithms 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.

Index