

# Package ‘digeR’

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**Type** Package

**Title** GUI tool for analyzing 2D DIGE data

**Version** 1.0

**Date** 2009-06-16

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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: 1.0  
 Date: 2009-06-16  
 License: GPL ( $\geq 2$ )  
 LazyLoad: yes

**Author(s)**

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 digeR

*digeR GUI*


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**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:**

<b>File</b>	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
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<b>Correlation</b>	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
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
<hr/>	
<b>Score Plot</b>	PCA and PLSR score plot
Plot Type	select either PCA or PLSR score plot
Top N component	plot score plot with top N components

Pairwise	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
<hr/>	
<b>Classification</b>	Classification
Methods	select the method for the classification
Scaling	scale the data before classification
<i>Arguments</i>	
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
<hr/>	
<b>Feature Selection</b>	Select important features
Method	select feature selection method
Scaling	scale the data before feature selection
<i>Arguments</i>	
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
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 featurers	store the selected features in the selected items
Save features	save the features into an R workspace
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<b>Power</b>	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)

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prostate

*Prostate cancer serum 2D DIGE data*

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### 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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