

Package ‘ER’

September 11, 2020

Encoding UTF-8

Type Package

Title Effect + Residual Modelling

Version 1.0.2

Date 2020-09-10

Description Multivariate modeling of data after deflation of interfering effects (EF Mosleth et al. (2020) <doi:10.1016/B978-0-12-409547-2.14882-6>). The effects can be estimates from designed experiments, non-overlapping clusters or continuous effects.

Depends R (>= 3.0)

Imports ggplot2, scales, gridExtra, glmnet, pls, plsVarSel, methods

License GPL

LazyData TRUE

RoxygenNote 7.1.1

NeedsCompilation no

Author Kristian Hovde Liland [aut, cre],
Ellen Færgestad Mosleth [ctb]

Maintainer Kristian Hovde Liland <kristian.liland@nmbu.no>

Repository CRAN

Date/Publication 2020-09-11 08:10:17 UTC

R topics documented:

confints	2
Diabetes	3
elastic	4
ER	5
Lactobacillus	6
pls	7
Index	8

 confints

Confidence Intervals of Effect Differences

Description

Confidence Intervals of Effect Differences

Usage

```
confints(X1, X2, confidence = 0.95, df.used = 0)
```

```
## S3 method for class 'confints'
plot(
  x,
  y,
  xlab = "",
  ylab = "normalised log2",
  sorted = TRUE,
  nonZero = FALSE,
  xlim = NULL,
  ylim = NULL,
  text.pt = 16,
  ...
)
```

Arguments

X1	data.frame containing first effect.
X2	data.frame containing second effect.
confidence	Level of confidence, default = 0.95.
df.used	Optional argument indicating how many degrees of freedom have been consumed during deflation. Default = 0.
x	Object of class confint.
y	Not used.
xlab	X label (character)
ylab	Y label (character)
sorted	Logical indicating if intervals should be sorted according to their mean values.
nonZero	Logical indicating if intervals are required not to include zero.
xlim	Limits of the horizontal scale.
ylim	Limits of the vertical scale.
text.pt	Size scaling of text in the plot (default = 16).
...	Further arguments to qplot.

Value

An object of class `confints`, which holds the information needed to perform statistics or plot the confidence intervals is returned from `confints`. The plotting routine returns a `ggplot` structure for plotting.

Diabetes

Diabetes data

Description

A data frame with a design and transcriptomic data.

Usage

```
data(Diabetes)
```

Details

Clinical study on humans was performed as a 2-way factorial design with two factors both on two levels: bariatric surgery on two levels (before and after the bariatric surgery) and type 2 diabetes (T2D) on two levels (with and without T2D). There were 8 patients without T2D and 7 with T2D. It was discovered that the patients with T2D would be separated in two groups: 3 patients in the group called T2D1 and 4 patients in the group called T2D2. The experiment can therefore also be analysed as a 2-way factorial design where the disease factor is on three levels. All patients were obese before bariatric surgery (BMI >45). Transcriptome in the subcutaneous adipose tissue was obtained before and one year after bariatric surgery.

Author(s)

Ellen Færgestad Mosleth

References

Dankel et al. 2010. Switch from Stress Response to Homeobox Transcription Factors in Adipose Tissue After Profound Fat Loss. *Plos One* 5.

Examples

```
data(Diabetes)
str(Diabetes)
```

elastic

Elastic-net modeling of ER objects.

Description

Elastic-net modeling of ER objects.

Usage

```
elastic(er, ...)  
  
## S3 method for class 'ER'  
elastic(  
  er,  
  effect,  
  alpha = 0.5,  
  newdata = NULL,  
  validation,  
  segments = NULL,  
  measure = measure,  
  family = family,  
  ...  
)
```

Arguments

er	Object of class ER.
...	Additional arguments for <code>pls::cvsegments</code> .
effect	The effect to be used as response.
alpha	The elasticnet mixing parameter.
newdata	Optional new data matrix for prediction.
validation	Optional validation parameters.
segments	number of segments or list of segments (optional)
measure	Type of performance summary, default = 'class' (see glmnet)
family	Type of model response, default = 'multinomial'.

Description

Effect + Residual Modelling

Usage

```
ER(formula, data)

## S3 method for class 'ER'
plot(
  x,
  y = 1,
  what = "raw",
  col = NULL,
  pch = NULL,
  model.line = !(what %in% c("fits", "residuals")),
  ylab = "",
  xlab = "",
  main = NULL,
  ...
)

tableER(object, variable)
```

Arguments

formula	a model formula specifying features and effects.
data	a data.frame containing response variables (features) and design factors or other groupings/continuous variables.
x	Object of class ER.
y	Response name or number.
what	What part of ER to plot; raw data (default), fits, residuals or a named model effect (can be combined with 'mean', see Examples).
col	Color of points, defaults to grouping. Usually set to a factor name.
pch	Plot character of points, defaults to 1. Usually set to a factor name.
model.line	Include line indicating estimates, default = TRUE. Can be an effect name.
ylab	Y label (character)
xlab	X label (character)
main	Main title, defaults to y with description from what.
...	Additional arguments to plot
object	ER object.
variable	Numeric for selecting a variable for extraction.

Value

An object of class ER containing effects, ER values, fitted values, residuals, features, coefficients, dummy design, symbolic design, dimensions, highest level interaction and feature names.

References

E.F. Mosleth et al. (2020) <doi:10.1016/B978-0-12-409547-2.14882-6>. Comprehensive Chemometrics, 2nd edition; Brown, S., Tauler, R., & Walczak, B. (Eds.). Chapter 4.22. Analysis of Megavariate Data in Functional Omics. Elsevier.

Lactobacillus

Lactobacillus data

Description

A data.frame with a design and proteomic data, transcriptomic data and phenotypic data.

Usage

```
data(Lactobacillus)
```

Details

Experiment on *Lactobacillus sakei* was performed as a 2-way factorial design with two factors both on two levels: strain (*L. sakei* strains LS25 and 23K) (factor A) and growth condition (high and low glucose availability) (factor B) both on two levels, and their interaction term (factor AB). There were three biological replicates within each group. Transcriptome, proteome and end product profile (lactate, formate, acetate and ethanol) were observed.

Author(s)

Ellen Færgestad Mosleth

References

McLeod et al. 2017. Effects of glucose availability in *Lactobacillus sakei*; metabolic change and regulation of the proteome and transcriptome. Plos One 12, e0187542.

Examples

```
data(Lactobacillus)
str(Lactobacillus)
```

Description

Partial Least Squares modelling of ER objects.

Usage

```
pls(er, ...)

## S3 method for class 'ER'
pls(
  er,
  effect,
  ncomp,
  newdata = NULL,
  er2,
  validation,
  jackknife = NULL,
  shave = NULL,
  df.used = NULL,
  ...
)
```

Arguments

<code>er</code>	Object of class ER.
<code>...</code>	Additional arguments for <code>pls</code> .
<code>effect</code>	The effect to be used as response.
<code>ncomp</code>	Number of PLS components.
<code>newdata</code>	Optional new data matrix for prediction.
<code>er2</code>	Second object of class ER for comparison.
<code>validation</code>	Optional validation parameters for <code>pls</code> .
<code>jackknife</code>	Optional argument specifying if jackknifing should be applied.
<code>shave</code>	Optional argument indicating if variable shaving should be used. <code>shave</code> should be a list with two elements: the PLS filter method and the proportion to remove. <code>shave = TRUE</code> uses defaults: <code>list("sMC", 0.2)</code> .
<code>df.used</code>	Optional argument indicating how many degrees of freedom have been consumed during deflation. Default value from input object.

Index

`confints`, [2](#)

Diabetes, [3](#)

elastic, [4](#)

ER, [5](#)

`glmnet`, [4](#)

Lactobacillus, [6](#)

`plot.confints` (`confints`), [2](#)

`plot.ER` (ER), [5](#)

`pls`, [7](#)

`tableER` (ER), [5](#)